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2, 2004, 14:35:42 ; Search time 44.9 Seconds (without alignments) 950.215 Million cell updates/sec
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1 MKLIKVAAFAAIVVSGSALA......VTRVVTHEMAHANNATANQY
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15.1.6
Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                1586107 segs, 282547505 residues
GenCore version
Copyright (c) 1993 - 2004
                                                                        - protein search, using sw model
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries A Geneseq 29Jan04:\*

1: geneseqp1980s:\*
2: geneseqp2000s:\*
4: geneseqp2001s:\*
5: geneseqp2001s:\*
6: geneseqp2003s:\*
7: geneseqp2003bs:\*
8: geneseqp2003bs:\* seq length: 0 seq length: 200000000 Minimum DB s Maximum DB s Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## Aar74625 Agra. 15.0 Aab56341 Salmonell Aab36352 Agra.: PT3 Aab36352 Agra.: PT3 Aab36350 Agra.: PT3 Aab36354 Agra.: PT3 Aab36354 Agra.: PT3 Aab36355 Agra.: PT3 Aab36358 Agra.: PT3 Aab36358 Agra.: PT3 Aab36358 Agra.: PT3 Aab36348 Agra.: PT3 Aab36348 Agra.: PT3 Aab36343 Agra.: PT3 Aab36348 Agra.: PT3 Aab36348 Agra.: PT3 Aab36346 AgfA::PT3 Aab36347 AgfA::PT3 Description AAR74625 AAB36341 AAW23570 AAB36352 AAB36353 AAB36349 AAB36350 AAB36354 AAB36354 AAB36355 AAB36348 AAR62761 AAW23569 AAB36346 AAB36347 Length Query 100.0 66696 Score Result

ala	E. coli c Salmonell	Salmonell	Salmonell Salmonell	ophi	Drosophil		E. coli c	Protein e	Candida a	Plectreur	Escherich	Human tru	Truncated	Human tru	Truncated	Human tan
Aab36339 Aab36320	Abr82644 Aab36340	Aab36324	Aab36319 Aab36342	Abb65764		Abr82645	Abr82647	Abu36649	Abp74039	Aae36890	Aab36331	Aay44403	Aau79538	Aay44404	Aau79539	Aay44402
AAB36339 AAB36320	ABR82644 AAB36340	8	AAB36319 AAB36342	ABB65764	ABB62708	ABR82645	ABR82647	ABU36649	ABP74039	AAE36890	AAB36331	AAY44403	AAU79538	AAY44404	AAU79539	AAY44402
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115	113	109	100	98.5	98.5	96	95	94.5	94.5	93	92	92	92	92	92	92
26 27	28	30	31 32	33	34	35	36	37	38	33	40	43	4.2	43		<b>4</b> .

## ALIGNMENTS

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal. Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; AgfA::PT3#1 amino acid sequence SEQ ID NO:12. Kay WW; Disclosure; Page 135; 139pp; English. vaccine; immune response; immunogen Collison SK, AAB36346 standard; protein; 151 AA 05-APR-2000; 2000WO-CA000356. 99US-0127888P. (first entry) Salmonella enteritidis (UYVI-) UNIV VICTORIA Doran JL, WPI; 2000-672631/65. N-PSDB; AAC64622 Escherichia coli WO200060102-A2 05-APR-1999; 26-FEB-2001 12-0CT-2000 White AP, Synthetic. AAB36346; AAB36346 

The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEP17/TAF) nucleation depended assembly system of strains of Salmonella. Bscherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA. CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombinantion of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of back into the chromosome of the pack into the chromosome of the back into the chromosome of the back into the chromosome of the pack into

Escherich E. coli C Fibronect

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ABR82651 AAR52664 AAB36343

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FNB curli Salmonell Salmonell

Aar52663 1 Aab36316 8 Aab36318

AAB36316 AAB36318 AAB36321

AAB36338 AAB36325

AAB36326

Salmonell Salmonell Salmonell

Aab36321 Aab36326 Aab36338 Aab36338

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compy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or segment or assumental a. Coli or brotein containing a replacement segment or assumental and introducing the sequence or sequence grown on a Salmonella, B. coli or brotein which the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein passesses both the immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbride are usually strong inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AgfA::PT3#2 amino acid sequence SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB36347 standard; protein; 151 AA.
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                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 151; Conservative
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Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYVI-) UNIV VICTORIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000-672631/65.
                                                                                                                                                                                                                                                 Sequence 151 AA;
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Best Local Similarity
Matches 141; Conserv
                                                                                                                                                                      Sequence 151 AA;
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26-JUN-1995
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                                                                                                                                                                                                         Query Match
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                                                                        1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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                                                                                               1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella, agfA, chromosomal gene replacement, fimbrin, epitope, vaccine, immune response, immunogen.
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0
 DB 3; Length 151;
                                     Indels
100.0%; Score 779; DB 3; 100.0%; Pred. No. 2e-66; ive 0; Mismatches 0;
                                                                                                                                                                                                                         NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
                                                                                                                                                                                                                                            NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA cequence which encodes a foreign epicope or antigen. Also described are: (1) use of thin aggregative finbriae (SPEPI/TAP) nucleation depended assembly system of strains of Salmonella. Escherichia coli and Entertabacteriaces for the production of fimbriae comprising recombinant GAFA, CSAA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombinant gene into the chromosome of the homologue species; (3) directing recombinant gene into the chromosome of the homologue species, replacing the native comprising separating an amologous species, replacing the native comprising separating an amologous species, replacing the native comprising separating an amologous species of foreign an immune and containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino acid polymer comprising separating an amino acid polymer comprising the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for useful for the expension of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to copies/cell), the hybrid finbrin protein see usually strong immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier finbrial submitt proteins are usually strong immunogensity in large amount. The present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89.3%; Score 696; DB 3; Length 151; ilarity 87.6%; Pred. No. 1.7e-58; Conservative 0; Mismatches 0; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 NNAALVNYDQLVTRVVTHEMAHA------NNATANQY 151
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KING J.

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 136; 139pp; English

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cc (1) use of thin aggregative fimbriae (SEP17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterbacteriaceae for the production of fimbriae comprising recombinant C AgfA, CspA and AgfA-homologue fimbrian subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the composition of a recombinant gene back into the chromosome of the homologus species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA comprising separating an amino acid polymer comprising a recombinant of protein containing a replacement segment or segments of foreign amino cortesion containing a replacement segment or segments of foreign amino cortesion containing a replacement segment or segments of foreign amino cortesion of segments of coli or acid sequence or sequences grown on a Salmonella, E. Coli or confercion animal in conjunction with a carrier or diluent. (I) is coliver into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for coli expension of recombinant AgfA protein which is useful for the expression of recombinant in Ainbrial presentation system the hererologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid finbrin protein sequence is given in manogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogensive to purify in large amount. The present sequence is given in consumption of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 695; DB 3; Length 151;
Pred. No. 2.2e-58;
4; Mismatches 11; Indels
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90.1%;
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(first entry)
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Best Local Similarity
Matches 136; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 151 AA;
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29-SEP-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                            09
                                                                                                                                                                                      The Salmonella AgfA protein and DNA are used in vaccine and genetic immunization compositions, respectively, to elicit an immune response to Salmonella in animals (God producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are:
                                                                                                  Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                          1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                    MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGFDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen.
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                                                                                                                                                                                                                                                                                                                    Score 695; DB 2; Length 151;
Pred. No. 2.2e-58;
                                                                                                                                                                                                                                                                                                                                                      Indels
             Doran JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151
                                                                                                                                                                                                                                                                                                                                       Pred. No. 2.2e
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NNAALVNYDQLVTRVVTHEMAHANNATANQY
             Clouthier SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Page 135; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collison SK,
                                                                                                                                                        7B; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB36341 standard; protein; 151
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                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 90.1%;
Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella enteritidis.
             Collinson SK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-672631/65.
N-PSDB; AAC64617.
                                                 WPI; 1994-358275/44
                                                                    N-PSDB; AAQ87467
                                                                                                                                                                                                                                                                                   Sequence 151 AA;
                                                                                                                                                          Disclosure, Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200060102-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB36341;
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               Kay WW,
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Page 138; 139pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB36353 standard; protein; 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                  Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sscherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200060102-A2.
                     Disclosure;
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                                                                                              The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 2765-3b. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                   SDARKSETTITQSGYGNGADVGQGADNSTIELLYQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                           1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                               MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                      Gaps
                                         Isolated Salmonella gene agfA - used for diagnosis of Salmonella or enteropathogenic bacteria of the Enterobacteria family.
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                                                                                                                                                                                                                                               Length 151;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                               Score 690; DB 2;
Pred. No. 6.5e-58;
4; Mismatches 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AgfA::PT3#7 amino acid sequence SEQ ID NO:24.
                                                                                                                                                                                                                                                                                                                                                                                  151
                                                                                                                                                                                                                                                                                                                                                                                                  121 NNPALVNQTASDSSVAVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                  NNAALVNYDOLVTRVVTHEMAHANNATANOY
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                                                                           Example 2; Fig 7; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB36352 standard; protein; 151
                                                                                                                                                                                                                                               88.6%;
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                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella enteritidis.
Escherichia coli.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Doran JL,
         WPI; 1997-309886/28.
N-PSDB; AAT74142.
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N-PSDB; AAC64628.
                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                         Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200060102-A2.
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA concentration by the concentration of the production of sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbrine (SFET)/TAF) nucleation depended assembly system of strains of Salmonella. Escherichia coli and Entertorial acade for the production of fimbriae comprising recombinant CC directing recombination of a recombinant gene composing species; (3) directing recombinant gene into the chromosome of the homologous species; replacing the native comprising separating an amino acid polymer comprising a recombinant pack into the chromosome of the homologous species; replacing the native comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. Coli or Enterobacteriaceae host cell, from the host cell and introducing the contenting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to coli or system the heterologous antigens are presented in high numbers (up to confort, the carrier finbrial submit protein are usually strong immunogens, which may be important for directing an immune response conformation and adhesion properties relevant for an efficient live vaccine, the carrier finbrial submit, proteins are usually strong immunogens, which may be important for directing an immune response against the inserted equitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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protein useful for eliciting immune response in animal
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84.1%; Score 655; DB 3; L

Best Local Similarity 79.8%; Pred. No. 1.4e-54;

Matches 134; Conservative 0; Mismatches 0;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epicope or antigen. Also described are: (1) use of thin aggregative finbries (SEPIT/TAP) nucleation depended a sembly system of strains of Salmonella. Escharichia coli and Enterobacteriaceae for the production of fimbries comprising recombinant of Enterobacteriaceae for the production of fimbries comprising recombinant of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a replacement sequent or sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the containing a replacement sequencion with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogens, which may be important for directing an immune response immunogens, which may be important for directing an immune response in expression of recombinate are easy and inextend epicope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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                                                                                                                                                                            Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYOYGSANAALYDO 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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Pred. No. 1.2e-50;
6; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AgfA::PT3#4 amino acid sequence SEQ ID NO:18.
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                                                                             Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 138; 139pp; English.
                                                                             Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB36349 standard; protein; 151 AA.
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99US-0127888P.
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                                    (UYVI-) UNIV VICTORIA.
                                                                             Doran JL,
                                                                                                                    2000-672631/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 151 AA;
05-APR-1999;
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                                                                             White AP,
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative finbriae (SEP1/7RE) nucleation depended assembly system of strains of Salmonella, Escherichia coli and aggregative finbriae (SEP1/7RE) nucleation depended assembly system of strains of Salmonella, Escherichia coli and combinant of intecting recombination of a recombinant gene correcting recombination of a recombinant gene incoming species; (3) directing recombinant gene into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a recombinant and an interpet comprising separating an amino acid polymer comprising a replacement segment or segments of foreign anino acid sequence or sequences grown on a Salmonella, E coli or acid sequence or sequences grown on a Salmonella, E coli or acid sequence or sequences grown on a Salmonella, E coli or acid sequence or sequences grown on a Salmonella, E coli or acid sequence or sequences grown on a Salmonella, E coli or acid sequence or sequences of recombinant AgfA protein which is useful for useful for the expension of recombinant AgfA protein which is useful for useful for the carrier fimbrial submit proteins are usually strong immunogens, which may be important for directing an immune response in an animal submit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKLLKVAAPAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 613; DB 3; Length 151;
Pred. No. 1.5e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNAALVNYDOLVTRVVTHEMAHANNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WW.
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                                                                                                                                                                                                                                                                                                                                            Kay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 136; 139pp; English.
                                                                                                                                                                                                                                                                                                                                          Collison SK,
                                                                                                                                                                                                        05-APR-2000; 2000WO-CA000356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78.7%;
80.8%;
                                                                                                                                                                                                                                                   99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 122; Conservative
                        Salmonella enteritidis.
                                                                                                                                                                                                                                                                                              (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                          Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-672631/65
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                                             Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAC64625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 151 AA;
                                                                                                              WO200060102-A2
                                                                                                                                                                                                                                                05-APR-1999;
                                                                                                                                                                                                                                                                                                                                            White AP,
                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
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The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA segment which encodes a foreign epitope or antigen. Also described are:

(1) use of thin aggregative fimbriae (SEP1/TAR) nucleation depended assembly system of strains of Salmonella. Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant of a recombinant gene into the chromosome of the homologue species, respectively; (2) directing recombination of a recombinant gene into the chromosome of the copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or comprising acid sequence or sequences grown on a Salmonella, E. coli or coll sequence or sequences grown on a Salmonella, E. coli or coll to the animal in conjunction with a carrier or dilutent. (I) is useful for the expression of recombinant AgfA protein which is useful for the heterologous antigens are presented in high numbers (up to Sou, 8000 copies/cell), the hybrid fimbrin protein possesses both the containing the properties relevant for an efficient live containing the containing the properties relevant for an efficient live containing the containing the properties relevant for an efficient live containing the containing the properties relevant for an efficient live containing the containing the properties relevant for an efficient live containing the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                    Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.4%; Score 611; DB 3; Length 151; 80.8%; Pred. No. 2.3e-50; ive 7; Mismatches 22; Indels
                                                                                                                                                             AgfA::PT3#5 amino acid sequence SEQ ID NO:20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Σ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 137; 139pp; English.
                                                                                                                                                                                                                                                vaccine; immune response; immunogen.
AAB36350 standard; protein; 151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-APR-2000; 2000WO-CA000356.
                                                                                                          26-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                    Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                White AP, Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-672631/65.
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Best Local Similarity
Matches 122; Conserv
                                                                                                                                                                                                                                                                                                                        Escherichia coli.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                           WO200060102-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-OCT-2000
                                                      AAB36350;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA segment with encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative finbriae (SBF1/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of finbriae comprising recombinant of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the homologous species, splacing in an animal. Comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the coll seful for the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to compicine, the expression properties relevant for an efficient live vaccine, the expression properties relevant for an efficient live vaccine, the expression properties relevant for an efficient live vaccine, the expression properties relevant for an emalally strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present easy and inexpensive to purify in large amount. The present sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                        SDARKYDOLVIRVVIHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella, agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                      AgfA::PT3#9 amino acid sequence SEQ ID NO:28.
                                                                                                                        ||||||||
| NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                           NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Page 138; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccine; immune response; immunogen.
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                                                                                                                                                                                                                                                     AAB36354 standard; protein; 151
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                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYVI-) UNIV VICTORIA.
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                                                                                                                                                                                                                                                                                                  AAB36354;
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                                                                                                                                      121
                                                                                                                                                                                                         RESULT 10
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Conservative

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05-APR-1999;
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                                                                                                                                                                     Query Match
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AAB36355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                       SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                              09
                                                                                                       MKLLKVAAFAAIVVSGSALAGVVPQWGGGONHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                        1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                  Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                   ..
                                             Length 151
                                          , DB 3; Length 15
8.5e-50;
ches 25; Indels
                                                                                                                                                                                                                                                                                                                             AgfA::PT3#6 amino acid sequence SEQ ID NO:22.
the exemplification of the present invention
                                                                                                                                                                                151
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                                            Score 605; DB
Pred. No. 8.5e-
5; Mismatches
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                                                                                                                                                                                              NNAALVNYDQLVTRVVTHEMAHANNATANQY
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                                                                                                                                                                                                                                                                                                                                                              vaccine; immune response; immunogen.
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                                                                                                                                                                                                                                                          AAB36351 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-APR-2000; 2000WO-CA000356.
                                            77.7%;
80.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0127888P
                                                                                                                                                                                                                                                                                                       (first entry)
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                   Salmonella enteritidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-672631/65.
                                                        Similarity
                      À.
                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
Synthetic.
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                      Sequence 151
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                                          Query Match
Best Local Simil
Matches 121; (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDARKSETTITOSGYGNGADVGOGADNYDQLVTRVVTHEMAHADOWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                              무
Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) useful for the expression of recombinant AgfA protein which is useful eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copieso/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 604; DB 3;
Pred. No. 1.1e-49;
6; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AgfA::PT3#10 amino acid sequence SEQ ID NO:30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||||||||
| NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB36355 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-APR-2000; 2000WO-CA000356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 80.8
18s 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enteritidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-672631/65.
N-PSDB; AAC64631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella enteri
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200060102-A2.
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N-PSDB; AAC64624.
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cc assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and cc assembly system of strains of Salmonella, Escherichia coli and defended coli and strains of strains of sepactively, (2) directing recombination of a recombination of comprising separating an aimon acid polymer comprising a replacement sequent or sequence of sequences or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or consequity of an animal in conjunction with a carrier or diluter. (1) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to concorne, the carrier fimbrial submuit protein are usually strong immunogens, which may be important for directing an immune response or inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDARKSETTITOSGYGNGADVGQGADNSTIELTONGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                  Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                             23; Indels
                                                                                                                                                                                                                                                                                                                                                                               Query Match
Pest Local Similarity 80.8%; Pred. No. 1.3e-49;
Matches 122; Conservative 6; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AgfA::PT3#3 amino acid sequence SEQ ID NO:16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine; immune response; immunogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-APR-2000; 2000WO-CA000356.
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                                                                                                                                                                                                                                                                                                                                                      Sequence 151 AA;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA cequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbrise (SETIA/TAP) nucleation depended assembly system of strains of Salmonella, Escherichia coli and contained by a comprising recombination of the comprising recombinant of directing recombination of a recombinant gene into the chromosome of the composition of a recombinant gene copy of that gene; and (4) eliciting an immune response in an animal, comprising separating a manimo acid polymer comprising recombinant AgfA protein containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments or dilutent. (I) is useful for the expression of recombinant AgfA protein which is useful containing an immune response in an animal. In a fimbrial presentation system the hererologous antigens are presented in high numbers (up to system the hererologous antigens are presented in high numbers (up to concise, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an easy and carrier the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.5%; Score 580; DB 3;
80.1%; Pred. No. 2.1e-47;
iive 7; Mismatches 23
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                                                                                                                                                                      Disclosure, Page 136; 139pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Matches 121; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 151 AA;
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26-JUN-1995
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Gaps

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The present sequence represents an agfA fragment encoded by an agfA gene fragment derived from Salmonella enteritidis 27655-3b ThiphoA mutant strain. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide proteins or primers which can specifically hybridise to nucleic acid molecules from premers which has been seen as a serial strains that are pathogenic to warmblooded animals relative to uncleic acid molecules from other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                           1 VVPOWGGGGNHNGGGNSSGPDSTLSIYOYGSANAALALOSDARKSETTITOSGYGNGADV 60
                                                                                                                                                                                                                                                                                                                              VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
                                                                                                                                                                                                                                                        71.9%; Score 560; DB 2; Length 120; 100.0%; Pred. No. 1.2e-45; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  61 GOGADNSTIELTONGFRNNATIDOWNAKNSDITVGQYGGNNAALVN 106
                                                                                                                                                                                                                                                                                                                                                                                                82 GOGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2, 2004, 14:48:24
Example 2; Fig 7; 85pp; English.
                                                                                                                                                                                                                                                                         al Similarity 100.
106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    completed: August
e : 45.9 secs
                                                                                                                                                                                                                         Sequence 120 AA;
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Best Local
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Job time
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                                                                                                                                                                                                                                                                                                        The sequence represents the Salmonella enteritis 27655-3b InphoA mutant strain AgfA protein. The encoding DNA and isolated AgfA protein are used in genetic immunization and vaccine compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                         using attenuated Salmonella g. fimbrial type proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated Salmonella gene agfA - used for diagnosis of Salmonella or enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella enteritidis 27655-3b InphoA mutant agfA fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVN 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.9%; Score 560; DB 2; Length 120; 100.0%; Pred. No. 1.2e-45; Ative 0; Mismatches 0; Indels
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                                                                                                                                     Doran JL;
                                                                                                                                                                                                                      Eliciting an immune response to Salmonella - us strains, vector constructs, or compsns. contg.
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                                                                                (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP
                                                                                                                                     Clouthier SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW23569 standard; protein; 120 AA
                                                                                                                                                                                                                                                                           Disclosure; Fig 7A; 95pp; English
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                94WO-IB000207
                                                 93US-00054452.
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(first entry)
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nes 106; Conservative
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                                                                                                                                     Collinson SK,
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                                                                                                                                                                    WPI; 1994-358275/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-309886/28.
N-PSDB; AAT74141.
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                                                                                                                                                                                     N-PSDB; AAQ73066
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 120 AA;
                                                                                                  KING/) KING J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-APR-1994;
                26-APR-1994;
                                               26-APR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5635617-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                   Kay WW,
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79 10.1 941 4 US-09-336-447A-9 Sequence 78:5 10.1 2123 3 US-08-96-68-A-10 Sequence 78 10.0 906 1 US-08-254-573-2 Sequence 78 10.0 906 1 US-08-687-379-2 Sequence	78 10.0 906 1 US-08-687-379-4 Sequence 78 10.0 906 4 US-08-172-332-1 Sequence 70 10.0 906 4 US-08-172-332-1 Sequence 70 10.0 906 4 US-08-176-352-1 Sequence 70 10.0 906 4 US-08-176-176-176-176-176-176-176-176-176-176	77.5 9.9 702 4 US-09-252-291A-2219 Sequence 77.5 9.9 714 4 US-09-841-786-4 Sequence 77.5 9.9 878 4 US-09-841-236-3401 Sequence 77.5 9.9 878 4 US-09-540-236-3401 Sequence 77.5 9.0 9.0 9.0 9.0 9.0 9.0 9.0 9.0 9.0 9.0	39 77 9.9 528 4 US-09-025-7695-280 Sequence 20.7 App. 40 77 9.9 1690 4 US-09-595-684B-39 Sequence 39, Appl. 41 77 9.9 215 4 US-09-595-684B-39 Sequence 5434, Appl. 41 77 9.9 215 4 US-09-595-681A-5434 Sequence 5434, Appl. 41 77 9.9 215 4 US-09-595-681A-5434 Sequence 5434, Appl. 41 US-09-595-781A-5434 Sequence 5434 Sequence	76.5 9.8 139 5 09-00-00-22 Sequence 76.5 9.8 605 4 US-09-382-276-2 Sequence 76.5 9.8 605 4 US-09-489-38A-13002 Sequence 76.5 6 10-00-00-00-00-00-00-00-00-00-00-00-00-0	/5.5 V. 624 4 US-0V-535-44/A-/	ALIGNMENTS	RESULT 1	Sequence 59, Application US/08233788A ; Patent No. 5635617 ; GENERAL INFORMATION:	APPLICANT: Doran, James L. APPLICANT: Kay, William W. APPLICANT: Collinson, Karen S. APPLICANT: Cluthier, Sharon C. TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION TITLE OF INVENTION: OF SALWONELLA NUMBER OF SEQUENCES: 61 CORRESPONDENCE ADDRESS: ADDRESPONDENCE ADDRESS:	STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle Sattle Santington Fifth Avenue	COUNTRY: U.S.A.  ZIONIRA: 98104-7092	MEDIUM TYPE: Floppy disk COMPUTER: Ploppy disk COMPUTER: Order of the computer	CURRENT APPLICATION DATA:  CURRENT APPLICATION DATA:	; APPLICATION NUMBER: US/08/233,788A ; FILING DATE: 26-APR-1994	CLASSIFICATION: 435 ATTONEY/ASTION:	REGISTRATION UNMERS. 35,570	TELECOMMUNICATION INFORMATION:  TELECOMMUNICATION 1.000 0.00	; ILLEFAUNE: (200) 682-63-1900 ; TELEFAX: (200) 682-631 : TELEX: 3723836 SEEDANBERRY	; INPORMATION FOR SEQ ID NO: 59:	LENGTH: 151 amino acids	DGY: 1 E TYPE: 8A-59	Query Match 88.6%; Score 690; DB 1; Length 151; Best Local Similarity 89.4%; Pred. No. 7.1e-62; Matches 135; Conservative 4; Mismatches 12; Indels 0; Gaps	Qy 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 6
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	OM protein - protein search, using sw model	Run on: August 2, 2004, 14:40:48; Search time 12 Seconds (without alignments) 649.627 Million cell updates/sec	Title: Perfect score: 779 Sequence: 1 MKLLKVAAFAAIVVSGSALAVIRVVTHEMAHANNATANQY 151	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 389414 segs, 51625971 residues	Total number of hits satisfying chosen parameters: 389414	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 100% Maximum Match 100% Listing first 45 summaries	Database: Issued_Patents_AA:*  1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*  2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*  3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*  4: /cgn2_6/ptodata/2/iaa/pcTuS.comB.pep:*  5: /cgn2_6/ptodata/2/iaa/pcTuS.comB.pep:*  6: /cgn2_6/ptodata/2/iaa/pcTuS.comB.pep:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		Result Query No. Score Match Length DB ID Description	690 88.6 151 1 US-08-233-788A-59 Sequence 560 71.9 120 1 US-08-233-788A-57 Sequence	92 11.8 673 3 US-09-196-387-8 Sequence 92 11.8 673 4 US-09-841-835-8 Sequence	92 11.8 949 3 US-09-196-387-10 Sequence 92 11.8 949 4 US-09-841-385-10 Sequence Sequence	92 11.8 1327 4 US-09-841-835-2 Sequence Sequence 5.0 11.8 1327 4 US-09-841-835-2 Sequence 5.0 11.8 1327 4 US-09-841-835-2	9 90 11.8 13.7 4 08-09-34/Z-115A-8 Sequence 0 90 5 11.6 745 4 08-09-336/115C-6 Sequence 0 90 5 11.6 745 4 08-09-336/2-115C-6	1 89.5 11.5 /38 3 US-U8-864-U38A-3 Sequence 2 89 11.4 943 4 US-09-056-556-204 Sequence 3 89 11.4 943 4 US-09-056-556-199 Sequence	4 89 11.4 943 4 US-09-477-135A-131 Sequence	6 87.5 11.2 892 4 US-09-336-447A-5 Sequence 7 85 10.9 956 4 US-09-134-078-63 Sequence	8 82.5 10.6 186 4 US-09-382-276-3 Sequence 9 82.5 10.6 873 4 US-09-336-447A-13 Sequence 0 81.5 10.5 339 4 US-09-252-991A-32096 Sequence	81 10.4 568 4 US-09-543-681A-6966 Se 81 10.4 1739 4 US-09-540-236-3739 Se 81 10.3 234 4 US-08-804-227-3 80 10.3 232 4 US-09-252-991A-30263 Se	5 80 10.3 975 4 US-09-328-352-4764 Sequence 6 80 10.3 3241 4 US-09-841-786-1 Sequence 7 79.5 10.2 361 4 US-09-540-236-2164 Sequence

10.1 941 4 US-09-336-447A-9 10.1 2123 3 US-08-968-685A-10 10.0 906 1 US-08-968-685A-10 10.0 906 1 US-08-968-685A-10 10.0 906 1 US-08-687-379-2 10.0 906 4 US-08-1732-1 9.9 702 4 US-09-25-991A-22119 9.9 702 4 US-09-91-26-386-3 9.9 1690 4 US-09-91-8 9.9 1690 4 US-09-936-25-2 9.8 159 4 US-09-936-25-2 9.8 159 3 US-08-85-253-2 9.8 159 3 US-08-85-253-2 9.8 159 4 US-09-38-276-3 9.8 159 3 US-08-85-253-2 9.8 159 4 US-09-38-276-3 9.8 159 3 US-08-85-253-2 9.8 159 4 US-09-38-255-29-88-3 9.9 160 4 US-09-84-39-3 100 US-08-85-253-2 100 US-08-85-20	DETECTION	
15 10.1 2941 4 15 10.1 2123 3 16 10.0 906 1 178 10.0 906 4 15 10.0 906 4	ALIGNMENTS  COMPOSITIONS FOR  LLA  701 Fifth Avenue  3,788A  3,788A	
) - R KODZRA / B PPAHB OK - NRA HHHHUN P NORON - 1777-1777-1777-1778-1778-1778-1778-17	-59 Application US/08 635617 CORMATION: DOTALL JAMES L. RAY, William W.: COLLINSON, KARE: INVENTION: RETHOLINE SALE SECUENCES: 61 DENCE ADDRESS: 6 WASHINGTON IN SECUENCES: 6 DENCE TON WABER: US/C DATION NUMBER: US/C DATION UMBER: US/C DATION UMBER: US/C DATION UMBER: US/C DATION UNFORMATION: RATION ON US/C SEC ESDANBER STARSS SEC ESDANBER STARSS SEC ESDANBER	HARACIE 151 am mino ac : line. YPE: p
28	RESULT 1 US-08-233-786A- Sequence 53-786A- Sequence 53-786A- Patcht No56 GENERAL INFO APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: CORRESPOND ADDRESSE STATE: CONPUTER R MEDIUM T COMPUTER R MEDIUM T COMPUTER R APPLICAT REPERBUC TELECOMOUN TEL	SEQUENCE CF DENGTH: TYPE: an TOPOLOGY: MOLECULE TY US-08-233-788A-5

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6 VAAFAAI-VVSGSALAGVVPOWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
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; Sequence 8, Application US/09841835
; Patent No. 6506587
; GENERAL INFORMATION:
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack
STATE: New Jersey
COUNTRY: USA
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 1
COUNTRY: USA
TITLE OF TOWN OF USE
T
                                                                                                 A PROTEIN THAT BINDS TO TRF1 AND METHODS OF USE THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUW TYPE: Floopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/09/196,387
FILING APPLICATION:
PRIOR APPLICATION NUMBER: 09/095,225
FILING APPLICATION NUMBER: 09/095,225
FILING APPLICATION NUMBER: DATE: DATE
                                                                                                                                                                                                                                                                               ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       600-1-230 CIP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFRENCE/DOCKET NUMBER: 600-1 TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800 TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 07601
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEII
TITLE OF INVENTION: OF USE TI
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 673 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                       New Jersey
USA
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Best Local Similarity
Matches 35; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-841-835-8
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                                                                                                          SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                        61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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              1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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APPLICANT: Ray, William W.
APPLICANT: Clouthier, Karen S.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
SIREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GGGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVN 106
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COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,788A
FILING DATE: Z6-APR-1994
CLASSIFICATION: 435
ATTOREY/AGENT INFORMATION:
NAME: King, Joshua
REGISCHATION NUMBER: 35,570
REPRENCE/COCKET NUMBER: 35,570
REPRENCE/COCKET NUMBER: 35,570
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION INFORMATION:
TELEFAX: (206) 682-6031
TELEFAX: (206) 682-6031
TELEFAX: 3346 SEBDANBERRY
INFORMATION FOR SEO ID NO: 57:
SEQUENCE CHARACTERISTICS:
TEMMETH: 120 amino acids
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Matches 106; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                         121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                  121 NNPALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 57, Application US/08233788A Patent No. 5635617 GENERAL INFORMATION:
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US-09-196-387-8
; Sequence 8, Application US/09196387
; Parent No. 6277613
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOHN TOPOLOGY: 1:-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 6300 Co
CITY: Seattle
STATE: Washingt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-233-788A-57
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6 VAAFAAI -VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/09841835
; Sequence 10, Application US/09841835
; Patent No. 6506587
; GENERAL INFORMATION:
    APPLICANT: de Lange, Titia
    APPLICANT: de Lange, Titia
    APPLICANT: Smith, Susan
    IITLE OF INVENTION: OF USE THEREOF
    IITLE OF INVENTION: OF USE THEREOF
    IITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
    IITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
    ITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
    ITLE OF INVENTION OF USE THEREOF
    CORRESPONDENCE ADDRESS:
    APPRICATION TOWNER: A Jackson
    CONFUTER: READABLE FORM:
    COMPUTER: IBM PC compatible
    COMPUTER: IBM PC compatible
    COMPUTER: IBM PC compatible
    COMPUTER: BATCHING SYSTEM: PC-DOS/MS-DOS
    CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/841,835
    FILTMA DAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.8%; Score 92; DB 4; Length 949; 30.4%; Pred. No. 0.94;
                                                                                                                                                                                                                                                 Length 949,
                                                                                                                                                                                                                                                                                                 57; Indels
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE:
ATTONEY AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26/742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEFONE: 201-487-5800
TELEFONE: 201-343-1684
TELEF: 133521
INFORMATION FOR ESQ ID NO: 10:
SEQUENCE REARACTERISTICS:
LENGTH: 949 amino acids
                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 30.4%; Pred. No. 0.94;
Matches 35; Conservative 15; Mismatches 5
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TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 949 amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 30.44
Matches 35; Conservative
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                                                                                                                                                                   MOLECULE TYPE: protein US-09-196-387-10
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US-09-841-835-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/09196387

Patent No. 6277613

GENERAL INFORMATION:

APPLICANT: de Lange, Titia

APPLICANT: Smith, Susan

TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS

TITLE OF INVENTION: OF USE THEREOF

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.8%; Score 92; DB 4; Length 673; 30.4%; Pred. No. 0.6; tive 15; Mismatches 57; Indels
          SOFTWARE: PC-DUS/MS-DUS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
FILING DATE:
CLASSIFICATION NUMBER: US/09/841,835
FILING DATE:
APPLICATION NUMBER: 09/196,387
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIPI
TELEPHONE: 201-487-5800
TELEPHONE: 201-43-1684
INPORMATION FOR ESQ ID NO: 8:
SEQUENCE CHRARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: ATTORNEY/AGENT
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COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REBERBENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
     OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 30.49
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear;
MOLECULE TYPE: protein
US-09-841-835-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
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6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR Indels

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TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                              ADDRESSEE:
                                                                                                                                                                                       COUNTRY: L
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99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPFISS-SSSSPSSPGSSIAESPEAA 157
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                                                     65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
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                                                                                                                                                                                                                                APPLICANT: de Lange, Titia
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 1327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patenti robos/mobbos
SOFTWARE: Patenti Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION DATA:
APPLICATION UMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.8%; Score 92; DB 3 30.4%; Pred. No. 1.5; ive 15; Mismatches
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FP: 600-1-230 CIP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Pelocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REPERCE/DOCKET NUMBER: 600-1 TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
                                                                                                                                                                                 Sequence 2, Application US/09196387
Patent No. 6277613
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1327 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 30.49
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . protein
NO
                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                        CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                              New Jersey
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: lin
MOLECULE TYPE:
HYPOTHETICAL: N
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US-09-841-835-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Sequence 2, Application US/09841835; Patent No. 6506587; GENERAL INFORMATION:

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99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLBACRNGDVSRVKRLVDAANVNAKDM 212
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 1327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57; Indels
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APPLICANT: Walter, Funk D.
APPLICANT: Walter, Funk D.
APPLICANT: Walter, Funk D.
TITLE OP INVENTION: A Second Mammalian Telomerase
FILE REFERENCE: 080/003C
CURRENT APPLICATION NUMBER: US/09/972,115A
CURRENT APPLICATION NUMBER: US 60/128,577
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR PLING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Jackson Bsq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELERA: 201343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                      STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 92; DB 4; Pred. No. 1.5; 15; Mismatches
                                                                                                                                                                                                                                                                                                          COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS OSTWARE: Patentin Pol-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/09972115A
Patent No. 6599728
                                                                                                                                                   Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 30.4%;
Matches 35; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1327 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6599728
GENERAL INFORMATION:
APPLICANT: Geron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
NO
                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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218 GVYQPCKAKNGS-SSSSNGGNGSSTQTTATTTQDGVTITTTYNNNKATVKFD-----IT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 AYQAVFLAINAAVGL---WNTIGYAVMCGNGNGTESGPGSVIFNDQPGQDSTQITCNRFE 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 G-----ADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNYDQLVTRVVT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 VAAAPVVPANSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSFGSSLAESPEAA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----- 37
                                                                                                                                                                                                                                                                                                                                                                                                                             6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNG-------ADVGQ 83
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61;
                                                                                                                                                                                                                                                                                                                                                   ..
w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 745;
                                                                                                                                                                                                                                                                    DB 4; Length 1327;
                                                                                                                                                                                                                                                                                                                                          57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 AFAAIVVSGSALAGVVPQW-------GGGGNHNGGGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.6%; Score 90.5; DB 4; 20.8%; Pred. No. 0.97; attive 28; Mismatches 63;
                                                                                                                                                                                                                                                            ch 11.8%; Score 92; DB 4
1 Similarity 30.4%; Pred. No. 1.5;
35; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: 721
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-336-115C-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-08-864-038A-3
; Sequence 3, Application US/08864038A
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271 NNAEQLLNQAAN 282
                                                                                                                                            ; ORGANISM: Homo sapiens
US-09-972-115A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 40; Conserv
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                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 35; Conserv
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                                                                      1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
US-09-336-115C-6
                                                                                                               TYPE: PRT
                                 SEQ ID NO 8
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TREAT
GENERAL INFORMATION:
APPLICANT: KUNIO NAKASHIMA et al.
APPLICANT: KUNIO NAKASHIMA et al.
TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
TITLE OF INVENTION: SAID POLYPEPTIDE. DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
TITLE OF INVENTION: TO SAID POLYPEPTIDE
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 LLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD 62
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
ITILE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------GGGAGALA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONTACT.

COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM Compatible
Computer: IBM Computer: IBM Compatible
Computer: IBM Compatible
Computer: IBM Computer: IBM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 89.5; DB 3;
Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: From 1 to 738
IDENTIFICATION METHOD: E (by experiment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPACTION COMPACTABLE
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/864,038A
FILING DATE: May 28, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-184459
FILING DATE: LS-UA)-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pinctada fucata
CELL TYPE: mantle epithelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----AALAAAGAGGIGGGGG 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 ARKSETTITQSGYGNGADVGQG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: C. Bruce Hamburg
REGISTRATION NUMBER: 22,389
REFERENCE/DOCKET NUMBER: F'-I
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.5%;
35.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (212) 986-2340
(212) 953-7733
                                                                                                                                                                                                                                                                                                                                                                                                             812-5 Hirano
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mie-prefecture: JAPPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
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Best Local Similarity
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STREET: IS
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TYPE: PRT;
CORGANISM: Mycobacterium tuberculosis
US-09-477-135A-131
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Best Local Similarity
Matches 33; Conserv
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US-09-477-135A-131
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US-09-072-596-199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 NSYNTGFGNSGDANTGFFNSGIANTGVGNAGNYNTGSYNPGNSNTGGFNMGQYNTGYLNS 265
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F. Skeiky, Yasir A.W.
F. Dillon, Davin C.
F. Campos-Neto, Antonia
F. Houghton, Raymond
F. Wedvick, Thomas S.
F. Twardzik, Daniel R.
F. Hendrickson, Robald C.
F. Hendrickson, Robald C.
F. Hendrickson, COMFOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
11.4%; Score 89; DB 4; Length 943;
Best Local Similarity 25.6%; Pred, No. 1.9;
Matches 33; Conservative 15; Mismatches 55; Indels
                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUN TYPE: Floppy disk
MEDIUN TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM:
PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FLING DATE: 07-APR-1998
CLASSITCATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVId J. 392
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,392
RELEPAX: (206) 622-4900
TELEPAX: (206) 622-4900
TELEPAX: (205) 682-6031
INFORMATION FOR SEQ ID NO: 204:
SEQUENCE CHARACTERISTICS:
LENGTH: 943 amino acids
TYPE: AMINO acids
THENDER THE PROBLEM AND ACIDS AND
S: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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Patent No. 6458366
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BE
STREET: 6a00 Columbia
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNYNTGLAN 274
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APPLICANT: Skelky, Y.
APPLICANT: Dillon, D.
APPLICANT: Campos-Ne
APPLICANT: Twardich,
APPLICANT: Twardick,
APPLICANT: Twardik,
APPLICANT: Hendricks
APPLICANT: Hendricks
                                                                                                 Washington
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ZIP: 98104-7092
                                                              Seattle
   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-056-556-204
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                                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 IVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR---KKSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 TITQSGYGNGADVGQGADNSTIELTQNGPRNNATIDQMNAKNSD---ITVGQY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                               11.4%; Score 89; DB 4; Length 943;
llarity 25.6%; Pred. No. 1.9;
Conservative 15; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 943;
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRINI APPLICATION DUATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLEASSIFICATION:
ATTORNEY/AGBNT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 210121.417C9
REFERENCE/DOCKET NUMBER: 210121.417C9
TELEFORMUNICATION INFORMATION:
TELEFAM: (206) 622-4900
TELEFAM: (206) 622-4900
TELEFAM: (206) 622-4900
SELEFAM: (206) 622-6031
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55;
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11.4%; Score 89; DB 4
Best Local Similarity 25.6%; Pred. No. 1.9;
Matches 33; Conservative 15; Mismatches
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Job time : 13 secs
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313 NSYNTGFGNSGDANTGFFNSGLANTGVGNAGNYNTGSYNPGNSNTGGFNMGQYNTGYLNS 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 IVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR---KSET 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55; Indels 26; Gaps
                                                                                                                              Sequence 204, Application US/09072967

Sequence 204, Application US/09072967

GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dampos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Wardzik, Thomiel R.
APPLICANT: Wardzik, Daniel R.
APPLICANT: Wardzik, Daniel R.
APPLICANT: Houghton, Rohald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY:
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6510 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
11.4%; Score 89; DB 4; Length 943;
Best Local Similarity 25.6%; Pred. No. 1.9;
Matches 33; Conservative 15; Mismatches 55; Indels
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                              119 GGNNAALVN 127
                                                           373 GNYNTGLAN 381
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US-09-072-967-204
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Search completed: August 2, 2004, 14:58:31

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August 2, 2004, 14:54:48; Search time 36.8 Seconds (without alignments) 1287.123 Million cell updates/sec
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779
1 MKLLKVAAFAAIVVSGSALA.......VTRVVTHEMAHANNATANQY 151
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18: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1291235
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1291235 segs, 313682936 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Listing first 45 summaries
                                                                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0 Maximum DB seq length: 20000000000
                                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                           Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 4, Appli	Sequence 4, Appli	Sequence 2, Appli			Sequence 49960, A	Sequence 64573, A	Seguence 7876, Ap	Sequence 147343,	Sequence 8, Appli	Sequence 10, Appl	Sequence 2, Appli	Sequence 8, Appli	Sequence 4, Appli	Sequence 203823,
SOMMAKTES		ΔI	US-09-741-873B-4	US-09-741-873B-4	US-09-741-873B-2	US-09-741-873B-2	US-10-369-493-20638	US-10-425-114-49960	US-10-282-122A-64573	US-10-032-585-7876	US-10-437-963-147343	US-09-841-835-8	US-09-841-835-10	US-09-841-835-2	US-09-972-115A-8	US-10-199-937-4	US-10-437-963-203823
		DB	12	12	12	12	15	12	12	14	16	σ	σ	6	10	14	16
		Match Length DB	151	151	131	131	445	263	678	688	271	673	949	1327	1327	1327	705
	Ouerv	Match	66.4	66.4	56.4	56.4	12.8	12.5	12.1	12.1	11.9	11.8	11.8	11.8	11.8	11.8	11.7
		Score	517	517	439	439	100	97.5	94.5	94.5	93	92	92	92	92	92	91.5
	Result	NO.	н	7	e	4	Ŋ	φ	7	œ	σ	10	11	12	13	14	15

2284	Sequence 6, Appli	683		263	19						369	748	413		067	193	269		m	685	854	921	345	757	4	4			
16 US-10-437-963-16	US-08-834-666	2 US-10-282-12	-238-	6 US-10-437-96	5 US-10-369-49	US-09-996-634-13:	0 US-09-997-182-1	US-09-997-181-13	4 US-10-193-002-1	4 US-10-084-843-2	2 US-10-282-122A-0	US-10-437-963-1	5 US-10-437-963-1	0 US-09-820-843A-	6 US-10-437-963-1	6 US-10-437-963-1	2 US-10-282-122A-	0 US-09-952-267-5	4 US-10-156-7	6 US-10-437-9	2 US-10-282-13	6 US-10-437-9	Z US-10-282-13	2 US-10-282-13	US-09-880-1	2 US-10-293-4:	3 US-10-121-032-6	4 US-10-093-037-6	
ا 4 ک			1778	270	486	943						145																	
11.7	11.6	11.6	11.6	11.5	11.5	11.4	11.4	11.4	11.4	11.4	11.4	11.4	11.4	11.3	11.3	11.2	11.2	11.2	11.2	11.0	11.0	11.0	11.0	11.0	10.9	10.9	10.9	10.9	
16	90.5	0.00	96	89.5	6.0	, co	. co	80	.00	8	68	88.5	88.5	88	88	87.5	87.5	87.5	87	86	86	85.5	85.5	85.5	100	ري 80	80	ιΩ 00	
7	21	18	119	20		22	23	24	25	26	27	28	29	30	31	32	33	3.4	in in	98	37	38	3.9	40	4.1	4.2	43	44	

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RESULT 1

US-09-741-873B-4

Sequence 4, Application US/09741873B

Sequence 4, Application Would No. US20020001722A1

Sequence 6, Application No. US20020001722A1

SEQUENCE NO. USCO02001722A1

SEQUENCE NO. USCO02001722A1

APPLICANT: Normark. Staffan

APPLICANT: Normark. Staffan

APPLICANT: Normark. Staffan

APPLICANT: NORMER: US/09/741,873B

CURRENT RILING DATE: 1090-05-06

PRIOR FILING DATE: 1990-05-06

PRIOR FILING DATE: 1990-05-04

PRIOR FILING DATE: 1990-05-04

PRIOR FILING DATE: 1990-05-04

PRIOR FILING DATE: 1990-05-04

PRIOR FILING DATE: 1991-11-06

PRIOR FILING DATE: 1991-10-05

PRIOR FILING DATE: 1991-10-05

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PRIOR FILING DATE: 1991-10-05

PRIOR FILING DATE: 1994-10-05

NUMBER OF SEQ ID NOS: 10

SEQ ID NO 4

LENGTH: 151

TYPE: PRECEDIATION UNMER: US 08/187,865

PRIOR FILING DATE: 1994-10-05

NUMBER OF SEQ ID NOS: 10

SEQ ID NO 4

LENGTH: 151

TYPE: PRECEDIATION UNMER: US 08/187,865

PRIOR FILING DATE: 1994-10-05

NUMBER OF SEQ ID NOS: 10

SEQ ID NO 4

CONGANISM: Escherichia coli

US-09-741-873B-4

QUENTY MATCH

GEG-4%: Score 517; DB 12; Length 151;

Best Local Similarity 65.2%; Priod: No. 1.76-43;

Best Local Similarity 65.2%; Mismatches 29; Indels 0; Gaps 0;
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PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR FILING DATE: 1989-05-04
PRIOR FILING DATE: 1992-11-06
PRIOR PAPLICATION NUMBER: US 07/970,846
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR PILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 2
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.4%; Score 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09741873B Publication No. US20040096965A9 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Escherichia coli
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Publication No. US2004009695A9

GENERAL INFORMATION:

APPLICANT: Olsen, Arne

ITILE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation

FILE REPRENCE: 012889-084

CURRENT APPLICATION NUMBER: US/09/741,873B

CURRENT APPLICATION NUMBER: US/09/741,873B

CURRENT APPLICATION NUMBER: US 003-06-06

FRIOR APPLICATION NUMBER: US 08/978,978

FRIOR APPLICATION NUMBER: US 09/347,189

FRIOR APPLICATION NUMBER: US 07/347,189

FRIOR APPLICATION NUMBER: US 07/347,189

FRIOR FILING DATE: 1989-05-06

FRIOR APPLICATION NUMBER: US 07/370,846

FRIOR APPLICATION NUMBER: US 08/187,865

FRIOR APPLICATION NUMBER: US 08/187,865

FRIOR FILING DATE: 1994-01-05

FRIOR FILING DATE: 1994-10-05
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Publication No. US20020081722A1
GENERAL INFORMATION
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENITON: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084
CURRENT APPLICANION NUMBER: US/09/741,873B
CURRENT FILING DATE: 2003-04-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                         121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
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SOFTWARE: Patentin version 3.0
SEQ ID NO 4
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ORGANISM: Escherichia coli
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GENERAL INFORMATION:

APPLICANT: Normark, Staffan.

APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012899-084
CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT APPLICATION NUMBER: US 8801723-1
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR PILING DATE: 1999-05-04
PRIOR PELING DATE: 1999-11-06
PRIOR PELING DATE: 1991-11-06
PRIOR PELING DATE: 1994-01-28
PRIOR PILING DATE: 1994-01-28
PRIOR PELING DATE: 1994-01-28
PRIOR PELING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Version 3.0
SEQ ID NO 2:
FUNCTUR: 1131
                                                                                                                                                                                                                                                     91 VGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNYDQLVTRVVTHEM 140
                                                                                                                                                                                                                                                                                          61 VGQGSDDSSIDLTQRGFGNSATLDQWNGRNSEMTVKQFGGGNGAAVDQTASNSSVNVTQV 120
                                                                                                                                                                                   1 GVVPQYGGGGNHGGGGNNSGPNSELNTYQYGGGNSALALQTDARNSDLTITQHGGGNGAD
                                                                                                                          21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
                                                               Gaps
                                                               .
0
   DB 12; Length 131;
                                                           Indels
Query Match 56.4%; Score 439; DB 12; Best Local Similarity 62.6%; Pred. No. 8e-36; Matches 82; Conservative 21; Mismatches 28;
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DB 12; Length 131;

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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
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12.5%; Score 97.5; DB 12;
Best Local Similarity 26.6%; Pred. No. 0.17;
Matches 34; Conservative 18; Mismatches 53;
                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: 700071884_FLI.pep
US-10-425-114-49960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 64573, Application US/10282122A publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-02-16
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Zyskind, Judith
Wall, Daniel
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Trawick,
                                                                                                                                                               TYPE: PRT
ORGANISM: Zea mays
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                                                                                                                                      LENGTH:
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Publication No. US2003023675A1

GENERAL INFORMATION:

APPLICANT: Gao, Yongwei

APPLICANT: Slater, Steven C.

APPLICANT: Goodwan, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES

TITLE OF INVENTION: USABATE US/10/369,493

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT PILING DATE: 2003-02-28

PRIOR FILING DATE: 2002-02-21

NUMBER: OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-425-114-49960

Sequence 49960, Application US/10425114
Sequence 49960, Application US/10425114
Sequence 49960, Application No. US20040034888A1
SEMENAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jinda
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 GSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKN 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 GNSNSV-----GRDIQGKQSGAGNSAAIFQEGTGSDVELQQTGTSNGAVPSGWNWTN 129
                                                                                                                                                                 81 VGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNYDQLVTRVVTHEM 140
                                                                                                                                                                                         61 VGQGSDDSSIDLTQRGFGNSATLDQWNGRNSEMTVKQFGGGNGAAVDQTASNSSVNVTQV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 AAFAA-----IVVSGSALAGVVPQWGGGG-----NHNGG-----GNSSGPDSTLSIYQY 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----SDITVGQYGGNNAALVNYDQLVTRVVTHEMAHANNATA-NQ 150
                                                                                                      1 GVVPQYGGGGHHGGGGNNSGPNSELNTYQYGGGNSALALQTDARNSDLTITQHGGGNGAD
                                                                      21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
                             Gaps
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12.8%; Score 100; DB 15; Length 445;
Best Local Similarity 26.6%; Pred. No. 0.18;
Matches 47; Conservative 20; Mismatches 56; Indels 5.
                             Indels
                             28;
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; OTHER INFORMATION: unsure at all Xaa locations US-10-369-493-20638
62.6%; Prec. ....
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       Best Local Similarity 62.69
Matches 82; Conservative
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|21 GFGNNATAHQY 131
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US-10-369-493-20638
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LENGTH: 445
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84 SSIAG-----GGGGGGGGGGGGTNGGSGSGGGSGYGSGSSSTAASGPSSGNYADAEGKGAG 138 75 -------YGNGA--DVGQGADNSTIEL--TQNGFRNNATIDQWNAKNSDITVGQYGG 120 17 SALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSG-- 74 Gaps TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 49960 23; Length 263; 53; Indels

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TOPOLOGY:
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US-09-841-835-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Terry, Roemer D.
APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-99
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Referentin version 3.1
EDRIGH: 688
                                                                                                                                                                                                                                                 73 SGYGNGADVGQGADNS-----TIELTQNGFRNNATIDQ--WNAKNSDITVGQYGGNN 122
                                                                                                                                                                                                                                                                                                                             90 IELTQNGFRNNATIDQWNAIGNSDITVGQYGGNNAALVNYDQLVTRVVTHEMAHANNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ--SDARKSETTITQ 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 GNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNST 89
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                                                                                                                                           Length 678;
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                                                                                                                                     Query Match
12.1%; Score 94.5; DB 12;
Best Local Similarity 25.7%; Pred. No. 1.1;
Matches 39; Conservative 24; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.1%; Score 94.5; DB 14; 25.8%; Pred. No. 1.1; tive 24; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                123 AALVNYDQLVTRVVTHEM-----AHANNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
US-10-437-963-147343
i Sequence 147343, Application US/10437963
i Sequence 147343, Application US/10437963
i Publication No. US20040123343A1
i GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buukharov, Andrey A.
APPLICANT: Barbarak, Brad
                                                         TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7876, Application US/10032585 Publication No. US20030180953A1
SOFTWARE: Patentin version 3.1
SEQ ID NO 64573
LENGTH: 678
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US-10-032-585-7876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 31, Conserve
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59 GGEGGGSESGGGLGRQR------YWNSRLSTERQRLVDHVFKNSDVVCDVF 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 VVGRAAAAYPEVGSGDGGESGGGGGGGGGG------GGDGSVAAVNPEAGSGDGDRSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/09841835

Patent No. US20020076795A1

GENERAL INCRAMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDERORS 12
CORRESPONDERORS JOACKSON
STREET: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                          11.9%; Score 93; DB 16; Length 271; 22.2%; Pred. No. 0.49; ive 18; Mismatches 59; Indels
                                                                                                                                                                                                                                 OTHER INFORMATION: Clone ID: PAT_MRT4530_47881C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 SGVGPIAIS----AARKVKYVYANDLNPTAVEY 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 SGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 GGNNAALVNYDQLVTRVVTHEMAHANNATANQY 151
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FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 147343
LENGTH: 271
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APPLICATION NUMBER: 09/196,387
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Jackson Esg., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600 TELECOMMUNICATION INFORMATION: TELEPHONE: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                 Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-09-841-835-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                           ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                       US-10-437-963-147343
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linear
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US-09-972-115A-8
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                                                                                       6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
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                                                                                                                                                                                                             Gaps
                                                                                                                                                                              65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
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                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/09841835
Fatent No. US20020076795A1
GENERAL INFORMATION:
APPLICANT: Gall Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: All Hackensack Avenue, 4th Floor
COUNTRY: USA
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Query Match 11.8%; Score 92; DB 9; Length 673; Best Local Similarity 30.4%; Pred. No. 1.9; Matches 35; Conservative 15; Mismatches 57; Indels
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11.8%; Score 92; DB 9; Length 949;
Best Local Similarity 30.4%; Pred. No. 2.9;
Matches 35; Conservative 15; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DCS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Jackson Eq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 13521
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 949 amino acids
TYPE: amino acid
TOPOLOGY: linear
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US-09-841-835-10
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                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                   DB 10; Length 1327;
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                                                                                                                                                                                                                                                           57; Indels
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Publication No. US2003019073941

GENERAL INFORMATION:

APPLICANT: Christenson, Erik

APPLICANT: Christenson, Erik

APPLICANT: Goldman, Phyllis S.

APPLICANT: McElligott, Anthony J.

TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS

FILE REFERENCE: 27866/36559

CURRENT FAPLICATION NUMBER: US/10/199,937

CURRENT FILING DATE: 2002-07-22

PRIOR APPLICATION NUMBER: US/09/606,035

PRIOR FILING DATE: 2002-06-28

PRIOR FILING DATE: 1999-06-29

NUMBER OF SEQ ID NOS: 178

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4

LENGTH: 1327
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15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15; Mismatches
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Conservative 15; Mismatch
                                                                                                                                                                                                                     11.8%; Score 92; 30.4%; Pred. No.
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PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR FILING DAME: 1999-04-13
NUMBER OF SEQ ID NOS: 64
SEQ ID NO 8
LENGTH: 1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
                                                                                                                                                                                                                   Query Match
Best Local Similarity 30.4%
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT

) ORGANISM: Homo sapiens

US-10-199-937-4
                                                                                                                                                            ORGANISM: Homo sapiens
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Best Local Similarity
Matches 35; Conserv
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                                                                                                                                           TYPE: PRT
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APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Moreont
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21/63221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 203823
LENGTH: 705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 IVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYG---SANAALALQSDARKSET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----NEWYKK-----GHYG---EALRHYDQAVALCPDSAACRSNRAAA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT4530_98970C.1.pep
US-10-437-963-203823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match. 11.7%; Score 91.5; DB 16; Best Local Similarity 24.7%; Pred. No. 2.3; Matches 42; Conservative 19; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: August 2, 2004, 15:36:09 Job time : 37.8 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 TITQSG---YGNG--
                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Oryza sativa
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Sequence 16, Appl
Sequence 15, Appl
Sequence 75, Appl
Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 5834, Ap
Sequence 5834, Ap
Sequence 5834, Ap
Sequence 5834, Ap
Sequence 2, Appli
Sequence 34, Appli
Sequence 37, Appli
Sequence 37, Appli
Sequence 35, Appli
Sequence 36, Appli
Sequence 58, Appli
Sequence 58, Appli
Sequence 58, Appli
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5833. Ap
5833. Ap
20638. Ap
20638. Ap
358. App
358. App
358. App
3137. App
3137. App
24084. App
241179. App
19019. App
14916. App
  Sequence 12, 3
Sequence 14, 4
Sequence 57, Ar
Sequence 24, A
Sequence 24, A
Sequence 28, A
Sequence 20, A
Sequence 31, A
Sequence 31, A
Sequence 32, A
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APPLICANT: White, Aaron P.

APPLICANT: White, Aaron P.

APPLICANT: Collinson, S. Karen

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

FILE REFERENCE: 920043.406

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12

LENGTH: 151
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Sequence
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OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: Sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
19 US-09-543-407-12

US-09-543-407-14

US-09-543-407-14

US-09-543-407-24

US-09-543-407-24

US-09-543-407-24

US-09-543-407-20

US-09-543-407-30

US-09-552-691-5833

US-10-417-886-5833

US-10-417-886-5833

US-10-417-886-5833

US-10-117-313-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-317-318-3
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US-09-614-150-14916
US-09-614-150A-14916
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US-60-191-637-24179
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        RESULT 1
US-09-543-407-12
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                                                                                                                                                                                                                                                                         US-09-543-407-12
779
1 MKLLKVAAFAAIVVSGSALA.....VTRVVTHEMAHANNATANQY 151
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1: /cgn2 6/ptodata/2/paa/BCTUS CONB.pep:*

2: /cgn2 6/ptodata/2/paa/BCTUS CONB.pep:*

3: /cgn2 6/ptodata/2/paa/US08 CONB.pep:*

5: /cgn2 6/ptodata/2/paa/US081_CONB.pep:*

6: /cgn2 6/ptodata/2/paa/US082_CONB.pep:*

6: /cgn2 6/ptodata/2/paa/US082_CONB.pep:*

7: /cgn2 6/ptodata/2/paa/US082_CONB.pep:*

8: /cgn2 6/ptodata/2/paa/US083_CONB.pep:*

10: /cgn2 6/ptodata/2/paa/US083_CONB.pep:*

10: /cgn2 6/ptodata/2/paa/US083_CONB.pep:*

11: /cgn2 6/ptodata/2/paa/US083_CONB.pep:*

12: /cgn2 6/ptodata/2/paa/US083_CONB.pep:*

13: /cgn2 6/ptodata/2/paa/US083_CONB.pep:*

14: /cgn2 6/ptodata/2/paa/US083_CONB.pep:*

15: /cgn2 6/ptodata/2/paa/US083_CONB.pep:*

16: /cgn2 6/ptodata/2/paa/US093_CONB.pep:*

17: /cgn2 6/ptodata/2/paa/US093_CONB.pep:*

18: /cgn2 6/ptodata/2/paa/US093_CONB.pep:*

19: /cgn2 6/ptodata/2/paa/US093_CONB.pep:*

19: /cgn2 6/ptodata/2/paa/US093_CONB.pep:*

19: /cgn2 6/ptodata/2/paa/US093_CONB.pep:*

10: /cgn2 6/ptodata/2/paa/US093_CONB.pep:*
                          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            6019581 segs, 976053577 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                           protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length DB
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Best Local Similarity
Matches 135; Conserv
                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 136; Conserv
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                                                                                                                                                                                                                                 61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                        1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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                                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Col, Milliam W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGGUS PEPTIDE SEQUENCES
FILE REPERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILIS DATE: 2000-04-05
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09543407
GENERAL INFORMATION:
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
CURRENT APPLICATION NUMBER: US/09/543,407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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                                          Length 151;
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Best Local Similarity 87.6%; Pred. No. 2e-65;
Matches 141; Conservative 0; Mismatches 0; Indels 20
                                                                                          Indels
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                                     100.0%; Score 779; DB 19;
100.0%; Pred. No. 2.9e-74;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                 121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
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                                                                                       Matches 151; Conservative
                                             Query Match
Best Local Similarity
US-09-543-407-12
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US-09-543-407-5
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TITLE OF INVENTION: BASED VACCINES
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                        Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88.6%; Score 690; DB 6; Length 151; Lonsity 89.4%; Pred. No. 8.6e-65; Conservative 4; Mismatches 12; Indels
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/233,642A FILING DATE: 26-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3: Seed and Berry
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                        Score 695; DB 19;
Pred. No. 2.5e-65;
4; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
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REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 920043.403C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                  NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS OSTWARE: PatentIn Policy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Sequence 57, Application US/08233642A, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kay, William W.
APPLICANT: Collinson, S. Karen
APPLICANT: Clouthier, Sharon C.
APPLICANT: Doran, James L.
                                                                                                                              ) ORGANISM: Salmonella enteritidis US-09-543-407-5
2000-04-05
59
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INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                           89.2%;
nilarity 90.1%;
Conservative 4
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104-7092
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                                                                                                                                      61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: White, Aaron P.

APPLICANT: White, Aaron P.

APPLICANT: With G. S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

TITLE OF INVENTION: BACTERIAL FIMERIAL SYSTEM FOR

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 26

LENGTH: 151
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MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                             1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                       SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: RAy, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 NNAALVNYDQLVTRVVTHEMAHA--------NNATANOY 151
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84.1%; Score 655; DB 19;
Best Local Similarity 79.8%; Pred. No. 4.6e-61;
Matches 134; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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US-09-543-407-26
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US-09-543-407-24
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US-09-543-407-24
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LENGTH: 151
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                                                                                                                                                                                                                                                                                                                                                                  61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                            Gaps
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OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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                                       OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA orther INFORMATION: sequence containing the replacement fragment; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-26
                                                                                                                                                 Length 151;
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80.8%; Pred. No. 1.4e-56;
iive 7; Mismatches 22;
                                                                                                                                              Score 614; DB 19;
Pred. No. 1.1e-56;
6; Mismatches 23;
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTE)
TITLE OF INVENTION: PRESENTATION OF HETEROLG
TITLE REPERBNCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
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; Sequence 20, Application US/09543407
; GENERAL INFORMATION:
; APPLICANT: Mitte, Aaron P.
; APPLICANT: Doran, James L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 18, Application US/09543407; GENERAL INFORMATION:
                                                                                                                                                   78.8%;
ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                   Query Match
Best Local Similarity 80.8
Matches 122; Conservative
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Matches 122, Conservative
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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Matches 122;
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LENGTH: 151
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APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ITANS: PRT
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APPLICANT: Collinson, S. Karen
APPLICANT: KAY, William W.
TITLE OF INVENTION: BASSENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASUSEQ for Windows Version 4.0
LENGTH: 151
TYPE: PRT
CYRANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 151;
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78.4%; Score 611; DB 19; Length 1
Best Local Similarity 80.8%; Pred. No. 2.2e-56;
Matches 122; Conservative 7; Mismatches 22; Indels
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Pred. No. 3.9e-56;
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; Sequence 31, Application US/09543407
; GENERAL INFORMATION:
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Best Local Similarity 88.5%;
Matches 116; Conservative
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GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FOR HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.466
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 151
TYPE: PRT
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                                                 APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Colling.
S. Karen
APPLICANT: Colling.
S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REPERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
SOFTWARE: FASTSEQ for Windows Version 4.0
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larity 80.8%; Pred. No. 1.2e-55;
Conservative 6; Mismatches 23; Indels 0
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Pred. No. 9.8e-56;
5; Mismatches 25;
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Sequence 28, Application US/09543407 GENERAL INFORMATION:
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Best Local Similarity 80.1%;
Matches 121; Conservative
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US-08-233-642A-55
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                                                                                 61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                              61 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGFDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
US-09-543-407-16
Sequence 16, Application US/09543407
Sequence 16, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: RAy, William W.
TILLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TILLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
: SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
APPLICANT: RAY, William W.
APPLICANTON: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFRENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT PILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SEQ ID NO 30
LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 77.4%; Score 603; DB 19; Length 151; Best Local Similarity 80.8%; Pred. No. 1.6e-55; Matches 122; Conservative 6; Mismatches 23; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
                                                                                                                                                                                                                          121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
                                                                                                                                                                                                                                                                                                                      RESULT 12
US-09-543-407-30
'Sequence 30, Application US/09543407
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                         .
FEATURE:
COTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
COTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
US-09-543-407-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Clouthier, Sharon C.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: MATHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: BASED VACCINES
NUMBER OF SEQUENCES: 58
NUMBER OF SEQUENCES: -
CORRESPONDENCE ADDRESS: -
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                            74.5%; Score 580; DB 19; Length 151; 80.1%; Pred. No. 4.5e-53; ive 7; Mismatches 23; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
71.9%; Score 560; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 4.5e-51;
Matches 106; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,642A
FILING DATE: 26-APR-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
US-08-233-642A-55
Sequence 55, Application US/08233642A,
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
ATTORNEY AGENT IN PORNATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 92004
TELECOMPUNICATION INFORMATION:
TELESPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEFAX: 3723846 SEEDANBERRY
INFORMATION FOR SEO IN NO: 55:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 120 amino acids
amino acid
                                                                                                                                                                  Query Match
Best Local Similarity 80.1%
Matches 121; Conservative
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STATE: Washington
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1 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                           WESULY 15

WESULY 12

WESULY 12

WESULY 12

SEQUENCE 7, Application US/09543407

SEQUENCE 7, Application US/09543407

SEQUENCE 7, Application US/09543407

APPLICANT: White, Aaron P.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: REPRENCE 12

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

TITLE OF INVENTION: WANDER: US/09/543,407

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 66.8%; Score 520; DB 19; Length 151; Best Local Similarity 66.9%; Pred, No. 1.1e-46; Matches 101; Conservative 21; Mismatches 29; Indels
                                                                                61 GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVN 106
                                             82 GOGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT

ORGANISM: Escherichia coli
US-09-543-407-7
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Search completed: August 2, 2004, 15:26:42 Job time : 168.9 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:
August 2, 2004, 14:49:38 ; Search time 17:8 Seconds (without alignments)

Run on:
August 2, 2004, 14:49:38 ; Search time 17:8 Seconds (without alignments)

Bucklet score:
779
Sequence:
1 MKLLKVAAFAAIVVSGSALA.....VTRVVTHEMAHANNATANQY 151

Scoring table:
Gapop 10.0 , Gapext 0.5
Searched:
601315 segs, 104695340 residues

Total number of hits satisfying chosen parameters:
601315

Minimum DB seg length: 0
Maximum DB seg length: 2000000000
```

Pending\_Patents\_AA\_New:\*

1: /cgn2\_6/ptodata/2/paa/PCT\_NEW\_COMB.pep:\*
2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep:\*
3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pep:\*
4: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep:\*
5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep:\*
6: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep:\*
7: /cgn2\_6/ptodata/2/paa/US0\_NEW\_COMB.pep:\*
7: /cgn2\_6/ptodata/2/paa/US0\_NEW\_COMB.pep:\*
7: /cgn2\_6/ptodata/2/paa/US0\_NEW\_COMB.pep:\*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 2, Appli Sequence 2, Appli Sequence 300390, Sequence 312468, Sequence 35751, A Sequence 35751, A Sequence 30134, Sequence 7608, Ap Sequence 7906, Ap Sequence 7906, Ap Sequence 7907, Ap Sequence 317, App Sequence 317, App Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 7905, Ap Sequence 5, Appli Sequence 1905, Ap Sequence 21, Appli Sequence 21, Appli
SUMMARIES	US-09-741-873C-4 US-09-741-873C-4 US-09-741-873C-4 US-10-425-115-302468 US-10-425-115-302468 US-10-170-205E-35751 US-110-170-205E-35751 US-110-170-205E-35751 US-110-170-205E-35751 US-10-425-115-30133-4 US-10-425-115-30133-4 US-10-425-115-30133-4 US-10-10-683-7906 US-60-56-632-7907 US-10-757-701-45603 US-60-56-632-7907 US-10-757-701-7907 US-10-757-701-7907 US-10-757-701-7907 US-10-757-701-7907 US-10-757-701-7907 US-10-757-701-7907 US-10-757-701-7905
Length DB	1110 1110 1110 1110 1110 1110 1110 111
ery	44 w w u u m m m c c c c c c c c c c c c c c c
Score	888 8999999999999999999999999999999999
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Sequence 13, Appl Sequence 13, Appl Sequence 254240, Sequence 10326, Sequence 10327, A Sequence 10327, A Sequence 3, Appli Sequence 3, Appli Sequence 9, Appli Sequence 25, Appli Sequence 255214, Sequence 255214, Sequence 265214, Sequence 26514, Sequence 4, Appli Sequence 26514, Sequence 21109, A Sequence 11109, A Sequence 11109, A Sequence 11109, A		well As Its Preparation	ength 151; Indels 0, Gaps 0;	PDSTLSIYQYGSANAALALQ 60  :   :	IIDQWNAKNSDITVGQYGG 120 
US-10-872-267B-13 US-10-872-768-13 US-10-872-768-13 US-10-425-115-254340 US-10-100-683-10326 US-10-100-683-10327 US-10-798-513-100 PCT-USO4-13211-3 US-10-170-205E-16599 PCT-USO4-09388-9 US-10-425-115-285214 PCT-USO4-09388-9 US-10-425-115-285214 PCT-USO4-09388-9 US-10-425-115-285214 US-10-425-1109 US-10-425-11109 US-60-555-632-11109 US-60-555-632-11109 US-10-425-1115-285214	ALIGNWENTS	1873C 1 Binding Protein As 109/741,873C 201723-1 1/978,878 1/347,189 1/789,437 1/970,846 1/187,865	Score 517; DB 5; Le: Pred. No. 1.1e-36; 22; Mismatches 29;	LAGVVPQMGGGGNHNGGGNSSGP:	SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDOWNAKNSDITVGQY 
8873 6 8873 6 8873 6 8873 6 8873 6 8 886 6 6 8 886 6 6 8 886 6 6 8 886 6 6 8 886 6 6 8		braffan frie 19-084 19-084 19-084 19-084 10MBER: US 1908-11-26 198-11-26 198-11-26 1998-11-26 1998-11-26 1998-11-26 1998-11-26 1998-11-06 1988: US 1991-11-06 1988: US 1994-01-28 111 3.	66.4%; y 66.2%; rvative	FAAIVVSGSA           IAAIVFSGSA	IITQSGYGNG            IITQHGGGNG
000000000000000000000000000000000000000		SSULT 1 5.09-741-873C-4 Sequence 4, Application GENERAL INFORMATION: APPLICANT: Normark, St APPLICANT: Normark, St APPLICANT: Normark, St APPLICANT: Normark, Art TILE OF INVENTOR: DISEN, FILE REFERENCE: 012885 CURRENT FILING DATE: 199 PRIOR PILING DATE: 199 PRIOR PILING DATE: 199 PRIOR PILING DATE: 199 PRIOR FILING DATE: 199	Similarity 0; Conser	mklikvaa          mklikvaa	SDARKSETTI       :    TDARNSDLTI
8888 2022 111111 1 111111 888888888888888888888	Į.	UT 1 9-741-873C- 9-741-873C- WERAL INFORM PPLICANT: PPLICANT: ILE REFEREN ILE REFEREN URRENT APPLIC RIOR PILING RI	Match Local	ਜ <b>ਜ</b>	6 6 1
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GENERAL INFORMATION:
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GENERAL INFORMATION:
MILLS OF INVENTION:
FOR DIAGNOSTICS AND THERAPEUTICS
TILLS OF INVENTION:
FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/248,796A

PRIOR FILING DATE: 1998-02-13
NUMBER: OF SEQ ID NOS: 28208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: La Rosa, Thomas J.
APPLICANT: Experiment Revalic, David K.
APPLICANT: Shou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
FITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 312468
LENGTH: 295
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                                                                                                                                                                                                                                       -----YGNGA--DVGQGADNSTIEL--TQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                      133 GEMGGGANGAYGSGAGGGVGKGEGVSGVALAPSSNGYYNGGAADATGGGSG--AGGGHGG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74
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                                                                                                                                                                                             17 SALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 DNSTIELTQNGFRN------NATIDQWNAKN-----SDITVGQYGGNNAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGA
                                                               12.5%; Score 97.5; DB 6; Length 258; 26.6%; Pred. No. 0.86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 29.7%; Pred. No. 1;
Matches 38; Conservative 15; Mismatches 50; Indels 2
                                                                                                                                 Indels
                                                                                                                                 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: MRT4577_48027C.1.pep
US-10-425-115-312468
                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 312468, Application US/10425115; GENERAL INFORMATION:
                                                                                                                                 18;
                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 NNAALVNY 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 GAAGAPSY 198
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                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Zea mays
US-10-425-115-300390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
US-10-425-115-312468
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US-09-248-796A-17559
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GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Scou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, You a
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                                                                                                     APPLICANT: Normark, Staffan APPLICANT: Normark, Staffan APPLICANT: Olsen, Arne TITLE OF INVENTIONS Fibronectin Binding Protein As Well As Its Preparation FILE REFERENCE: 012889-084 CURRENT APPLICATION NUMBER: U5/09/741,873C
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OTHER INFORMATION: Clone ID: MRT4577_37025C.1.pep
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OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                               PRIOR PAPLICATION NUMBER: 2000-12-2-3

PRIOR FILING DATE: 1998-05-06

PRIOR FILING DATE: 1998-05-06

PRIOR PELING DATE: 1998-11-26

PRIOR APPLICATION NUMBER: US 07/347,189

PRIOR PILING DATE: 1999-11-06

PRIOR PILING DATE: 1991-11-06

PRIOR FILING DATE: 1991-11-06

PRIOR PAPLICATION NUMBER: US 07/970,846

PRIOR PILING DATE: 1991-11-03

PRIOR APPLICATION NUMBER: US 08/187,865

PRIOR PILING DATE: 1992-11-03

PRIOR PILING DATE: 1994-10-05

PRIOR FILING DATE: 1994-10-05

PRIOR FILING DATE: 1994-10-05

NUMBER: PRIOR PILING DATE: 1994-10-05

SEQ ID NOS: 11

SOFTWARE: PATENTIN VERSION 3.0

SEQ ID NOS: 11
                                                 Sequence 2, Application US/09741873C GENERAL INFORMATION:
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ORGANISM: Escherichia coli
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121 GFGNNATAHQY 131
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Best Local Similarity
Trahes 82; Conserva
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ORGANISM: Zea mays
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US-10-425-115-300390
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FULLEDAY CASSON AND TELL TO THE APC AND AXIN PATHWAYS AND METHODS OF THE OF INVENTION:

JAPPICANTE EXELIXES, INC.

JITLE OF INVENTION: MAPCASS AS MODIFIERS OF THE APC AND AXIN PATHWAYS AND METHODS OF THE BERERNER: EXCHOUSE-PC.

JUREAR APPLICATION NUMBER: PCT/USO4/02338

CURRENT FILING DATE: 2004-01-28

PRIOR PELLING DATE: 2003-01-29

PRIOR PILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: US60/447,358

PRIOR APPLICATION NUMBER: US60/441,799

PRIOR APPLICATION NUMBER: US60/441,799

PRIOR PILING DATE: 2003-04-10

PRIOR PILING DATE: 2003-04-10

PRIOR PILING DATE: 2003-04-10

PRIOR PILING DATE: 2003-05-14

PRIOR SPUICATION NUMBER: US60/470,684

PRIOR PILING DATE: 2003-05-14

PRIOR SPUICATION NUMBER: US60/479,650

NUMBER OF SEQ ID NOS: 54

SOFTWARE: PATCHIL VEISION 3.2
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Sequence 301334, Application US/10425115

Sequence 301334, Application US/10425115

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: APPLICANT: David K.
APPLICANT: Cao, Younge in the strength of t
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99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPFISS-SSSSPSSPGSSLAESPEAA 157
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                                                                                                                   65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
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11.8%; Score 92; DB 1; Length 1327;
Best Local Similarity 30.4%; Pred. No. 16;
Matches 35; Conservative 15; Mismatches 57; Indels
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US-10-425-115-301334
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Best Local Similarity
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TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: DEPTURE AGENTS, AND USES THEREOF
FILE REFERENCE: CL001381
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 1203
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GENERAL INFORMATION:
SPELICANT: ADAMS, Mark
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE REFERENCE: CL001381
CURRENT APPLICATION NUMBER: US/10/170,205E
SURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: PATENTIN version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              563 TGLTMN---NNSKSPAKSKKKSNFD----NNSNSALNNLDKSKLKINTNEITNISETTSN 615
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                                                                                                                                                                                                                                                       Query Match 12.1%; Score 94.5; DB 5; Length 719; Best Local Similarity 25.8%; Pred. No. 4.9; Matches 31; Conservative 24; Mismatches 42; Indels 23;
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11.8%; Score 92; DB 6;
Best Local Similarity 30.4%; Pred. No. 14;
Matches 35; Conservative 15; Mismatches 5
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Best Local Similarity 30.4%
Matches 35, Conservative
                                                                                                   ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-17559
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ORGANISM: Homo sapiens
US-10-170-205E-741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-10-170-205E-35751
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US-10-170-205E-35751
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LENGTH: 299
                        SEQ ID NO 17559
LENGTH: 719
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Query Match
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                                                                                                                        SSVAG-----GGGGGGGGGTNGGSGSGGGSGYGSGTSSTAASGPSSGNYANAEGKGAG 133
                                                                                                                                                                                       VGQGADNSTIEL - - TQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                            185 GMNPQGAPWGQGG--NGGPPNFGTNTQGAVAQPGYGSVRA----SNQNEGCTNPPPSGS 237
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                                                            17 SALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDA----RKSETTITQ 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TILE OF INVENTION: Human Secreted Proteins
TILE OF INVENTION: Human Secreted Proteins
CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT APPLICATION NUMBER: US 60/040,162
PRIOR APPLICATION NUMBER: US 60/040,162
PRIOR FILING DATE: 1997-03-01
PRIOR FILING DATE: 1997-03-01
PRIOR FILING DATE: 1997-03-03
PRIOR FILING DATE: 1997-04-11
PRIOR FILING DATE: 1997-04-12
PRIOR FILING DATE: 1997-04-13
PRIOR FILING DATE: 1997-04-13
PRIOR FILING DATE: 1997-04-11
PRIOR FILING DATE: 1997-04-13
PRIOR FILING DATE: 1997-04-13
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PRIOR PLING DATE: 1997-04-13
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PRIOR PLING DATE: 1997-04-13
PRIOR PLING DATE: 1997-04-13
PRIOR FILING DATE: 1997-04-13
PRIOR PLING DATE: 1997-04-13
PRIOR PLING DATE: 1997-04-13
PRIOR PLING DATE: 1997-04-13
PRIOR PLING DATE: 1997-06-22
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   23; Gaps
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52;
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Best Local Similarity 26.0%; Pred. No. 5.1;
Matches 33; Conservative 18; Mismatches 43;
16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
US-60-565-632-7906
; Sequence 7906, Application US/60565632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7608, Application US/10100683 GENERAL INFORMATION:
                                                                                                                                                                                       73 SGYGNGAD------
Conservative
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US-10-100-683-7608
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Matches
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APPLICANT: Larosa, Thomas J.
APPLICANT: Larosa, Thomas J.
APPLICANT: Lu, Maolong
APPLICANT: Lu, Maolong
APPLICANT: Lu, Maolong
APPLICANT: Roberts, James K.
APPLICANT: Chang, Bei
TITLE OF INVENTION: Compositions Thereof
FILE REFERENCE: 38-21(53403) B
FILE REFERENCE: 38-21(53403) B
FILE REFERENCE: SEQ ID NOS: 15449
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SEQ ID NO 7906
LENGTH: 841
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APPLICANT: Baum, James A
APPLICANT: Baum, James A
APPLICANT: Larosa Thomas J
APPLICANT: Larosa Thomas J
APPLICANT: Larosa Thomas J
APPLICANT: Larosa Thomas J
APPLICANT: Munykwa, Tichifa R. I.
APPLICANT: Winnykwa, Tichifa R. I.
APPLICANT: Win wel
APPLICANT: Munykwa, Tichifa R. I.
APPLICANT: Munykwa, Tichifa R. I.
APPLICANT: Munykwa, Tichifa R. I.
APPLICANT: Canag, Bala
APPLICANT: Canag, Bala
APPLICANT: Compositions thereof
TITLE OF INVENTION: Compositions thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      328 AAQGTDNGAAABNTGNADPAQGNDNGAA----AENSGNENGTAAGNNA---NPD---- 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:

NAME/KEY: misc feature

LOCATION: (810)

OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-60-565-632-7906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 7; Length 841;
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32.6%; Pred. No. 11;
:ive 12; Mismatches
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                                 Baum, James A

Kovalic, David K.

Larosa, Thomas J.

Lu, Maolong

Munyikwa, Tichifa R. I.

Roberts, James K.

Wu, Wei
Monsanto Technology, LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Diabrotica virgifera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   375 -VQNDAAQVNDNGTA 388
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Matches 44; Conservative
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APPLICANT: Baum, James A
APPLICANT: Baum, James A
APPLICANT: Kovalic David K.
APPLICANT: Kovalic David K.
APPLICANT: Larosa, Thomas J.
APPLICANT: Larosa, Thomas J.
APPLICANT: Munyikwa, Tichifa R. I.
APPLICANT: Munyikwa, Tichifa R. I.
APPLICANT: Wu, Wai, Bei
TITLE OF INVENTION: Compositions Thereof
FILE OF INVENTION: Compositions Thereof
FILE REFERENCE: 38-21 (53403) B
CURRENT FILING DATE: 2004-04-27
NUMBER OF SEQ ID NOS: 15449
SOFTWARE: Patentin version 3.2
SEQ ID NO 9907
                                                                                                                                                                                                                                                                                                                                                                          347 GGNFGGNNNGGGGFNSGNNFNSPGGVNNFGNNGGSNFGGNGGGGFNNGGNFVSSSGVGNF 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 GG--GGNHNGGG-----NSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNG
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                                                                                                                                                                                                                                   Query Match
Best Local Similarity 25.5%; Pred. No. 9.5;
Matches 28; Conservative 12; Mismatches 44; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 7907, Application US/60565632; GENERAL INFORMATION:
  PRIOR APPLICATION NUMBER: 60/422,377
PRIOR FILING DATE: 2002-10-29
NUMBER OF SEQ ID NOS: 381
SEQ TWARE: Patentin version 3.1
SEQ ID NO 317
LENGTH: 586
                                                                                                                                                                     ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT Monsanto Technology,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) ORGANISM: Diabrotica virgifera US-60-565-632-7907
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Best Local Similarity 26.29
Matches 38; Conservative
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Job time : 17.8 secs
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US-60-565-632-7907
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                                                                                                                                            TYPE: PRT
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Sequence 317, Application PC/TUS0324982A
GENERAL INFORMATION:
APPLICANT: Syngenta Participations AG
APPLICANT: Stam, Lynn
APPLICANT: Spana, Eric
APPLICANT: Bachmann, Jane
TITLE OF INVENTION: Nucleic Acid Sequences from Drosophila Melanogaster that Encode
TITLE OF INVENTION: Desential for Viability and Uses Thereof
TITLE OF DAPLICATION NUMBER: PCT/US03/24982A
CURRENT APPLICATION NUMBER: 2003-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 45603, Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yingwei
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 45603
LENGTH: 234
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                                                                                                                                          269 GNENGTGAENNANADAQTDAAQ-GSTNEANAENNANADVQNDAAQANENGAAAENSGNAD 327
                                                                                                                                                                                         81 VGQGADN-STIELTQN-----GFRNNATIDQWNAKNSDITVGQYGGNNAALVNYDQLVTR 134
                                                                                                                                                                                                                                     328 AAQGTDNGAAAENTGNADPAQGNDNGAA----AENSGNENGTAAGNNA---NPD---- 374
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                                                                                                GNHNGGG--NSSGPDSTLSIYQYGSANAALA----LQSDARKSETTITQSGYGNGAD 80
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                                                 48; Indels 31; Gaps
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       DB 7; Length 841;
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US-10-767-701-45603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.6%; Score 90.5; DB 6; 1
24.2%; Pred. No. 3;
tive 12; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: unsure
LOCATION: (1)..(234)
OTHER INFORMATION: unsure at all Xaa locations
th 11.7%; Score 91.5; Di Similarity 32.6%; Pred. No. 11; 44; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                    135 VVTHEMAHAN-NATA 148
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 24.2%
Matches 39; Conservative
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-10-767-701-45603
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:
August 2, 2004, 14:39:53 ; Search time 9.4 Seconds (without alignments)
1545.204 Million cell updates/sec
Title:
US-09-543-407-12
Perfect score:
779
Sequence:
1 MKLLKVAAFAAIVVSGSALA......VTRVVTHEMAHANNATANQY 151

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Total number of hits satisfying chosen parameters: 283366

283366 segs, 96191526 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		ok:				
Result No.	Score		Leng	DB		Description
	69	١ %	ı ın	7	603	fimbrin protein ad
(1)	695	89.2	LΩ	N	1063	major curlin chain
٣	52	9	S	7	078	curlin protein csq
4	501.5	4.	S	7	9080	ppr
ເກ	0		152	0	H85665	a]
9	106	13.6	4	N	2	cnjB protein - Tet
7	0	m	17	7	E95965	hypothetical glyci
œ	ij	ო	5	N	33	nucleation compone
σ	00	ď.	ß	7	4	fimbrin protein ad
10	98.5	ď.	3	~1	33	DNA-binding protei
11	œ,	ď.	21	~	55	ovo protein - frui
12	96	2	4	7	4	conserved hypothet
13	96	N.	4	7	4	hypothetical prote
4	94.5	ď	67	~	9	probable PPE prote
15	m.	ď.	m	N	33	probable exported
16	83	ä	7	N	8626	F3F19.21 protein -
17	Ξ.		ß	N	7078	curlin nucleator p
18	ä	ä	S	~	9080	minor curlin subun
19	91.5	ij	ß	0	9298	curlin minor chain
20	ä	ä	ß	~	0337	glycine-rich prote
21	91	н	7	~	5102	related to C2H2 zi
22	91	ä	S	~	9101	ical
23	91	ä	25	N	8586	ica
24	90.5	ij	4	~1	6455	mbrar
25	06	ä	0	7	2084	hypothetical prote
26	90	ä	7	7	3532	inase
27	σ	ä	œ	7	7067	PPE pro
28	89.5		Ø	7	027	z pr
50	6	11.5	4	2	0522	hypothetical prote

merozoite 45K surf probable PPE prote	- w	probable PPE prote hypothetical prote		nypornetical glycl probable PPE prote	protein F39D8.1b [	class 3 outer memb	probable sugar ABC	probable PPE prote	hemolysin (importe	CREB-binding prote
B39112 D70575	721956 G84687	D70604 B84533	B70663	E70663	D89723	S21409	D153	F70825	AI0452	T13828
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347	407	552 301	354	434 615	940 945	331	440	64	63	3190
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O O O	88 88.5	α0	. co	7 8	87:5	87	87	ω.	86.5	9
	3 E	ა ა 4 ი	9 0	~ 80 M M	w 4 ov ⊂	41				

### ALIGNMENTS

OV 12.1 NNAAL.VNYDOLVTRVVTHEMAHANNATANOV 15.1
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csg

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Curlin major subunit CsgA [imported] - Escherichia coli (strain O157:H7, substrain RIMD C.Species: Escherichia coli (c.Date: Escherichia coli (c.Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C.Accession: D90806 F.A.Flayashi, T.; Maxino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 F.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. A; Pitle: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gench A; Reference number: A99629; MUID:21156231; PMID:11258796 A; Accession: D90806 A; Accession: D90806 A; Accession: Dpreliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Description: major component of wild-type curli; interaction between CsgA and CsgB tr. A; Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli that and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers F;1-20/Domain: signal sequence #status predicted <SIG> F;21-151/Product: curlin #status experimental <MAT>
A.Title: The RpoS sigma factor relieves H-NS-mediated transcriptional repression of A;Reference number: S31202; MUID:93211294; PMID:8459772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs1420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          A.RESIGNES: 1-133. "...
A.Gross-references: EMBL.L04979; NID:9290424; PIDN:AAA23616.1; PID:9290425
A.Experimental source: strain K-12, substrain W3110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.9%; Score 520; DB 2;
66.9%; Pred. No. 4.7e-36;
ive 21; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
                                                                                                                                                                                                                                 A; Molecule type: protein
A; Residues: 21-42;44-50 < OLS2>
R; Olsen, A.N.; Arnqvist, A.M.
submitted to the EMBL Data Library, October 1992
A; Reference number: $34559
A; Accession: $34559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.9%;
Matches 101; Conservative 2
                                                                      A,Accession: S31202
A;Molecule type: DNA
A,Residues: 1-6,VV, 8-151 <OLS1>
A;Cross_references: EMBL:L04979
A,Accession: S34560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 23.15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: DNA
A,Residues: 1-152 <H
                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Simi
Matches 100;
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                                                                                                                                                                                                  "Gypecies: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09.Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: A10635
B;Parkhill, J; Dougan, G; James, K.D; Thomson, N.R; Pickard, D.; Wain, J.; Churcher, F., T.; Connerton, P; Cronnin, A.; Davis, P.; Davies, R.M; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gacra, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: A80502; MuID:21534947; PMID:11677608
A;Accession: A10635
A;Accession: A10635
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-151 - PARA
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A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-references: EMBL:X30754; NID:g1147558; PIDN:CAA62282.1; PID:g1147564
A; Experimental Source: strain Kl2, substrain W3110
A; Experimental Source: strain Kl2, substrain W3110
A; Experimental Source: strain Kl2, substrain W3110
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1895
B; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; A; Recession: G64846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Curlin protein csgA precursor - Escherichia coli (strain K-12)
NyAlternate names: csgA protein; major curlin protein
C;Speciaes: Escherichia coli
C;Speciaes: Bscherichia coli
C;Accession: S70788; G64846; S31202; S34560; S34559
E;Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S.
Mol. Microbiol. 18; 661-670, 1995
A;Thitle: Expression of two csg operons is required for production of fibronectin- and A;Reference number: S70783; MUID:96414468; PMID:8817489
                                                                                                                                                                              curlin chain precursor [imported] - Salmonella enterica subsp. enterica serovar
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A, Residues: 1-151 <PRE>
A, COSTO CADO8268.1; PID:g16502315; GSPDB:GN00176
C, Genetics:
A, Gene: STY1181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 695; DB 2;
Pred. No. 1.8e-50;
4; Mismatches 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                       NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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larity 90.1%;
Conservative
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Best Local Similarity
Matches 136; Conserv
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C,Accession: E95965
R,Finan, T.M.; Weldner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 989, 9889-9894, 2001.
A,Title: The complete sequence of the 1.683-4kb pSymB megaplasmid from the N2-fixing end: A,Reference number: A95842; MUID:21396508; PMID:11481431
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Abdubnors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, KA; Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
                                                                                                                                290/2; 327/3; 499/1; 573/2; 607/3; 708/3; 777/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical glycine-rich protein [imported] - Sinorhizobium meliloti (strain 1021)
C,Species: Sinorhizobium meliloti
C,Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----CQSNVQESTTTSSGGWGSSGSGN 1685
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A;Molacule type: DNA
A;Residues: 1-2174 <KUR>
A;Cross-references: GB:ALS91985; PIDN:CAC49389.1; PID:g15140875; GSPDB:GN00167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----GGYANTANVGFKGLTLTTQGSHAAGIVAQSVGGGGGGGGGTGCTASSYSAGIGFTASVAV 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 QWGGGGNHNGG---GNSSGPDSTLSIYQYGSANAALALQSDARKSETTIT----QSGYGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 AIVVSGSALAGVVPQ--WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 GADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQ--YGGNNAA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
13.4%; Score 104; DB 2; Length 2174;
Best Local Similarity 27.1%; Pred. No. 1.9;
Matches 35; Conservative 16; Mismatches 44; Indels 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 106; DB
; Pred. No. 1;
13; Mismatches
A,Cross-references: EMBL:X06462
C,Genetics:
A,Gene: cnjB.
A,Geneic code: SGC5
A,Introns: 85/3; 136/1; 157/3; 201/2; 290/2; C,Keywords: 21nd finger
F,1164-1450/Region: glyoine-rich
F;1451-1464/Region: zinc finger CCHC motif
F;1501-1514/Region: zinc finger CCHC motif
F;1501-1514/Region: zinc finger CCHC motif
F;1530-1543/Region: zinc finger CCHC motif
F;1551-1568/Region: zinc finger CCHC motif
F;1559-1568/Region: zinc finger CCHC motif
F;1559-1568/Region: zinc finger CCHC motif
F;1602-1615/Region: zinc finger CCHC motif
F;1602-1615/Region: zinc finger CCHC motif
F;1626-1748/Region: zinc finger CCHC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OFGGGGNSNGGOSWGTSSGSDWN---
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32.1%;
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Best Local Similarity
Matches 35; Conserv
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A;Gene: SMb21548
A;Genome: plasmid
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A;Cross-references: GB:AE005174; NID:g12514574; PIDN:AAG55788.1; GSPDB:GN00145; UWGP:Z16
A;Cross-references: ctrain O157:H7, substrain EDL933
C;Genetics:
A;Gene: csgA
                                                                                                                                                                                                                                                                                            hypothetical protein csgA [imported] - Escherichia coli (strain O157:H7, substrain EDL93
                                                                                                                                                                                                                                                                                                                                                                                                                   D.J.; Mayhew
K.; Apodaca,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A/Residues: 1-1748 <TAY>
B/Across-references: EmBL-103710; NID:g161751; PID:g161752
B/Taylor, F.M.; Martindale, D.W.
Nucleic Acids Res. 21, 4610-4614, 1993
A/Tesidue Retroviral-type zinc fingers and glycine-rich repeats in a protein encoded by cay. A/Residue type: DNA
A/Residue type: DNA
A/Residues: 1164-1174;1179-1198;1233-1252;1285-1293;1297-1309;1316-1326;1331-1341;1343-134;
A/Residues: 1164-1174;1179-1198;1233-1252;1285-1293;1297-1309;1316-1326;1331-1341;1343-134;
A/Residue Acids Res: 16, 2189-2201, 1988
A/Title: Multiple introns in a conjugation-specific gene from Tetrahymena thermophila.
A/Reference number: 803650; MUID:88189811; PMID:3357771
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   QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG 119
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                                                                                                                                                                                                                                                                                                                    Gispecies: Bacherichia con imported, particular cui (brian cui), sum cispecies: Bacherichia coli (c) bace; le Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 RyPerna, N.T., Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Inature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession. H85665
A;Accession. H85665
A;Accession. H85667
A;Accession. Preprintary
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Pred. No. 1.6e-34;
1; Mismatches 30; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cnjB protein - Tetrahymena thermophila
C;Species: Tetrahymena thermophila
C;Date: 19-Mar. 19-Mar. 19-Mar.
C;Accession: 842136; 842135; 830850
R;Taylor, F.M.; Martindale, D.W.
B;Equited to the EMBL Data Library, October 1992
A;Reference number: 842136
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A,Residues: 236-250,'I',252-255,'N',257-773 <MAR>
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64.4%; Score 501.5;
Best Local Similarity 65.8%; Pred. No. 1.6e
Matches 100; Conservative 21; Mismatches
                                                                                                                                   GGNGAAVDQTASNSTVNVTQVGFGNNATAHOY
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C;Species: Drosophila melanogaster
C;Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 21-Jul-2000
C;Accession: ASG038
B;Gartinkel, M.D.; Wang, U.; Liang, Y.; Mahowald, A.P.
Mol. Cell. Biol. 14, 6809-6818, 1994
A;Title: Multiple products from the shavenbaby-ovo gene region of Drosophila melanogast
A;Accession: ASG038
A;Accession: ASG038
A;Actus: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1028 cGAR>
A;Cross-references: GB:U11383; NID:g520526; PIDN:AAB60216.1; PID:g520527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ovo protesin - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Feb-1997
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Feb-1997
C;Accesion: 316356
EMBO J 10, 2259-2266, 1991
A;Title: The ovo gene of Drosophila encodes a zinc finger protein required for female shakeference number: $16356, MUID:91293102; PMID:1712294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 LLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1028;
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protein ovo - fruit fly (Drosophila melanogaster)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.6%; Score 98.5; DE ilarity 24.5%; Pred. No. 2.3; Conservative 15; Mismatches
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12.6%; Score 98.5; DE
Best Local Similarity 24.5%; Pred. No. 2.8;
Matches 46; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Gene: FlyBase:ovo
A,Cross-references: FlyBase:FBgn0003028
A,Introns: 931/3; 1152/3
                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: FlyBase: FBgn0003028
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A;Cross-references: EMBL:X59772
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                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
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DNA-binding
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                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: ovo
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S16356
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                 nuccase monoment of curlin monomers [imported] - Salmonella enterica subsp. enterica fingorted] - Salmonella enterica subsp. enterica serovar Typhi G; Species: Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi C; Baccession: AH0635
C; Accession: AH0635
R; Parkhill, J; Dougan, G; James, K.D; Thomson, N.R.; Pickard, D; Wain, J; Churcher, L, T. Connerton, P.; Cronin, A; Davis, P.; Davies, R.M.; Dowd, L.; Wain, J.; Farrar, S.; Moule, S; O'Gacra, P.
Nature 413, 848-852, 2001
A; Athile: Complete genome sequence of a multiple drug resistant Salmonella enterica serova; Ricture: Davies and A; Reference number: AB0502; MUD:21534947; PMID:1167608
A; Reference number: AB0502; MUD:21534947; PMID:1167608
A; Retains: preliminary
A; Molecule Cype: DNA
A; Residues: 1-151 < PAR>
A; Residues: 1-151 < PAR>
A; Residues: 1-151 < PAR>
A; Genetics:
A; Genetics:
A; Genetics:
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A. Cross-references: GB:U43280; NID:g1184712; PIDN:AAC43598.1; PID:g1184713
A. Cross-references: GB:U43280; NID:g1184712; PIDN:AAC43598.1; PID:g1184713
A. Experimental source: strain 276755-3b
A. Conetics:
A. Conetics:
A. Conetics:
A. Conetics:
A. Description:
A. Description:
A. Description:
A. Cross-reference and the fibronectin, plasminogen, tissue plasminogen activator
A. Note: fimbriae bind to fibronectin, plasminogen, tissue plasminogen activator
A. Note: fimbriae bind to fibronectin, plasminogen, tissue plasminogen activator
B. 1-21/Domain: signal sequence #status predicted <AMT>
F;22-151/Product: fimbrin protein agfB #status predicted <AMT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IGQVGTDNSA-RVRQEGSKLLSVISQEGENNRAKVDQAGNYNFAYIEQTGNANDASISQS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Salmonella enteritidis
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999
C;Accession: UC6040
R;Collinson, S.K.; Clouthier, S.C.; Doran, U.L.; Banser, P.A.; Kay, W.W.
J. Bacteriol. 178, 665-667, 1996
A;Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fin
A;Reference number: UC6039; MUID:96146512; PMID:8550497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 NAKNSDITVGQYGGNNAALVNYDQLVTRVVTHEMAH 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 AYGNSAAIIQKGSGNKANITQYGTQKTAVVVQKQSH 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.0%; Score 101.5; DB
30.2%; Pred. No. 0.15;
:ive 17; Mismatches
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Best Local Similarity
Matches 29; Conserv
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A;Molecule type: DNA
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probable exported protein YPO0309 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AH0038
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 1.7-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 15-Sep-2003
C;Accession: A70762
R;Cole, S.T. Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, T.; Connor, R.; Davies, R.; Perkhill, M.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Sequers, S.; Squares, S.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Squares, S. Ayukhors, Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Reference number: A70500; MUID:9829597; PMID:9634230
A;Accession: A70762
A;Accession: 
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A;Cross-references: GB:Z74020, GB:AL123456; NID:g3261584; PIDN:CAA98335.1; PID:e1300075
A;Eross-references: strain H37Rv
C;Genetics:
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A; Cross-references: GB: AL590842; PIDN: CAC89171.1; PID: g15978410; GSPDB: GN00175
                                                                                                                                                                                                                  61 IVGHQYGRHNLS-AVGQEGHDNYGSTTQNGNRNVAGIGQFGSNHTTLTJQDGNGNIAAGV 119
                                                                                                                                                                        45 LSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATID 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGYGNGADVGQGADNS-----TIELTQNGFRNNATIDQ--WNAKNSDITVGQYGGNN 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   384 SGSGNLG----FGNSGNGNIGFFNSG-NNNIGMGNSGNGGVGALSVEFGSSAERS-----
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                                 --- OMG---- GGGNHNGGGN--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           th 12.1%; Score 94.5; DB 2; Scimilarity 25.7%; Pred. No. 3.1; 39; Conservative 24; Mismatches 48;
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                                 LLKVAAFAAIVVSGSALAGVVP----
                                                                                                                                                                                                                                                                                                                   OWNAKNSDITVGQYGGNNAA 124
                                                                                                                                                                                                                                                                                                                                                                                       120 Q-VGRGCSANVSQGGNDNVA 138
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Best Local Similarity
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A, Status: preliminary
A, Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                   Conserved hypothetical protein Atu4768 [imported] - Agrobacterium tumefaciens (strain C5 (5) pecies: Agrobacterium tumefaciens C5 Joate: Il-Jan-2002 #sequence_revision Il-Jan-2002 #text_change 18-Nov-2002 (5) Accession: Ab3143 R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I Fragp, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 A; Aththors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pypothetical protein AGR L 228 [imported] - Agrobacterium tumefaciens (strain C58, Cered C, Species: Agrobacterium_tumefaciens C, Species: Agrobacterium_tumefaciens C, Species: Agrobacterium_tumefaciens C, Species: Agrobacterium_tumefaciens C, Species: C, Saccession: H98144
R, Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liuu F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A, Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A, Reference number: A97359; MUD:21608551; PMID:11743194
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-145 < KURA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ster, E.W.

A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A,Fitle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A,Accession: AD3143

A,Status: preliminary

A,Molecule type: DNA

A,Rolecule type: DNA

A,Rolecule type: DNA

A,Ecssidees: 1-145 < KKR>

A,Experimental source: strain C58 (Dupont)

A,Experimental source: strain C58 (Dupont)

A,Gene: Atu468

A,Gene: Atu468

A,Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .,
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   ----LVTRVVTHEMAHA 143
                                             45 LSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATID 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 LLKVAAFAAIVVSGSALAGVVP-----OWG----GGGNHNGGGN----SSGPDST 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 145;
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   ---ÖUÄNIA----
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0.41;
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Pred. No. 0.41;
3; Mismatches
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GenCore version 5.1.6
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779
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Title: Perfect score: Sequence:

Scoring table:

141681 seqs, 52070155 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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# ALIGNMENTS

STANDAR	01-OCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Major curlin subunit precursor (Fimbrin SEF17).	GN CSGA OR AGFA OR STWII44 OR STWII81 OR T1776.		OS Salmonella enteritidis. OC Bacteria: Proteobacteria: Gammaproteobacteria: Enterobacteriales:	Enterobacteriaceae; Salmonella.			RC SPECIES=S.typhimurium; STRAIN=SR-11; RX MEDLINE=98117058; PubMed=9457880;	Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;	RT "Curli fibers are highly conserved between Salmonella typhimurium and	KI ESCHERICHIA COLI WICH FESPECE CO OPERON SEINCEULE ANN LEGULACION: ; RL J. Bacteriol, 180:722-731(1998).			MEDLINE=21534948; PubMed=11677609;	RA MCCIelland M., Sanderson K.E., Spiech U., Cilicon S.W., Latzellie F., RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.	Leonard S., Nguyen C., Scott K., Holmes A			RT IT2."; DI Natura 413.852-856/2001)		RP SEQUENCE FROM N.A.		RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.	N Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,	RA Cronin.A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,			RA Whitehead S., Barrell B.G.;		KI Enceilca Selovar Iyphi Clis."; RL Nature 413:848-852(2001).		RP SEQUENÇE FROM N.A. RC SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;	MEDLINE=22531367; PubMed=12644504;	KA Delig W., Dicu WK., Fillinger G Litt, Mayica G.:
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J. Bacteriol. 173:4773-4781(1991).
-!- FUNCTION: CURLIN IS THE STRUCTUREL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURPRICE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 21-33.
SPECIES=S.enteritidis; STRAIN=27655-38;
MEDLINE=91310586; PubMed=1677357;
Collinson S.K., Emcedy L., Mueller K.-M., Trust T.J., Kay W.W.;
"Purification and characterization of thin, aggregative fimbriae from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                      SEQUENCE FROM N.A. STRAIN=27655-3B;
SPECIES=S.enteritidis; STRAIN=27655-3B;
MEDLINE=96146512; PubMed=8550497;
Collinson S.K., Clouther S.C., Doran J.L., Banser P.A., Kay W.W.;
"Salmonella enteritidis agfBAC operon encoding thin, aggregative
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 21-151 FROM N.A.
SPECIES-S. enteritidis; STRAIN-27655-3B;
MEDLINE-9401373; PubMed-8104955;
Doran J.L., Collinson S.K., Burian J., Sarlos G., Todd E.C.D.,
Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., Kay W.W.;
Manzo C.K., Tay C.M., Banser P.A., Peterkin P.I., Kay W.W.;
Inha-based diagnostic tests for Salmonella species targeting agfa, the structural gene for thin, aggregative fimbriae.";
J. Clin. Microbiol. 31:2263-2273(1993).
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Pred. No. 4.6e-51;
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Stygene, SG10608, csgA.
Fimbria, Signal, Complete proteome.
                                                                        Bacteriol. 185:2330-2337(2003)
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SEQUENCE OF 21-31.

MEDLINE=91310586; PubMed=1677357;

Collinson S.K., Emoedy L., Trust T.J., Kay W.W.;

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Collinson and characterization of thin, aggregative fimbriae from Salmonella enteritidis.";

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-!- FUNCTION: CTRLIN IS THE STRUCTUREL SUBUNIT OF THE CURLI. CURLI ARI COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN.
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Yano M., Horiuchi T.;
Yano M., Horiuchi T.;
And Sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
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SEQUENCE FROM N.A.
MEDLINE=9426617 PubMed=9278503;
Blatcher F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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MEDLINE=93023873; PubMed=1357528;

Arnqvist A., Olsen A., Pfeifer J., Russell D.G., Normark S.,

Arnqvist A., Olsen A., Pfeifer J., Russell D.G., Normark S.,

fine Cri protein activates cryptic genes for curli formation and
fibronectin binding in Escherichia coli HB101.";

MOI. Microbiol. 6:2443-2452(1992).
                                                                                                                                                                                                                                                                       MEDLINGERGALL.
Olsen A., Annqvist A.;
Olsen A., Annqvist A.;
The Rpos sigma factor relieves H-NS-mediated transcriptional
repression of csgA, the subunit gene of fibronectin-binding or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Ross
Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                               01-DEC-1992 (Rel. 24, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FFB-2003 (Rel. 41, Last annotation update)
151 AA.
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-K12 / W3110;
MEDLINE-93211294; PubMed-8459772;
                                                                                                                                                                                                                                                                                                                                       Escherichia coli.";
Mol. Microbiol. 7:523-536(1993).
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                                                                                                                                                             Enterobacteriaceae; Escherichia.
                                                                                             Major curlin subunit precursor
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/ MC4100;
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                                                                                                                               Escherichia coli.
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SEQUENCE FROM N.A.
[3]
SEQUENCE FROM N.A.
STRAIN=0157:H7 / R
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   SOUR DESIGNATION OF THE SERVICE SERVIC
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                                                              This SWISS-PROT entry is copyright, It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most fine institutions as long as its content is in no way modified and this statement is not removed, Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=21218556; PubMed=11319125;
Uhlich G.A., Keen J.E., Blder R.O.;
Mutations in the csgD promoter associated with variations in curli expression in certain strains of Escherichia coli 0157:H7.";
Appl. Environ. Microbiol. 67:2367-2370(2001).
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Enterobacteriaceae, Escherichia.
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C003470D208D395F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAJOR CURLIN SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.8%; Score 520; DB 1;
66.9%; Pred. No. 1.5e-36;
iive 21; Mismatches 29.
      SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY
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ID CSGA ECOS7

STANDARD; PRT; 152 AA.

AC 033U24.

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

Major curlin subunit precursor.

GN CSGA OR 21676 OR ECS1420.

OS Escherichia coli 0157:H7.
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STRAIN=0157:H7 / EDL933 / ATCC 700927;
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EMBL; X90754; CAA62282.1; -.
EMBL; AB000205; AAC74126.1; -.
EMBL; D90741; BAA35832.1; -.
EMBL; D90742; BAA35840.1; -.
PIR; S70789; S70788.
ECOGene; EG11489; Complete proteome.
SIGNAL:
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Matches 101; Conservative
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SEQUENCE FROM N.A..

SINGALN=6157.H. FIRD 0509952;

MEDLINE=21156231; PubMed=11258796;

Hayashi,T., Makino K., Ohnishi W., Kurokawa K., Ishii K., Yokoyama K., Hayashi,T., Makino K., Ohnishi W., Murata T., Tanaka M., Tobe T.,

Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

Kuhara S., Shiba T., Hattori M., Shinagawa H., Shinagawa H.,

"Complete genome sequence of enterohemorrhagic Escherichia coli

O157:H7.and genome sequence of enterohemorrhagic Escherichia coli

O157:H7.and genome comparison with a laboratory strain K-12.";

DNA Res: 8:11-22(201).

-! FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE

- FUNCTION: CURLIN STRUCTURES THAY ASSERMEDE PREFERENTIALLY AT GROWTH

TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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R EMBL; AP27573; AAK53212.1; -..

R EMBL; AP00554; BAB34843.1; -..

R EMBL; AP00254; BAB34843.1; -..

R EMBL; AP00256; Boodso.

PR; Dogoso, Dogoso.

RW Fimbria; Signal; Complete proteome.

BY SIMILARITY.

T 152 MAJOR CURLIN SUBUNIT.

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T 152 MAJOR CURLIN SUBUNIT.

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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Minor curlin subunit precursor.
SCSB OR STY180 OR T1777.
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Best Local Similarity 65.8
Matches 100, Conservative
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RESULT 6
OVO_DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 IYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQW 106
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                                                                                                                                                                                                                                                                                                                                                                J. Bacteriol. 185:2330-2337(2003).
-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELGIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-TZ-/ ATCC 700931, STRAIN-TZ-/ ATCC 700931, MEDLINE-22231367; PubMed=12644504; MeDLINE-22231367; PubMedt G. III, Mayhew G.F., Rose D.J., Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J., Burland V., Kodoylanni V., Schwartz D.C., Blattner F.R.; "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S., "Curli fibers are highly conserved between Salmonella typhimurium and Escherichia coli with respect to operon structure and regulation."; J. Bacteriol. 180:722-731(1998).
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Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBI_TaxID=602, 592;
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01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Minor curlin subunit precursor (Fimbrin SEP17 minor subunit).
CSGB OR AGFB OR STM1143.
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MINOR CURLIN SUBUNIT.
161C54326E573495 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 NAKNSDITVGQYGGNNAALVNYDQLVTRVVTHEMAH 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 AYGNSAAIIQKGSGNKANITQYGTQKTAVVVQKQSH 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 30.2%; Pred. No. 0.071
Matches 29; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=S.typhimurium; STRAIN=SR-11;
MEDLINE=98117058; PubMed=9457880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE016840; AA069400.1; -. Fimbria; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL627269; CAD08267.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 AA; 16254 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella typhimurium, and Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                   Nature 413:848-852(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURLIN MONOMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SALTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P55226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteriol. 178:662-667(1996).
- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COILED SURPACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DESCREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                           SPECIES=S.typhimurium, STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 IGQVGTDNSA-RVRQEGSKLLSVISQEGGNNRAKVDQAGNYNFAYIEQTGNANDASISQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 IYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQW
                                                                                                                                                                                                                           Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=96146512; PubMed=8550497;
Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W.W.;
"Salmonella enteritidis agfBAC operon encoding thin, aggregative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
MINOR CURLIN SUBUNIT.
; COFC5430E6DD361D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.9%; Score 100.5; DB 1;
30.2%; Pred. No. 0.086;
iive 17; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 AYGNSAAIIQKGSGNKANITQYGTQKTAVVVQKQSH 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P51521; 09XZU4;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
0VO protein (Shaven baby protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ā
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ002301; CAA05316.1; -.
EMBL; AB008749; AAL20073.1; -.
EMBL; U43280; AAC43598.1; -.
PIR; JC6040; JC6040
StyGene; SG10609; csgB.
Fimbria; Signal; Complete protecome.
SIGNAL
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Best Local Similarity 30.2%
Matches 29, Conservative
                                                                                                                                                                                                                                                                                                                                                               Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURLIN MONOMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 AA;
[2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fimbriae."
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LONDADADAYIMSAGSG-----GGGCTGNGGGGASGPGGGSANSGGGGGGGG----- 104

LLKVAAFPAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD

65;

Length 1028;

5; DB 1; 1.1; 62;

12.6%; Score 98.5; w. 24.5%; Pred. No. 1.1; iive 15; Mismatches

46; Conservative

... 50.

1028 AA; 110620 MW; D7068BB2BC0F6F77 CRC64;

Query Match Best Local Similarity Matches 46; Conserv SEQUENCE S gg g 엄 ò ò ò ò RECURRICE FROM N.A.

SEQUENCE FROM N.A.

(2) SEQUENCE FROM N.A.

(2) STARIN=Oregon-R;

WEDLINE=91233102; PubMed=1712294;

Mevel-Naio M.T.M., Terracol R., Kafatos F.C.;

Mevel-Naio M.T.M. Terracol R., Terraco SEQUENCE FROM N.A.

TISSUE-Ovary,
MEDLINE=95021209; PubMed=7935398;
Garfinkel M.D., Wang J., Liang Y., Mahowald A.P.,
"Multiple products from the shavenbaby-ovo gene region of Drosophila
melanogaster: relationship to genetic complexity.";
Mol. Cell. Biol. 14:6809-6818(1994). HERETEREREES AND DRAWN NO DRAW BRANK NA BRANK NA

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EMBL, X59772; CAB36921.1; ALT\_SEQ.
HST, ASCO38, ASCO38.
HSSP, P07248; ZADR.
TRANSFAC; T00669; -.

Repeat; Nuclear protein; 5 POLIY-GLY.
POLIY-GLY.
POLIY-GLY.
POLIY-GLY.
POLIY-GLN.
POLY-GLN.
POLY-GLN.
POLY-GLN.
POLY-ALA.
POLY-GLN.
POLY-GLN.
POLY-GLN.
POLY-CLN.
POLY-TYPE J.
CZHZ-TYPE J. | FlyBase | Troubbe | TryBase | TryB

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30-MAY-2000 (Rel. 39, Created)
40-MAY-2000 (Rel. 39, Last sequence update)
50-MAY-2010 (Rel. 40, Last annotation update)
60-CT-2011 (Rel. 40, Last annotation update)
60-CT-2011 (Rel. 40, Last annotation update)
60-CT-2011 (Rel. 40, Last annotation)
60-CT-2011 (Lel. 80, Last antigen)
60-CT-2011 (Lel. 80, Last antigen)
60-CT-2011 (Surface antigen)
60-CT-2011 (Surface protein (Surface protein antigen)
61-CT-2011 (120 kDa outer membrane protein ompB); 32 kDa beta peptidel. similarity).

-!- FUNCTION: THE 32 KDa BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR (BY similarity).

-!- SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a Stager with hexagonal symmetry.

-!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY. 63 ARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDI-----VERAIN-YH;
UCHIYAMA I.;
Uchiyama I.;
"Sequencing of the gene encoding the protein rOmp B of Rickettsia
"Sequencing",
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR
-I- FUNCTION: THE PACTOR WHICH MAY PLAY A ROLE AS A RICKETISIAL
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (By Rickettsia japonica. Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales, Rickettsiaceae, Rickettsieae, Rickettsia. NCBI\_TaxID=35790, 120 kDa SURFACE-EXPOSED PROTEIN. 32 kDa BETA PEPTIDE. POLY-GLY. 1656 AA. EMBL; AB003681; BAA20138.1; -.
InterPro; IPR006315; Autotransport.
InterPro; IPR006346; Autotransporter.
Pfan; PF03797; Autotransporter; 1.
TIGRFAMS; TIGR01414; autotrans\_bar1; 2.
Autigen; S-layer; Cell wall.
CHAIN 1339 1656
DOMAIN 528 533 POLY-GLY. PRT; STANDARD; 144 NNATANOY 151 213 GQFNASAY 220 SEQUENCE FROM N.A. STRAIN=YH; RICJA 105 114 OMPB\_RICJA ID OMPB\_R 

432

72

Gaps

41;

491

511

Matches

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à g ò

S

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15 SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ--SDARKSETTITQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGYGNGADVGQGADNS-----TIELTQNGFRNNATIDQ--WNAKNSDITVGQYGGNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               384 SGSGNLG----FGNSGNGNIGFFNSG-NNNIGMGNSGNGVGALSVEFGSSAERS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21602874; PubMed=11739745;
Cook B.D., Dynek J.N., Chang W., Shostak G., Smith S.;
"Role for the related poly(ADP-Ribose) polymerases tankyrase 1 and 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith S., de Lange T.;
"Cell cycle dependent localization of the telomeric PARP, tankyrase,
to nuclear pore complexes and centrosomes.";
J. Cell Sci. 112:3649-3656(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20556282; PubMed=10988299;
Chi N.-W., Lodish H.F.;
Tankyrase is a Golgi-associated mitogen-activated protein kinase
substrate that interacts with IRAP in GLUT4 vesicles.";
J. Biol. Chem. 275:38437-38444(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OS271; 095272;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 41, Last annotation update)
11-OCT-2003 (Rel. 42, Last annotation update)
11-OCT-2003 (Rel. 42, Last annotation update)
11-OCT-2003 (Rel. 42, Last annotation update)
11-OCT-2003 (Rel. 41, La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith S., Giriat I., Schmitt A., de Lange T.,
"Tankyrase, a poly(ADP-ribose) polymerase at human telomeres.";
Science 282:1484-1487(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol. Cell. Biol. 22:332-342(2002).
-!- FUNCTION: May regulate vesicle trafficking and modulate the subcellular distribution of SLC2A4/GLUT4-vesicles. Has PARP activity and can modify TRFI, and thereby contribute to the
                                                                                                                                                                                                                                                                                                                                                                   / Match 12.1%; Score 94.5; DB 1; Length 678; Local Similarity 25.7%; Pred. No. 1.5; etc. 39; Conservative 24; Mismatches 48; Indels 4:
                                                                                                                                                                         Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                    258 D -> G (IN REF. 2).
66736 MW; 209F1593D52533A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION, AND MUTAGENESIS OF HIS-1184 AND GLU-1291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 AALVNYDQLVTRVVTHEM-----AHANNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------LVTGSMGLFNSGHTNTGSFN
Tuberculist, Rv1548c; -.
InterPro; IPR000030; Microbac_PPE.
InterPro; IPR002989; Mycobac_Dentapep.
Pfam; PF01469; Pentapeptide_2; 11.
Pfam; PF00823; PPE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
TISSUE=Testis;
                                                                                                                                                                                                                                        POTENTIAL
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Mol. Cell. Biol. 22:332-342(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [3] FUNCTION, AND PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                     34
200
258
                                                                                                                                         3; Frb, 14 34 14 34 180 200 258 256 678 AA; 6
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                                                                                                                                                                  Hypothetical p
TRANSMEM 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN
                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                          Query Match
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TNK1 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
       AND AND TEFFS
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                                                                                                                                                                                                                                            66 SETTITQSG----YGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVG--QYG 119
                                                                                                                                                                                                                                                                                                                                                                                            ---TLTLGGANIISANGGTINFQANGGTIKLTST--QNNIVVD-----CDLAIATDQTG 596
                                                                                                                                                                                              6 VAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=9825987; PubMed=9634230; Carnier T., Churcher C., Harris D., Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Cordon S.V., Englaneir K., Gas S., Barry C.E., III, Trekaia F., Badcock K., Englaneir K., Gas S., Barry C.E., III, Tekaia F., Davies R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Seeger K., Skelton R., Radiandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; Bocchhering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Mature 393:537-544(1998).
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STRAIN-CDC 1551 / Oshkosh;
MEDLINE-22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Neidman J., Khouri H., Gill J., Mikula A.,
Bishal W., Jacobs W.R. Jr., Veneer J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                     38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                               12.5%; Score 97; DB 1; Length 1656; 28.3%; Pred. No. 2.6;
1656 AA; 168097 MW; 3132A69C9DD5999F CRC64;
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-!- SIMILARITY: Belongs to the mycobacterial PPE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical PPE-family protein Rv1548c/MT1599.
RV1548C OR MT1599 OR MTCY48.17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              597 VVDASSLTNAQTLİISGİIGİNANTTLGÖF 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 GNNAALVNYDQLVTRVVTHEMAHANNATANQY 151
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                                                                                                                                  19; Mismatches
                                                                                                                                                                                                                                                                 509 VLAAGAITLDGSATI-----TGDIGNGGG-
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EMBL, AE07026; AAK45866.1; ALT_INIT.
BIR; A70762; A70762.
TIGR; WT1599; -.
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                                                                                                                                  Conservative
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                                                                                           Similarity
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Q10778;
SEQUENCE
                                                               Query Match
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regulation of telomere length.

-!-CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribosyl} (N)-acceptor = nicotinamide + {ADP-D-ribosyl} (N-1)-acceptor.
-!-SUBUNIT: Oligomerizes and associates with TNKS2. Interacts with the Cytoplasmic domain of LNEEP/Ordse in SLC2A4/GLUT4-vesicles.
-!-SUBCELLULAR LOCATION: Cytoplasmic, associated with the Golgi and with juxtanuclear SLC2A4/GLUT4-vesicles.
-!-SUBCELLULAR LOCATION: Cytoplasmic, associated with the Golgi and with juxtanuclear sore scores of a minor proportion is also found at nuclear pore complexes and around the pericentriolar matrix of mitotic centromeres. During interphase, a small fraction of TNKS is found in the nucleus, associated with TRF1.
-!-ALTERNATIVE PRODUCTS:
-!-Event-Alternative splicing, Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF082555; AAC79841.1; -.

R EMBL; AF082555; AAC79841.1; -.

R EMBL; AF082555; AAC79844.1; -.

R EMBL; AF082559; AAC79844.1; -.

R EMBL; AF082559; AAC79844.1; -.

R HSSP; Q00420; LAWC.

Genew; HGNC:11941; TNKS.

MIM; 603303; Protein binding; IPI.

GO; GO:0003950; F:NAD ADP-ribosyltransferase activity; IDA.

GO; GO:0005115; F:Protein binding; IPI.

GO; GO:0005115; F:Protein binding; IPI.

GO; GO:0005115; F:Protein binding; IPI.

GO; GO:0007004; P:telomerase-dependent telomere maintenance; NAS.

R InterPro; IPR00160; SAW.

R InterPro; IPR01606; SAW.

R Fam; PF0013; ANK; 19.

R PRINT; SM00449; ANK; 17.

SMART; SM00449; ANK; 17.

SMART; SM00454; SAW; 1.

R PROSITE; PS50089; ANK REPERT; 15.

R PROSITE; PS50105; SAW_DOMĀIN; 1.

R PROSITE; PS50105; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; ANK REPERT; 
                                                                                                                                                                                                                                                                                                                                                                    IsoId=095271-2; Sequence=VSP 004538, VSP 004539;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Ubiquitous; highest levels in testis.
PTM: Upon insulin-stimulation, phosphorylated on serine residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PTM: ADP-ribosylated (-auto).
-!- SIMILARITY: Belongs to the PARP family.
-!- SIMILARITY: Contains 15 ANK repeats.
-!- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
                                                                                                                                                                                                                                                                                                                               IsoId=095271-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANK 1. ANK 2. ANK 2. ANK 3. ANK 4. ANK 4. ANK 5. ANK 6. ANK 6. ANK 9. ANK 11. ANK 112. ANK 113. ANK 113. ANK 115. ANK 115.
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99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
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STRAIN=K12 / MC4100;
MEDLINE=96414648; Pubmed=8817489;
Hammar M., Arnqvist A., Bian Z., Olsen A., Normark S.;
Hammar M., Actorist A., Bian Z., Expension of two csg operons is required for production of fibronectin- and congo red-binding curli polymers in Escherichia coli
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                                                                                                                                                                                                                 EST -> GHS (in isoform 2).
/FIId=VSP 004538.
Missing (in isoform 2).
/FIId=VSP 004539.
H-A: LOSS OF ACTIVITY; WHEN ASSOCIATED WITH A-1291.
E-A: LOSS OF ACTIVITY; WHEN ASSOCIATED
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STRAIN=K12 / MG1655;
STRAIN=K12 / MG1655;
STRAIN=K12 / MG1655;
SILON STRAIN=K12 / MG1655;
Blattner F.R., Plunket G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.,
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1995 (Rel. 31, Created)
01-CT-1996 (Rel. 34, Last sequence update)
01-CT-1996 (Rel. 34, Last sequence update)
Minor curlin subunit precursor.
CSGB OR: B1041 OR Z1675 OR BCS1419.
Escherichia coll, and
Escherichia coll, and
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacterials, Enterobacteria, Escherichia.
Enterobacteriaceae; Escherichia.
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1327 AA; 142010 MW; B14DB985C710B957 CRC64;
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POLY-PRO.
POLY-SER.
POLY-SER.
EST -> GH
    SAM.
PARP.
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MEDLINE=97061202; PubMed=8905232;
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Best Local Similarity 30.4%
Watches 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses, dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
T4-like viruses.
NCBI_TaxID=10664;
          89 NLAYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQYGTQKTAIVV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=91156685; PubMed=2000383;
Smythe J.A., Coppel R.L., Day K.P., Martin R.K., Oduola A.M.J.,
Kemp D.J., Anders R.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum (isolate Nig32 / Nigeria).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
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01-0cT-1996 (Rel. 34, Last sequence update)
01-0cT-1996 (Rel. 34, Last annotation update)
Merozoite surface antigen 2 precursor (MSA-2).
                                                                                                                                                                                                                                                                 01-AUG-1988 (Rel. 08, last sequence update) 01-AUG-1990 (Rel. 15, last annotation update) Receptor recognizing protein (Protein Gp38).
                                                                                                                                                                            262 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.3;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         347 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 NSTIELTQNGFRNNATIDQWNAKNSDIT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----RGWGKNVYTSEGGAAGAAVT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.5%; Score 89.5; 34.1%; Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, X05312; CAA28935.1; -.
PIR; S00275; S00275.
InterPro; IPR007932; Tall_fibre_GP38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam, PP65268, GP38, 1. Fiber protein, Phage recognition. SEQUENCE 262 AA, 25801 MW, 05
                                                                                                                                                                                                                                         01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequ
01-AUG-1990 (Rel. 15, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Best Local Similarity
Matches 30; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AS RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                              Bacteriophage T2
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                                                                                                                                                                         VG38 BPT2
P07875:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arngvist A., Olsen A., Normark S.,
"Sigma S-dependent growth-phase induction of the csgBA promoter in
"Sigma S-dependent growth-phase induction of the csgBA promoter in
Escherichia corli can be achieved in vivo by sigma 70 in the absence
of the nucleoid-associated protein H-NS.";
Mol. Microbiol. 13:1021-1032(1994).
-! FUNCTION: CRELIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE
COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-0157.H7 / RIMD 0509952;
MEDLINE-21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                    STRAIN=015:H7 | EDL933 / ATCC 700927;

MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Appodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
corresponding to the 12.7-28.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 SETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
MINOR CURLIN SUBUNIT.
; B18D266B964014B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURLIN MONOMERS.
SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AE000205; AAC74125.1; --
EMBL; D00741; BAA35831.1; --
EMBL; AE005315; AAG55787.1; --
EMBL, AE00554; BAB34842.1; --
FIR; C90806; C90806.
FIR; G90806; C90806.
FIR; S70787; S70787.
ECGGne; EG12621; CSGB.
Fimbria; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95157246; PubMed=7854117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15882 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [6]
SEQUENCE OF 1-21 FROM N.A.
                                   DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Best Local Similarity
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                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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RALE REPARE REPA

SEQUENCE

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RESULT 14
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                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 ETTITQSGYGNGA--DVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99
                                                                                                                                                                                                                                                                     POTENTIAL.

MEROZOTTE SURFACE ANTIGEN 2.

HYDROPHOBLELC, REMOVED DURING MATURATION

(BY SIMILARITY).

POLYMORPHIC REGION.

POLYTHR.

N-LINKED (GLCNAC. .) (POTENTIAL).

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 AAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 AGNGAGNGAGNGAGNGAGNGAGNGAVASAGNGAGNGAVASAGNGAVAERSSSTPATTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 AGNGAVASAGNGAGNGAGNGAGNGAGNGAGNGAG-----NGAGNGA---GNGÀGNG
'Structural diversity in the Plasmodium falciparum merozoite surface
                                                                                -!- DEVELOPMENTAL STAGE: During the trophozoite and schizont stages.
                                                          a GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
       antigen 2.",
Proc. Natl. Acad. Sci. U.S.A. 88:1751-1755(1991).
-!- FUNCTION: May play a role in the merozoite attachment to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773, 1765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES=M.tuberculosis; STRAIN=H37RV;
MEDLINE=98295997; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                              11.4%; Score 89; DB 1; Length 347; 23.4%; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82; Indels
                                                                                                                                                                                                                         InterPro; IPR001136; MSA_2.
Pfam; PF00985; MSA_2; 1.
Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypotherical glycine-rich protein Rv2098c/MT2159/Mb2125c.
RV2098C OR MTX159 OR MTX49.38C OR MB2125C.
Mycobacterium tuberculosis, and
                                                          ρχ
                                                          membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                491 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Mismatches
                                               erythrocyte.
-!- SUBCELLULAR LOCATION: Attached to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 TTTNDAEASTSTSSENSNHNNAETN 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 LVNYDQLVTRVVTHEMAHANNATAN
                                                                                                                                                                                                                                                                                                                                                                                                                        33786 MW;
                                                                                                                                                                                                    EMBL; M59765; AAA29691.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                     323
                                                                                                                                                                                                                                                                GPI-anchor; Merozoite
SIGNAL 1
                                                                                                                                                                                                                 PIR; B39112; B39112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                          144
222
224
226
326
3206
347
347
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347
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                                                                      (Potential).
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CARBOHYD
CARBOHYD
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CARBOHYD
CARBOHYD
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send; an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74
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Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SPECIES—M. unberculosis; STRAIN-CDC 1551 / Oshkosh;
MEDLINE-22206494; PubMed=12218036;
MEDLINE-22206494; PubMed=12218036;
MEDLINE-22206494; PubMed=12218036;
MEDLINE-22206494; PubMed=12218036;
MEDLINE-22206494; PubMed=12218036;
Melscher R.D., Mitchen D., Rickey E., Relson W., Deboy R., Gwinn M., Haft D., Hickey E., Rollony J.F., Nelson W., Gwinn M., Salzberg S.L., Bishai W., Jacobs W.R. Jr., Wendman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 59. Ref.1 sequence has been checked by authors in Ref.1 and they report that no errors have been found.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SPECIES=M.Dovis; STRAIN=AF2122/97;
SPECIES=M.Dovis; STRAIN=AF2122/97;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
The complete genome sequence of Mycobacterium bovis.";
The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100,7877-7882(5033).
-: SIMILARIIY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock, K., Babham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Humphy L., Olsborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., Complete genome sequence.", Barrell B.G., Complete genome sequence.", Mycobacterium tuberculosis from the Nature 393:537-544 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00934; PE; 1. Process; PF00034; PE; 1. Probom; PD001223; PE region; 1. Protochetical protein, Complete proteome. CONFLICT 312 312 G -> GG (IN REF. 1). SEQUENCE 491 AA; 41979 MW; 12C8630C59CA0C13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, 273966; CAA98228.1; ALT_FRAME.
EMBL, AE007065; AAK46440.1; -.
EMBL; BX248341; CAD96978.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory strains.";
J. Bacteriol. 184:5479-5490(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro, IPR000084; PE_region.
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nes 30; Conservative
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Tuberculist; Rv2098c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBFAMILY
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PER_DROWI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAALALQSDARKSETTITQSGYGN----GADVGQGADNSTIELTQNGFRNNATIDQWNA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 NGLKAIWQVEQKASIAGTDSGWGNRQSFIGLKGGFG--KLRVGRLNSVLKDTGDINPWDS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 LKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGS-----A 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 LPVAAMADVTLYGTIKAGV--ETSRSVEHNGGQVVSVETGT-GIVDLGSKIGFKGQEDLG 69
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAINS-CUG 37604 / M981 / Serogroup B / Serotype 4;
STRAINS-CUG 37604 / W981 / Serogroup B / Serotype 4;
WARDIANNE-99051225; PubMed-1330818;
Ward M.J., Lambden P.R., Heckels J.E.;
Ward M.J., Lambden P.R., Heckels J.E.;
Serotype proteins and relationships between meningococcal class 3
serotype proteins and other porins from pathogenic and non-pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Outer membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAJOR OUTER MEMBRANE PROTEIN P.IB.
                               01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Major outer membrane protein P.IB precursor (Protein IB) (PIB)
(Porin) (Class 3 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CU385 / Serogroup B / Serotype 4 / Subtype 15;
MEDLINE=93116587; PubMed=1335540;
Sapate G.A., Vann W.F., Rubinstein Y., Frasch C.E.;
"Identification of variable region differences in Neisseria meningitidis class 3 protein sequences among five group B
                                                                                                                                            Neisseria meningitidis (serogroup B).
Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: Homotriner.
-!- SUBUNIT: Homotriner.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Outer
-!- SIMILARITY: Belongs to the Gram-negative porin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 KNSDITVGQYGGNNAAL - VNYDQLVTRVVTHEMAHANNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol. Microbiol. 6:3493-3499(1992).
-!- FUNCTION: Serves as a slightly cation selective porin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NG -> KR (IN STRAIN CU385).
35EA35B7EBD28301 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S21409; S21409.
PIR; S28441; S28441.
InterPro; IPR001701; Porin Gram-ve.
Pfam; PF00267; Gram-ve_porins; 1.
PRINTS; PR00182; BCOLNEIPORIN.
PROSITE; PS0766; GRAM_NGS_PORIN.
Outer membrane; Porin, Transmembrane; Antigen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.5%; Pred. No. 2.8; ive 23; Mismatches
331 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.2%; Score 87;
                                                                                                                                                                                                                                                                                                                                                                       FEMS Microbiol. Lett. 73:283-289(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            331 AA; 35741 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X65531; CAA46501.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                   Neisseriaceae; Neisseria.
STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                         NCBI_TaxID=491;
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 OMB2 NEIMB
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Mol. Biol. Bvol. 10:127-139(1993).

Mol. Biol. Bvol. 10:127-139(1993).

Mol. Biol. Bvol. 10:127-139(1993).

-!-FUNCTION: Essential for biological clock functions. Determines the period length of circadian and ultradian rhythms; an increase in period length of circadian and ultradian rhythms and a decrease leads to shortened circadian rhythms and a decrease leads to lengthened circadian rhythms. Essential for the circadian rhythmic component of the male courtship song that originates in the thoracic nervous system. The biological cycle depends on the complex Light induces the degradation of TIM, which promotes complex. Light induces the degradation of TIM, which promotes elimination of PRR. Nuclear activity of the heterodamer coordinatively regulates PER and TIM transcription through a negative feedback loop. Behaves as a negative element in circadian transcriptional loop. Does not appear to bind DNA, suggesting indirect transcriptional inhibition (By similarity).

-!- SUBCELLULAR LOCATION: Nuclear at specific periods of the day.

-!- PTM: PHOSPHORYATED WITH A CIRCADIAN RHYTHMICITY, PROBABLY BY THE DOUBLE-TIME PROTEIN (DET). PHOSPHORYLATION COULD BE IMPLICATED IN THE STABILITY OF PER MONOMER AND IN THE FORMATION OF HETERODIMER DOUBLE-TIME PROTEIN (DET). PHOSPHORYLATION COULD BE IMPLICATED IN MISCELLANBOUS: THE SEQUENCE SHOWN IS THAT OF STRAIN ATLIXCO.

-!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                           STRAIN=Various strains;

MEDIJNE=97357421; PubMed=9214747;
Gleason J.M., Powell J.R.;
"Interspecific and intraspecific comparisons of the period locus in the Drosophila willistoni sibling species.";
Mol. Biol. Evol. 14:741-753(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peixoto A.A., Campesan S., Costa R.H., Kyriacou C.P., "Molecular evolution of a repetitive region within the per gene of
                                                                                                    Drosophila willistoni (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7260;
             003297; 018421; 018422; 191721; 191722; 01-0CT-1993 (Rel. 27, Created) 15-ULL-1998 (Rel. 36, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update)
1093 AA
                                                                                16-OCT-2001 (Rel. 40, Last annotati
Period circadian protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 579-646 FROM N.A.
MEDLINE=93196482; PubMed=8450754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, U51055, AAB41360.1, -..
EMBL, U51056, AAB41361.1; -..
EMBL, U51058, AAB41363.1; -..
EMBL, U51059, AAB41363.1; -..
EMBL, U51059, AAB41363.1; -..
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US1061; AAB41366.1;
US1062; AAB41367.1;
STANDARD;
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
PER DROWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
EMBL;
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721 GGGGGGGGGGGGGLPLFLDVTHTSS------SSQNKGPTGVAAGGAGGCVGGGGG-- 770
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POLY-LYS.
POLY-LYS.
POLY-CER.
POLY-CER.
POLY-CER.
POLY-CER.
POLY-CER.
POLY-ALA.
T -> A (IN STRAIN 0811.4).
G -> F (IN STRAIN 0811.4).
G -> A (IN STRAIN MANNUS 2).
G -> S (IN STRAIN MANNUS 2).
MISSING (IN STRAIN PORTO ALEGRE 4).
MISSING (IN STRAIN MANNUS 1 AND MANNUS 3).
MISSING (IN STRAINS MANNUS 1 AND MANNUS 3).
MISSING (IN STRAINS MANNUS 1 AND MANNUS 3).
MISSING (IN STRAINS DANNUS 1 AND MANNUS 3).
MISSING (IN STRAINS DANNUS 4, PORTO PORTO ALEGRE 1 AND MUSSING (IN STRAINS MANNUS 4, PORTO ALEGRE 1 AND MUSSING (IN STRAINS MANNUS 4, PORTO ALEGRE 1 AND MUSSING (IN STRAINS MANNUS 4, PORTO ALEGRE 1 AND MISSING (IN STRAINS MANNUS 2).
MISSING (IN STRAINS MANNUS 2).
MISSING (IN STRAINS MANNUS 3).
MISSING (IN STRAINS MANNUS 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
11.0%; Score 86; DB 1; Length 1093;
Best Local Similarity 27.2%; Pred. No. 13;
Matches 25; Conservative 6; Mismatches 45; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEAR LOCALIZATION SIGNAL (POTENTIAL) PAS 1.
PAS 2.
EMBL; US1063; AAB41368.1; -.

REMBL; US1066; AAB41369.1; -.

REMBL; US1066; AAB41370.1; -.

REMBL; US1066; AAB41370.1; -.

REMBL; US1066; AAB41370.1; -.

REMBL; US1066; AAB41370.1; -.

REMBL; US1069; AAB41370.1; -.

REMBL; US1069; AAB41370.1; -.

REMBL; US1070; AAB41370.1; -.

REMBL; US1070; AAB41377.1; -.

REMBL; US1070; AAB4137.1; -.

REMBL; US106011; PAS, 12.

REMBL; US1070; AAB4137.1; -.

REMBL; US10611; PAS, 12.

REMBL; 
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Search completed: August 2, 2004, 14:49:27 Job time : 6.3 secs

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August 2, 2004, 14:39:17; Search time 29.7 Seconds (without alignments) 1604.150 Million cell updates/sec
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779
1 MKLLKVAAFAAIVVSGSALA......VTRVVTHEMAHANNATANQY 151
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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1: Sp_archea:*
2: sp_bactera:*
3: sp_lungi:*
4: sp_lungi:*
5: sp_inverser:*
6: sp_mammal:*
7: sp_info:*
7: sp_phage:*
7: sp_phage:*
7: sp_plant:*
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7: sp_vir
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Gapop 10.0 , Gapext 0.5
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# Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	033802 salmonella	Q7x243 citrobacter	Q7x240 citrobacter	OBcw63 escherichia	07x237 enterobacte	Q54069 salmonella	Q9s3j5 escherichia	O8y106 ralstonia s	Q8xsd6 ralstonia s	Q7xdr3 oryza sativ	Oseih4 shewanella	094821 tetrahymena	09xcj4 salmonella	O8zn57 salmonella	Q841y5 campylobact	092uu8 rhizobium m
SUMMARIES	ΩI	033802	Q7X243	Q7X240	Q8CW63	Q7X237	Q54069	Q9S3J5	98Y106	Q8XSD6	Q7XDR3	Q8EIH4	094821	Q9XCJ4	Q8ZN57	Q841Y5	092UU8
	DB	7	7	7	16	7	7	7	16	16	10	16	Ŋ	7	16	7	16
	Query Match Length DB	152	150	149	152	150	76	29	3501	3552	191	502	1748	2035	2039	1286	2174
₩	Query	88.1	75.9	68.9	63.6	54.9	49.4	15.7	14.6	14.6	13.9	13.7	13.6	13.5	13.5	13.4	13.4
	Score	989	591.5	537	495.5	427.5	385	122	113.5	113.5	108.5	107	106	105	105	104.5	104
	Result No.	н	73	m	4	S	9	7	60	σ	10	11	12	13	14	15	16

	Q8u6n9 agrobacteri Q88B90 pseudomonas Q8914 bradyrhizob Q9n6m8 drosophila Q9kka8 rickettsia Q840u5 rickettsia Q8kb4 rickettsia Q8kb4 rickettsia Q9kb4 rickettsia Q9mgf6 drosophila
QBEIH3 QBNIV1 QSEFU3 QOEETU3 QOX241 QOX244 QOX85 QOW4F0 QORTEL9 QORTEL9 QORTEL9 QORTEL9 QORTEL9 QORTEL9 QORTEL9 QORTEL9 QOYGE	Q8U6N9 Q88HG0 Q89J14 Q9N6M8 Q9EKA8 Q9EKA8 Q9EKB4 Q9CKB4 Q9KKB4 Q9KKB4
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### ALIGNMENTS

Database :

28

Created)

01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel, 25, 01-OCT-2003 (TrEMBLrel. 25,

Curlin-csgA protein.

CSGA. Citrobacter

SEQUENCE FROM N.A. STRAIN=Fec2;

PRELIMINARY;

Q7X243; 07X243

RESULT 2 Q7X243

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60 QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG 119
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1 MKLLKVAAFAAIVVSGSALAGVVPQW--GGNHHGGGSNYGPDSSLSIYQYGSNNSANALQ
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriacee, Escherichia.
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STRAIN=Fec39;
Zogaj X., Bokranz W., Nimtz M., Romling U.;
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01-MAR-2003 (TrEMBLrel. 23, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
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STRAIN=Fec4;
Zogai X., Bokranz W., Nimtz M., Romling U.;
Zogai X., Bokranz W., Nimtz M., Romling U.;
Zogai X., Bokranz W., Nimtz M., Romling U.;
Zogai X., Bokranz W., Nimtz M., Romling U.;
Enreduction of Cellulose and Curli Fimbriae by Members of the Family
Enreduction of Cellulose and Curli Fimbriae by Members of the Family
Enreduction of Cellulose and Curli Find Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insurance Insura
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"Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract."; Infect. Immun. 72:4151-4158 (2003).
EMBL: AJS15700; CADS6672-11; -. SEQUENCE ISO AA, 15016 MW; 1D7141B8D6973DC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Enterobacteriaceae; Citrobacter.
NCBI_TaxID=213763;
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Enterobacteriaceae; Citrobacter.
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75.9%; Score 591.5; DB 2; Length 150;
Best Local Similarity 77.5%; Pred. No. 6.7e-38;
Matches 117; Conservative 14; Mismatches 19; Indels 1
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68.9%; Score 537; DB 2; Length 149;
Best Local Similarity 71.5%; Pred. No. 9.7e-34;
Matches 108; Conservative 17; Mismatches 24; Indels
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Last annotation update)
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Last annotation update)
            121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
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Q7X240 PRELIMINARY; Q7X340; 01-0CT-2003 (TEMBLEEL: 2: 01-0CT-2003 (TEMBLEEL: 2: 01-0CT-2003 (TEMBLEEL: 2: Curlin-csgA protein.

Citrobacter freundii.

SEQUENCE FROM N.A. NCBI\_TaxID=546;

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NCBI_TaxID=305;
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                                            SEQUENCE
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Matches
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Q8Y106
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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Cox J.M., Eglezos S., Woolcock J.B.;
Cox J.M., Eglezos S., Woolcock J.B.;
virulence of Salmonella enteritidis in chickens correlates with colony morphology and expression of SEF17 fimbriae.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; US3207; AAA98671.1; -.
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"Production of Cellulose and Curli Fimbriae by Members of the Enterobacteriaceae Isolated from the Human Gastrointestinal Infect. Immun. 72:4151-4158 (2003).
EMBL, AJ515702, CAD56678.1; -SEQUENCE 150 AA; 15112 MW; 5D8BB2D872DF15F3 CRC64;
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Pred. No. 1.9e-22;
0; Mismatches 1; Indels
                                                                                                                              Length
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Last annotation update)
                                                                                                                          Score 427.5; DB 2
Pred. No. 2.3e-25;
6; Mismatches 36
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58.3%; Pred
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                                                                                                                                            Local Similarity 58.3
les 88, Conservative
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Best Local
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Q9S3J5
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TRANSPOSON-Insertion sequence IS1;

MEDLINE=99314153; PubMed=10386375;

La Ragione R.M., Collighan R.J., Woodward M.J.;

La Ragione R.M., Collighan R.J., Woodward M.J.;

IS1 inserti on in csgB and reduced persistence in poultry infection.";

PEMS Microbiol. Lett. 175:247-253 (1999).

PEMS Microbiol. Lett. 175:247-253 (1999).

SEMBL; AJ131756; CA845380.1; -..

SEQÜENCE 29 AA; 2789 MW; E290DFC07ABBB243 CRC64;
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MEDLINEE=2081879; PubMed=11823852;
Salanoubat M., Ganin S., Artiguenave F., Gouzy J., Mangenot S.,
Salanoubat M., Choise N. Claudel-Renard C., Cunnac S., Demange N.,
Arlat M., Eillault A., Brottier P., Camus J.C., Cattolico L.,
Arlat M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
Chandlar M., Choisen N., Claudel-Renard C., Cunnac S., Demange N.,
Agapin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
Melsenbach J., Boudener C.A.,
Melsenbach J., Bouder C.A.,
Melsenbach J., Bouder C.A.,
Melsenbach J., Bouder C.A.,
Melsenbach J., Bouder C.A.,
Melsenbach J., Boudeler C.A.,
Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach J., Melsenbach
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
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Pred. No. 0.0078;
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Last annotation update)
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01-MAR-2002 (TrEMBLrel. 20, Last sequen
01-CCT-2003 (TrEMBLrel. 25, Last annota
Probable hemagglutinin-related protein.
RSC0887 OR RS06116.
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Best Local Similarity 28.8
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26; Conservative
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chromosome 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 LALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-GMI1000;
Manded=11823852;
Manded=121681879;
Manded Manin S., Artiguenave F., Gouzy J., Mangenot S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Genin S., Artiguenave F., Camus J.C., Cattolico L., Arlat M., Choisne N., Claudel-Frenard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Walseenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502(2002).
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OSJNBB0039P10.07G10.
OSJNBB0039P10.07G10.
Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 28.8%; Pred. No. 8.4;
Matches 36; Conservative 19; Mismatches 43; Indels 27;
                                                                                                                                                                                                                                                                                                                           Plasmid megaplasmid.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF05594; Fil haemagg; Z0.
Pfam; PF05860; Haemagg; act; 1.
PROSITE; PS01070; NUCLEASE NON_SPEC; 1.
Plaemid; Complete proteome: SEQUENCE 3552 AA; 352934 MW; CS432AABE2CCF59C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGSALAGVVPQWGGGGNHNGGG-NSSGPDSTLSIYQYGSANAA---
                                                                                                                                                                                                Last sequence update)
Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                   Probable hemagglutinin-related protein.
RSP0540 OR RS06117.
Ralstonia solanacearum (Pseudomonas solanacearum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gacule Alegan Alegan Alegan Alegan Bolt, I. J. Go. Go. 0046821; C:extrachromosomal DNA; IEA. Go. Go. 0046821; C:extrachromosomal DNA; IEA. Go. Go. 00046821; F:endonuclease activity; IEA. Go. Go. 0003676; F:nucleic acid binding; IEA. InterPro; IPR008619; Fil. haemagg. InterPro; IPR008619; Fil. haemagg. Fil. Pro5594; Fil. haemagg. Zo.
                                                                                                                           PRT; 3552 AA
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01-MAR-2002 (TrEMBLrel. 20, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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2542 DLGGN 2546
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Q7XDR3;
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                                                                          RESULT 9
                                                                                                     90SX8Ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 GGGGGGGYSQYGGSGSGSGSGSGSSQTSQNGYYGYGSSSAGGSGAGAGAGQAGGYWP 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 GSALAGVVPQWGGGGNHNGGGNSSGPDSTL--SIYQYGSANAALALQSDARKSETTITQS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 DARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGN 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 GYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAAL 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10; Length 191;
[1]
SEQUENCE FROM N.A.
STRAIN=cv. Nipponbare;
STRAIN=cv. Nipponbare;
Fig. Chromosome 10 Sequencing Consortium;
"In-depth view of structure, activity, and evolution of rice
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=cv. Nipponbare;
Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q
Submitced (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AE01701; AAPS4078.1; -.
SEQUENCE 191 AA; 17021 MW; 95A246FBIIDE3ACS CRC64;
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52441 MW; D08CA23D6C46B62D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59;
                                                                                                                                                                                                                                                                                                                                                                                                                                             13.9%; Score 108.5; DE 29.5%; Pred. No. 0.72; ative 15; Mismatches
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EMBL; AE015532; AANS3941.1; -.
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                                                                                                                                                                            Science 300:1566-1569(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33; Conservative
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Best Local Similarity 27.3%
Marches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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SEQUENCE 502 AA; 52
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Best Local Similarity
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MEDLINE-94051569; PubMed=8233798;

A Taylor F.M., Martindale D.W.;

Taylor F.M., Martindale D.W.;

Taylor F.M., Martindale D.W.;

Taylor F.M., Martindale D.W.;

The recoded by cnjB, a Tetrahymena gene active during meiosis.";

Nucleic Acids Res. 21:4610-4614(1993).

REBL; X06462; CAB3723.1; -.

REBL; X06462; CAB37323.1; -.

REBL; X06462; CAB37323.1; -.

REBL; X06462; Prucleic acid binding; IEA.

RESP; PO5889; LAAF.

RESP; PO5889; LAAF.

RESP; PO5889; LAAF.

RESP; PO003676; Prucleic acid binding; IEA.

REPROSTE: PRO01979; ZF.CCHC; 7.

REPROSTE: PS001973; ZF.CCHC; 7.

REPROSTE: PS0118; ZF.CCHC; 7.

REPROSTE: PS0118; ZF.CCHC; 7.

REPROSTE: PS0118; ZF.CCHC; 7.

THE CONFLICT 251 ZF.CCHC; 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tetrahymena thermophila.
Eukaryota, Alveolata, Ciliophora, Oligohymenophorea, Hymenostomatida;
Tetrahymenina, Tetrahymena.
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Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCB_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=88189811; PubMed=3357771;
Martindale D.W., Taylor F.M.,
Multiple introns in a conjugation-specific gene from Tetrahymena thermophila.";
Nucleic Acids Res. 16:2189-2201(1988).
                                                                                                                                                                                                                                                                      Q94821 PRELIMINARY, PRT; 1748 AA. 094821; P92146; P92147; P92143; P92141; Q94820; C1-FEB-1997 (TEMBLrel. O2, created) C1-FEB-1997 (TEMBLrel. O2, created) C1-FEB-1997 (TEMBLrel. O2, Last sequence update) C1-FEB-1997 (TEMBLrel. O2, Last sequence update) C1-CCT-2003 (TEMBLrel. 25, Last annotation update)
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I -> N (IN REF. 1).
dw; OBO3F210104008A3 CRC64;
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Last annotation update)
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Pred. No. 14;
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1748 AA; 199624 MW;
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2...дс. 7.
251
256
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32.1%;
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Best Local Similarity
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SEQUENCE FROM N.A.
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    N 122
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01-NOV-1999 (
01-NOV-1999 (
01-MAR-2003 (
ShdA.
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    122
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Q94821
Q94821
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Q9XCJ4
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to the C-terminal region of AIDA, ICAA, subspecies I specific,
Peyer's patch colonization and shedding factor.
SHDA OR STM2513.
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MEDLINE=21534948; PubMed=11677609;
McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
McClelland M., Sanderson K.E., Spieth J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
LTZ.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STLSIYQYGSANA--------ALALQSDARKS-ETTITQSGYGNGADVG
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                                                                                                                                                                                                                                                                                                                                                    "Complete sequence of the xseA-hisS intergenic region of the S. enterica serotype Typhimurium genome and its distribution within the genus Salmonella.";
Salmonella.";
Submittéd (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFT40550; AAD25110.2; -.
InterPro; IPR005546; Autotransporter.
InterPro; IPR004899; Pertactin.
InterPro; IPR002173; PfkB.
Pfam; PF03797; Autotransporter; 1.
Pfam; PF03797; Autotransporter; 1.
TICRFAMS; TIGR01414; autotrans_barl; 3.
PROSITE; PS00584; PFKB_KINASES_2; 2.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                              to Salmonella
to warm blooded
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                                                                                                                                                                                                                                                                                                Kingsley R.A., van Amsterdam K., Edwards E.W., Hargis B.M.,
Baumler A.J.,
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                                                                                                                                                                          to the EMBL/GenBank/DDBJ databases
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                                                    Kingsley R.A., van Amsterdam K., Baumler A.J.;
"The presence of a pathogenicity island specific
enterica subspecies I correlates with adaptation
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26.3%; Pred. No. 20;
tive 20; Mismatches
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tes 54; Conservative
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Submitted (JUN-1999)
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SEQUENCE FROM N.A STRAIN=ATCC14028;
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"Characterization of the Campylobacter fetus saph promoter: evidence
that the saph promoter is deleted in spontaneous mutant strains.";
J. Bacteriol. 174:5916-5922(1992).
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Campylobacteraceae; Campylobacter.
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MEDLINE=91035477; PubMed=2229082;
Blaser M.J., Gotschlich E.C.;
"Surface array protein of Campylobacter fetus. Cloning and gene
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"Surface array protein of Campylobacter fetus. Cloning and gene
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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26.3%; Pred. No. 20;
iive 20; Mismatches 61;
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                                                                                                                                              InterPro; IPR004899; Pertactin.
InterPro; IPR004899; Pertactin.
InterPro; IPR002173; PfkB.
Pfam; PF03797; Autoriansporter; 1.
Pfam; PF031212; Pertactin; 1.
TIGRPAMS; TIGR01414; autorians_barl; 3.
PR051TE; PS00584; PFKB_KINASES_2; 2.
Complete proteome.
SEQUENCE 2039 AA; 207127 MW; 894E41F81
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                             EMBL, AEO08813; AAL21407.1; -.
InterPro; IPR006315; Autotransport,
InterPro; IPR005546; Autotransporter.
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J. Biol. Chem. 265:19372-19372(1990)
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STRAIN=23D;
MEDLINE=90354448; Pubmed=2387868;
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Best Local Similarity 26.3
Matches 54: Conservative
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Nature 413:852-856(2001)
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STRAIN=23D;
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MEDLINE=93348254; PubMed=8346244;
Tummuru M.K., Blaser M.J.;
"Rearrangement of sapA homologs with conserved and variable regions in Campylobacter fetus.";
Proc. Natl. Acad. Sci. U.S.A. 90:7265-7269(1993).
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J. Bacteriol, 180:6450-6458(1998).
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PubMcd=12694614;
Tu Z.C., Wassenaar T.M., Thompson S.A., Blaser M.J.;
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                                                                                                                                    MEDLINE=55204338; PubMed=7896695;
Dworkin J., Tummuru M.K., Blaser M.J.;
M.A lipopolysaccharide-binding domain of the Campylobacter fetus S-
layer protein resides within the conserved N terminus of a family of
silent and divergent homologs.",
J. Bacteriol. 177:1734-1741(1995).
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Thompson S.A., Shedd O.L., Ray K.C., Beins M.H., Jorgensen J.P.,
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EMBL, AY211269; AAO64216.1; -.
InterPro; IPROGA64; Autoriansporter.
Ffam; P031997; Autoriansporter; 1.
SEQUENCE 1286 AA; 134079 MW; AIFF9CEG34158789 CRC64;
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13.4%; Score 104.5; Best Local Similarity 27.8%; Pred. No. 13; Matches 44; Conservative 26; Mismatches
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Job time : 31.7 secs
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OM protein - protein search, using sw model

Run on:
August 2, 2004, 14:35:42; Search time 44.9 Seconds
(without alignments)
950.215 Million cell updates/sec

Title:
Berfect score: 775
Sequence:
1 MKLLKVAAFAAIVVSGALA......HASVMVRQVGFGNNATANQY 151
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107
Minimum DB seq length: 2000000000
Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Database : A Geneseq 29Gan04:\*

1. geneseqp1980s:\*
2. geneseqp1990s:\*
3. geneseqp2000s:\*
5. geneseqp201s:\*
6. geneseqp2038s:\*
7. geneseqp2033as:\*
8. geneseqp2003bs:\*

8: geneseqp2004s:\*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		47 AgfA::	52 AgfA::	346	25 Agf	_	70	3355	353	5349	5350	332	3321	3348	5343	2651	7	3569	2664	2663 FN	5316 8	s S		5326	5338 5	Aab36325 Salmonell
SUMMARIES	ID		AAB36347	AAB36352	AAB36346	AAR74625	AAB36341	AAW23570	535	AAB36353	AAB36349	AAB36350	335	'n	AAB36348	AAB36343	ABR82651	AAR62761	AAW23569	AAR52664	AAR52663	AAB36316	AAB36318	AAB36321	AAB36326	AAB36338	AAB36325
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3 AAB36339	3 AAB36320	7 ABR82644	3 AAB36340	3 AAB36324	3 AAB36319	3 AAB36344	3 AAB36342	7 ABR82645	6 ABU21488	3 AAB36323	3 AAB36336	3 AAB36328	3 AAB36331		5 AAU79538	3 AAY44404	5 AAU79539	3 AAY44402	3 AAB27212
22	22	24	23	23	23	151	151	56	186	13	13	13	23	673	673	949	949	1327	1327
14.8	14.8	14.6		14.1	14.1	13.5	12.7	12.6	12.3	12.0	12.0	12.0	11.9		11.9	11.9		11.9	11.9
 115	115	113	109	109	109	104:5	98.5	.6	95	6	93	93	92	92	92	92	92	92	92
26	27	28	29	30	31	32	en en	34	i CC	36	37	38	36	4	43	42	43	44	4.5

# ALIGNMENTS

RESULT 1  ABB36347  ABB36347  ABB36347  XX  ABB36347  XX  ABB36347  XX  ABB36347  XX  ABB36347  XX  ABB36347  XX  ABB36347  XX  ABB36347  XX  ABB36347  XX  Salmonella, agfA, chromosomal gene replacement; fimbrin; epitope; waccine; immune response; immunogen.  XX  Salmonella enteritidis.  Synthetic.  XX  WO200061102-A2.  XX  YX  YX  YX  YX  YX  YX  YX  YX  Y
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copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant Agfa protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonalia, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant Agfa protein which is useful feliciting an immune response in an animal. In a finbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inspensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                           MKLLKVAĀFĀAIVVSGSALĀGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAĀLĀLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ
                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                , Score 775, DB 3; Length 151;
, Pred. No. 5.4e-67;
0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AgfA::PT3#7 amino acid sequence SEQ ID NO:24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 138; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB36352 standard; protein; 151 AA
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                                                                                                                                                                                                                                                                                                                                                  100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella enteritidis.
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                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 151; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAC64628
                                                                                                                                                                                                                                                                                                               Sequence 151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA control encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbries (SEF17/TAF) nucleation depended assembly system of strains of Salmonella. Escherichia coli and control control control coli and the production of fimbries comprising recombinant control conformation of a recombinant gene into the chromosome of the homologue species; (3) directing recombinant gene into the chromosome of the homologue species, replacing the native comprising separating an aminologue species, replacing the native comprising separating an aminologue of the homologue species in an animal, comprising separating a replacement segment or segments of foreign animo containing a replacement segment or segments of foreign animo containing a replacement segment or segments of foreign animo containing a replacement segment or segments of foreign animo containing a replacement segment or segments of foreign animo containing a replacement segment or segments of foreign animo containing a replacement segment or segments of foreign animo containing a replacement segment or segments of foreign animo containing a replacement segment of a limbrial presentation containing a response in an animal. In a fimbrial presentation cyperced to system the hererologues antigens are presented in high numbers (up to system the hererologues antigens are presented in high numbers (up to concine, the carrier fimbrial submit protein are usually strong immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial submit proteins are usually strong immunogenist the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKN-----YDQ 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 LVTRVVTHEMAHA-----SVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 714; DB 3; L. Pred. No. 4.3e-61; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AgfA::PT3#1 amino acid sequence SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccine; immune response; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ā
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-OCT-2000
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(UYVI-) UNIV VICTORIA.

WO9425598-A2

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative finbriae (SERIY/TAR) nucleation depended assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and AgfA, homologue finbrin subunits, respectively; (2) directing recombination of a recombinant gene compounds to the chromosome of the homologues species, (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the colymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a finhight in the contained that the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal.
                                                                                                                            Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SDARKSETTITQSGYGNGADVGQGADNSTIBLIQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQ--- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 696; DB 3; Length 151;
Pred. No. 2.4e-59;
0; Mismatches 0; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----YDQLVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
                   Kay WW;
                                                                                                                                                                                                                       Disclosure; Page 135; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR74625 standard; protein; 151 AA.
                   Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
                     Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                              WPI: 2000-672631/65.
                                                                                        N-PSDB; AAC64622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 151 AA;
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26-JUN-1995
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                     White AP,
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SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Salmonella AgfA protein and DNA are used in vaccine and genetic immunization compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                      Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
                                                                                                                                                                                                                                                                                                                                                                                                         1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                      Length 151;
                                                                                                                                                                                                                                                                                                                                                             11; Indels
                                                                                                                              Doran JL;
                                                                                                                                                                                                                                                                                                                                    Score 693; DB 2;
Pred. No. 4.7e-59;
3; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                           UNIV VICTORIA INNOVATION & DEV CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kay MW;
                                                                                                                              Clouthier SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB36341 standard; protein; 151 AA
                                                                                                                                                                                                                             Disclosure, Fig 7B; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-APR-2000; 2000WO-CA000356.
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                                            94WO-IB000207
                                                                     93US-00054452
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 90.7%;
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella enteritidis.
                                                                                                                              Collinson SK,
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                                                                                                                                                     WPI; 1994-358275/44.
N-PSDB; AAQ87467.
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                                                                                                                                                                                                                                                                                                                  Sequence 151 AA;
                                                                                                       KING J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200060102-A2.
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                                               26-APR-1994;
                                                                     26-APR-1993;
                       10-NOV-1994.
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                                                                                                                              Kay WW,
                                                                                            (DYVI-)
                                                                                                       (KING/)
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AAB36341
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AIND (-IAAD)
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US5635617-A.
                                          03-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-OCT-2000
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                                                                                                                                                            The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA segment of thin aggregative fimbriae (SEF1/7AE) muleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacterriaceae for the production of fimbriae comprising recombinant depended directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a recombinant gene into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence polymer into the animal in conjunction with a carrier or dilutent. (I) is useful for the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to 500,000 coptes/cell), the hybrid fimbrian protein possesses both the immunogenic the inserted epitope, and hybrid fimbriae are usually strong immunogens, which may be important for directing an immune response is given in the exemplification of the present invention in the exemplification of the present invention
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                                     Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 693; DB 3; Length 151;
Pred. No. 4.7e-59;
3; Mismatches 11; Indels
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Misc-difference 123
/note= "Encoded by GCC"
                                                                                                                              Disclosure; Page 135; 139pp; English.
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Best Local Similarity 90.7%;
Matches 137; Conservative 3
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(first entry)
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29-SEP-1997
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61 SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritdis 2765-3b. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or eneropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide propriet or the sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                           Isolated Salmonella gene agfA - used for diagnosis of Salmonella or enteropathogenic bacteria of the Enterobacteria family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.3%; Score 692; DB 2; 90.7%; Pred. No. 5.8e-59; iive 3; Mismatches 11;
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                                                                                                                        VICTORIA INNOVATION & DEV CORP.
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                                                                                                                                                                                        Doran JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Fig 7; 85pp; English
94US-00233788
                                                            93US-00054452
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                                                                                                                                                                                        Kay WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                                 WPI; 1997-309886/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                  N-PSDB; AAT74142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 151 AA;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA concerns which encodes a foreign epicope or antigen. Also described are: (1) use of thin aggregative fimbries (SERIA/TAR) mucleation depended assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and anticoli and control of a recombination of fimbries comprising recombinant of directing recombination of a recombination of a recombinant gene composed species, (3) directing recombination of a recombinant gene copy of that gene, and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or containing an immune response in an immune coli polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant for an efficient live of system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein see usually strong immunogencity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial submuit proteins are usually strong immunogens, which may be important for an elevant for an efficient live vaccine, the carrier fimbrial submuit protein see usually strong aminorems which may be important for an elevant for an efficient live the exemplification of the present invention
                                                                                                                                                                                                                              Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                     Kay WW;
                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 139; 139pp; English.
                                                                                                        Collison SK,
99US-0127888P
                                                  UYVI-) UNIV VICTORIA.
                                                                                                        Doran JL,
                                                                                                                                                                                      N-PSDB; AAC64631
  05-APR-1999;
                                                                                                        White AP,
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Sequence 151 AA;

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SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
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                                                                                                                  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                        30;
tch 85.0%; Score 659; DB 3; Length 151; al Similarity 81.9%; Pred. No. 9.1e-56; 136; Conservative 0; Mismatches 0; Indels 3
                                                                                                                                                                                                                                     121 LVTRVVTHEMAHA------SVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                        106 LVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
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        Query Match
                          Best Local
Matches 13
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Salmonella, agfA, chromosomal gene replacement, fimbrin, epitope, vaccine, immune response, immunogen.
                                                              AgfA::PT3#8 amino acid sequence SEQ ID NO:26.
                                          (first entry)
                                          26-FEB-2001
                     AAB36353;
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AAB36353 standard; protein; 151 AA.

AAB36353 RESULT

121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbried (SEPI)/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and control of a recombination control of the production of fimbried comprising recombinant GAGA, CSGA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene (comprising seperating a recombinant gene into the chromosome of the homologus species, replacing the native comprising separating an amino acid polymer comprising separating an amino acid polymer comprising separating an amino acid polymer comprising separating an amino acid polymer comprising separating an amino acid polymer comprising separating an amino acid polymer comprising separating an amino acid polymer comprising separating a replacement segment or segments of foreign amino correcting an immune response in an animal. Ecoli or correcting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to conquence) the carrier fimbrial subunit protein sale usually strong immunogens, which may be important for an efficient live vaccine; the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response confinence is given in the expensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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Pest Local Similarity 81.5%; Pred. No. 3.2e-51;
Matches 123; Conservative 5; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151
                                                                                                                                                                                                                                                                                                       Kay WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVTRVVTHEMAHASVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                                                                                                                         Collison SK,
                                                                                                                                                                                 05-APR-2000; 2000WO-CA000356.
                                                                                                                                                                                                                         99US-0127888P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 138; 139pp;
                 Salmonella enteritidis.
                                                                                                                                                                                                                                                                 (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                                                            Doran JL,
                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-672631/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAC64629
                                        Escherichia coli
                                                                                                 WO200060102-A2
                                                                                                                                                                                                                         05-APR-1999;
                                                                                                                                            12-OCT-2000
                                                                                                                                                                                                                                                                                                              White AP,
                                                            Synthetic.
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                            agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 611; DB 3; Length 151;
Pred. No. 4e-51;
6; Mismatches 22; Indels
                                                         AgfA::PT3#4 amino acid sequence SEQ ID NO:18.
                                                                                                                                                                                                                          Kay WW;
                                                                                                                                                                                                                                                                                                     Disclosure, Page 136, 139pp, English.
                                                                                   vaccine; immune response; immunogen.
        AA.
                                                                                                                                                                                                                          Collison SK,
      AAB36349 standard; protein; 151
                                                                                                                                                                       05-APR-2000; 2000WO-CA000356.
                                                                                                                                                                                        99US-0127888P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 81.5%;
Matches 123; Conservative
                                         (first entry)
                                                                                                  Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                        (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                          Doran JL,
                                                                                                                                                                                                                                          WPI; 2000-672631/65.
N-PSDB; AAC64625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 151 AA;
                                                                                                                                     40200060102-A2.
                                                                                                                                                                                        05-APR-1999;
                                         26-FEB-2001
                                                                          Salmonella;
                                                                                                                                                      12-OCT-2000
                                                                                                                    Synthetic.
                                                                                                                                                                                                                         White AP,
                       AAB36349;
AAB36349
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA casegment of the gene has been replaced by a segment of a foreign DNA casegment of this encodes a foreign epitope or antigen. Also described are: (1) use of this encodes a foreign epitope or antigen. Also described are: casembly system of strains of Salmonella, Escherichia coli and content of the comparising recombination of Enterobacteriaceae for the production of fimbriace comprising recombinant on of a recombination of a recombinant gene into the chromosome of the homologue species, replacing the native copy of that gene; and (4) eliciting an immune respons in an animal, copy of that gene; and (4) eliciting an immune respons in an animal, comprising separating a replacement sequent or sequence or sequences grown on a Salmonella, E. coli or comprising separating an amino acid polymer comprising a replacement sequence or sequences grown on a Salmonella, E. coli or contenting an ential in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the hererologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live carrier the inserted epitope, and hybrid fimbria are usually strong immunogens, which may be important for directing an immune response conservancing the inserted epitope, and hybrid fimbrial semined easy and incomined against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given the exemplification of the present invention

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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenticity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in

The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitcope or antigen. Also described are: (I) use of thin aggregative finbriae (SER17/RAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae compitising recombinant of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the back into the chromosome of the homologous species, replacing the native copy of that gene; (3) directing recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising apparating a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation eliciting an immune response in an animal. In a fimbrial presentation 61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKOSDITVGQYGG 120 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120 Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal. Salmonella, agfA, chromosomal gene replacement, fimbrin, epitope, vaccine, immune response, immunogen. AgfA::PT3#5 amino acid sequence SEQ ID NO:20. Kay WW; 121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY Disclosure, Page 137, 139pp, English. Collison SK, AAB36350 standard; protein; 151 05-APR-2000; 2000WO-CA000356. 26-FEB-2001 (first entry) Salmonella enteritidis. Escherichia coli. (UYVI-) UNIV VICTORIA. White AP, Doran JL, WPI; 2000-672631/65. N-PSDB; AAC64626. WO200060102-A2. 05-APR-1999; 12-OCT-2000 Synthetic 61 AAB36350; RESULT 10 AAB36350 ò d à g

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Doran JL,
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                                                                                                                                                           Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200060102-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                               SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
                                                                                                                                                                       SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                      9
                                                                                                                        1 MKLLKVAAFFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                  chromosomal gene replacement; fimbrin; epitope;
                                                                         .,
                                             Score 609; DB 3; Length 151;
Pred. No. 6.3e-51;
5; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                           AgfA::PT3#9 amino acid sequence SEQ ID NO:28.
 of the present invention
                                                                                                                                                                                               121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                        151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kay WW
                                                                                                                                                                                                                Disclosure; Page 138; 139pp; English.
                                                                                                                                                                                                                                                                                    AAB36354 standard; protein; 151 AA.
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                                                78.6%;
81.5%;
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                                                                                                                                                                                                                                                                                                                                                                                               vaccine; immune response;
                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Doran JL,
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N-PSDB; AAC64630.
the exemplification
                                                          Local Similarity
es 123; Conserv
                                                                                                                                                                                                                                                                                                                                                                                  agfA;
                          Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200060102-A2.
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                                                                                                                                                                                                                                                                                                                                   26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                  Salmonella;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              White AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
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                                                 Query Match
                                                               Best Loca
Matches
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SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
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Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a finbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid finbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier finbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  i MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmoneila; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 603; DB 3;
Pred. No. 2.4e-50;
4; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AgfA::PT3#6 amino acid sequence SEQ ID NO:22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
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Matches 122; Conservative
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cc (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and casembly system of strains of Salmonella, Escherichia coli and Enterbacteriacae for the production of fimbriae comprising recombinant of monologous species, (3) directing recombination of a recombinant gene of the chomosome of the homologous species, replacing the active the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a replacement sequent or sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is confirmed to the combinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the hererologous antigens are presented in high numbers (up to conjuct or copies (cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong communogens, which may be important for directing an immune response cagainst the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in constant of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.7%; Score 602; DB 3, 81.5%; Pred. No. 3e-50; iive 5; Mismatches ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 123; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA segment which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative finbriae (SEP1/7AR) incleation depended assembly system of strains of Salmonella, Escherichia coli and Encaraceae for the production of finbriae comprising recombinant of a recombination of a recombinant pene into the chromosome of the homologous species, replacing the native comprising species, 3) directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising are combinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or dilutent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to compise/Cell), the hybrid finbrin protein possesses both the
                                              Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient liv vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 578; DB 3; Length 15
Pred. No. 6.3e-48;
6; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli CsgA amino acid sequence SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
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                                                                                                                                          Disclosure; Page 136; 139pp;
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Best Local Similarity 80.8%;
Matches 122; Conservative
                                           agfA
N-PSDB; AAC64624
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Plasma protein; immune response; antibacterial; vaccine; gene therapy
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                                                                                                                                   30-JAN-2003; 2003WO-EP000943.
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                                                                                                                                                                                                    (HANS-) HANSA MEDICAL RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 68.2
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                   or Shigella infections
                                                                                                                                                                                                                                 Bjoerck L, Olsen A,
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Job time : 44.9 secs
                                                                                                                                                                                                                                                                   WPI; 2003-646136/61.
                                   Escherichia coli.
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                                                                                                                                                                                                                                                                                  N-PSDB; ACF36153
                                                                    WO2003064446-A2
                                                                                                  07-AUG-2003
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                                                                                                                                                                                                                                                                           The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epicope or antigen. Also described are: (1) use of thin aggregative finbries (SEPI/TAP) nucleation depended assembly system of strains of Salmonella, Eschericha coli and assembly system of strains of Salmonella, Eschericha coli and constraint of salmonella, Eschericha coli and adfact in the production of fimbries respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising the native copy of that gene, and (4) eliciting an immune response in an animal, comprising separating a replacement sequent or sequents of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or enteronome of the host cell, from the host cell and introducing the coliciting an immune response in an animal. The finbrial presentation system the heterologous antigens are presented in high numbers (up to cliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to concours, the carrier fimbrial subunit protein are usually strong immunogens, which may be important for directing an immune response consequence, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response in an invested epicope, and hybria fimbrial are are assy and inexted epicope, and hybrial fimbrial are are seasy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                    Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kay WW;
                                                                                                                                                                                                                                                   Disclosure; Page 135; 139pp; English.
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                                                                                                     Collison SK,
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     05-APR-2000; 2000WO-CA000356.
                                    99US-0127888P.
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Matches 104; Conservative
                                                                    (UYVI-) UNIV VICTORIA
                                                                                                     Doran JL,
                                                                                                                                     WPI; 2000-672631/65.
                                                                                                                                                    N-PSDB; AAC64619
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                                    05-APR-1999;
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                                                                                                     White AP,
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The invention relates to an isolated peptide capable of binding a mammalian plasma protein or of generating an immune response in a mammal selected from sequences shown in ABRR2642, ABR264649. The peptide or antibody is useful for treating a bacterial infection in a human or animal or in the manufacture of a medicament for the prophylactic treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infection. The peptide that is immobilized on a solid support is also useful as a reagent for determining the ability of a plasma protein, to bind to bacteria. The present sequence represents an E. coli 15 kba protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
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                                                                                                                                                                                         New isolated peptide capable of binding a mammalian plasma protein, useful in the manufacture of a medicament for the prevention and/or treatment of a bacterial infection, such as Escherichia coli, Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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Herwald
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                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 41-42; 42pp; English
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August 2, 2004, 14:40:48 ; Search time 12 Seconds (without alignments) 649.627 Million cell updates/sec
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I MKLLKVAAFAAIVVSGSALA.......HASVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                             389414 segs, 51625971 residues
                                                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### STIMMARTES

	g			8, Appli	8, Appli	10, Appl	10, Appl	2, Appli	2, Appli	8, Appli	3, Appli	10, Appl	32096, A	4	_	131, App	204, App	30227, A	3401, Ap	13, Appl	5, Appli	5187262	2, Appli	11518, A	2, Appli	4, Appli	4, Appli	4, Appli
SUMMARIES	Description	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Seguence	Seguence	Sequence	Seguence	Sequence	Seguence	Sequence	Seguence	Seguence	Seguence	Seguence	Sequence	Sequence	Seguence	Patent No.	Sequence	Seguence	Seguence	Seguence	Sequence	Seguence
	ID	US-08-233-788A-59		-09-196-3	83	-387-1	US-09-841-835-10	-196-387-	US-09-841-835-2	US-09-972-115A-8	US-08-864-038A-3	Ψ	US-09-252-991A-32096	39-056-556-20	US-09-072-596-199	US-09-477-135A-131	US-09-072-967-204	US-09-252-991A-30227	US-09-540-236-3401	m	US-09-336-447A-5	5187262-1	US-09-043-123-2	US-09-489-039A-11518	4	-09-841-7	-08-409-9	-4
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ob;	Query Match	. E. 60	66.3	٠,	٠.	11.9	11.9	11.9	11.9	11.9	11.5	11.2	10.8	10.8	10.8	10.8	10.8	10.6	10.5	10.4	10.3	10.3	10.3	10.3	10.1	10.1	10.1	10.1
	Score	692	514	92	92	92	92	92	92	92	89.5	87		83.5		83.5	83.5		81	80.5	08	σ.		79.5	78.5	æ	78.5	78.5
	Result No.		2	m	4	2	9	7	∞	o.	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

Sequence 33, Appl		-	-	equence 47,		1,	Sequence 5818, Ap	Sequence 257, App	Sequence 280, App	Sequence 39, Appl	Sequence 42, Appl	_	Sequence 21268, A	Sequence 41, Appl	Seguence 6, Appli	Sequence 6, Appli	Sequence 6, Appli	
US-09-377-155-33	US-08-913-942-4	US-09-669-974-33	US-09-797-862-33	US-09-268-347-47	US-09-268-347-36	US-09-841-786-1	US-09-107-532A-5818	US-09-453-702B-257	$^{\circ}$	-09-595-684B-3	US-09-495-880A-42	US-09-134-078-63	US-09-252-991A-21268	US-09-919-172-41	US-08-960-780-6	US-09-073-898-6	US-09-850-351A-6	
٣	m	4	4	4	4,	4	4	4	4	4	4	4	4	4	٣	m	41	
2353	2353	2353	2353	2354	2411	3241	318	3169	415	1690	238	926	1413	645	789	789	789	
10.1	10.1	10.1	10.1	10.1	10.1	10.1	10.0	10.0	9.9	6.6	9.6	9.	9.6	9.7	7.6	9.7	9.7	
78.5	78.5	78:5	78.5	78:5	78:5	78.5	77.5	77:5	77	77	76.5	76.5	76:5	75:5	75:5	75.5	75.5	
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4.	

### ALIGNMENTS

GENERAL INFORMATION:
APPLICANT: Doran, James L.
APPLICANT: Ray, Williams L.
APPLICANT: Collinson, Karen S.
APPLICANT: Collinson, Karen S.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TITLE OF INVENTION: OF SALMONBLIA.
OVERESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: Galo Columbia Center, 701 Fifth Avenue CITY: Seattle
STATE; Washington
COMPTRY: U.S.A.
ZOUNTRY: U.S.A.
ZONDUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTRE: IBM PC compatible
COMPTRE: BATENIN Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
FILING DATE: 26-APR-1994 PPLLCALLA.

PILING DARE

FILING DARE

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: King, Joshua

REGISTRATION NUMBER: 920043.403C2

REGISTRATION NUMBER: 920043.403C2

TELEPHONE: C206) 622-4900

TELEPRA: (206) 682-6031

TELEFAX: (206) 682-6031

TELERA: 1273846 SERDANBERRY

INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:

LENTH: 151 amino acids

"THOSE AND AND ADDRESS AND AND ADDRESS AND ADDRE RESULT 1 US-08-33-788A-59 ; Sequence 59, Application US/08233788A ; Patent No. 56635617 MOLECULE TYPE: protein US-08-233-788A-59

Gaps Query Match
Best Local Similarity 90.7%; Pred. No. 3.9e-62;
Matches 137; Conservative 3; Mismatches 11; Indels 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60

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ADDRESSEE:
                                                                                                                                                                                     STATE: No COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                      61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                          SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGCNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
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0
                                                                                                                                                                                                                                                              Sequence 57, Application US/08233788A

Patent No. 5635617

GENERAL INFORMATION:

APPLICANT: Doran, James L.

APPLICANT: Collinson, Karen S.

APPLICANT: Collinson, Karen S.

APPLICANT: Collinson, Marchols And Compositions For DETECTION TITLE OF INVENTION: OF SALMONELLA NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GOGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQY 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Seed and Berry 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.2e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.3%; Score 514; DB 1;
                                                                                                                         121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
                                                                                                                                                           121 NNPALVNOTASDSSVMVROVGFGNNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE JOCKET WITHDER: 920043.403C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.20,
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-233-788A-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington
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ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 6300 Co
CITY: Seattle
STATE: Washingt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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Sequence 8, Application US/09196387 Patent No. 6277613

RESULT 3 US-09-196-387-8 GENERAL INFORMATION:

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6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSPSSPGSSLAESPEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF UNENTION: OF USE THEREOF
UNDBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/09841835
Patent No. 6506587
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
APPLICANT: General Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3; Length 673;
0.54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57; Indels
                                                                                                                                                                                                                                                                                                                                   SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                   E: Klauber & Jackson
411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  600-1-230 CIP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.9%; Score 92; 30.4%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
FILING DATA:
CLASSIFCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
ATTORNEY/ACENT INFORMATION:
NAME: Jackson Esq., David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                  E: Floppy disk
IBM PC compatible
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                ZIP: 07601
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy dis
COMPUTER: IBM PC Compat
OPERATING SYSTEM: PC-DO.
SUFTWARE: Patent*
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Best Local Similarity 30.4%
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 673 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein US-09-196-387-8
                                                                                                                                                                           Hackensack
: New Jersey
RY: USA
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6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 949 amino acids
                  TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 949 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201-343-1684
201-343-1684
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                                                                                                                             MOLECULE TYPE: protein US-09-196-387-10
                                                                                             TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
3Y: linear
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  TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-196-387-10

Sequence 10, Application US/09196387

Sequence 10, Application US/09196387

Sequence 10, Application US/09196387

Sequence 10, Application US/09196387

SEMERAL INFORMATION:

APPLICANT: de Lange, Titia

APPLICANT: SMITCH, SUSAN

TITLE OF INVENTION: OF USE THEREOF

TITLE OF INVENTION: OF USE THEREOF

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue, 4th Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57; Indels
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  NYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/055,225
FILING DATE: Unue 10, 1998
AFTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; Mismatches
                                                                                                                                                                                                                                         600-1-230 CIP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 92;
Pred. No. (
                                                            APPLICATION NUMBER: US/09/841,835 FILING DATE:
                                                                                           CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-23
TELEPHONE: 201-487-5800
TELEPHONE: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 30.4%
Matches 35; Conservative
                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                    TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 673 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-09-841-835-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                                                       6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGFDSTLSIYQYGSANAALALQSDAR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                       Gaps
                                                                                                                                                                                                                                         158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACENGDVSRVKRLVDAANVNAKDM 212
                                                                                                                                                                                                         65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                                    US-09-841-835-10
Sequence 10, Application US/09841835
Sequence 10, Application US/09841835
GENERAL INFORMATION:
APPLICANT: Smitch, Susan
TITLE OF INVENTION: OF USE THEREOF
TITLE OF INVENTION: OF USE THEREOF
TOWNER, OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Alauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STREET: New Jersey
COUNTRY: USA
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Query Match
Best Local Similarity 30.4%; Pred. No. 0.84;
Matches 35; Conservative 15; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 949;
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Best Local Similarity 30.4%; Pred. No. 0.84;
Matches 35; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26,742
ER: 600-1-230 CIP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
WEDLUM TYPE: Floppy disk
COMPUTER: ISM PC COMPATIBLE
COMPUTER: ISM PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFRENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
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New Jersey
USA
                                                                                                                                          STREET: 411 Hack
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 35, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inear
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MOLECULE TYPE:
HYPOTHETICAL: N
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                                                                                                                                                                                  STATE: Ne
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99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSPSSPGSSLAESPEAA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 VAAAPUVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR
                                                             65 KSETTIT-----OSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                    158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: de Lange, Titia
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: All Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 11.9%; Score 92; DB 3; Length 1327; Best Local Similarity 30.4%; Pred. No. 1.3; Matches 35; Conservative 15; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               600-1-230 CIP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                 Sequence 2, Application US/09196387
Patent No. 6277613
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 133521
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1327 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
TELEX: 1:
                                                                                                                                                               RESULT 7
US-09-196-387-2
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Sequence 2, Application US/09841835 Patent No. 6506587 GENERAL INFORMATION:

RESULT 8 US-09-841-835-2

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99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
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APPLICANT: Smith, Susan
IIIILE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
IIIILE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 09/196,387
FILING DATE:
APPLICATION NUMBER: 09/196,387
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Ren Township Information:
NAME: Jackson Ren Township Information:
NAME: Jackson Ren Township Information:
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APPLICANT: Walter, Funk D.
APPLICANT: Walter, Funk D.
APPLICANT: Walter, Funk D.
APPLICANT: Walter, Funk D.
TITLE OP INVENTION: A Second Mammalian Telomerase
FILE REFERENCE: 080/003C
CURRENT APPLICATION NUMBER: US/09/972,115A
CURRENT APPLICATION NUMBER: US 60/128,577
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR PRING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                                                                                                                                            E: Klauber & Jackson
411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jackson Esq., David A. REGISTRATION VMBER: 26,742 REFERENCE/DOCKET NUMBER: 000-1-230 CIP1 TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/09972115A Patent No. 6599728 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1327 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFHONE: 201-487-5800
TELEFAX: 201-343-1684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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LENGTH: 1327 amino aci
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INFORMATION FOR SEQ ID NO:
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NO
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber &
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Sequence 10. 4514981

Batent No. 4514981

GENERAL INFORMATION:
APPLICANT: TUCKER, KENNETH
APPLICANT: TUCKER, LAURA
TITLE OF INVENTION:
PROTEIN-106 FOLYPEPTIDE, GENE SEQUENCE AND USES THEREOF
NUMBER OF SEQUENCES: 2.
CORRESPONDENCES: 2.
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 LALQSDARKSETTITQSGYGNGADVG-QGADNSTI----ELTQNGFRNNA--TIDQWNAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 NSDITVGQYDQLVTRV----- 140
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                                                                   3 LLKVAAFFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98 LGSQSIAIGDNKIVHNS--NNNANIGAKASGNESIAIGGDVLASGHASIAIGSDDLYLKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 LSFARIAALAVLVIGATLNGSAYAGIGISEADGG--KGGANARG-DKSIAI---GDIAQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKLLKVAAFAAIVV----SGSALAGVVPOWGGGGNHNGGGNSSGPDSTLSIYOYGSANAA
                                                                                                           419 LLKSSASASASASASAG----GGGGGGNGGGNGGGG------GGGAGALA
                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52;
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                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,685A
FILING DATE: No. 6214981ember 12, 1997
CLASSIFICATION:
                             26;
      Pred. No. 1.1;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31,232
ER: 7969-060
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NAME: Baldwin, Geraldine F.
REGISTRATION NUMBER: 31,232
REFERÊNCE/DOCKET NUMBER: 7969
TELEPHONE: (212) 796-9990
TELEPHONE: (212) 869-8864
                                                                                                                                                        63 ARKSETTITOSGYGNGADVGQG
        35.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2123 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 25.4
Matches 48; Conservative
                             29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-968-685A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 -GFGNNATA 148
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STRANDEDNESS:
    Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New York
                                                                                                                                                                                                                                                                                  US-08-968-685A-10
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STATE:
                                                                                                                                                                                                 461
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Sequence 10. 6001592
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CONTAINING SAID CDMA, HOST CELLS TRANSFORMED WITH SAID
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TO SAID POLYPEPTIDE
NAMER OF SEQUENCES:
A CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                    6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
                                                                                                                                                                                                                                                                                                                             KSETTIT----OSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                                                   158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
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                                                                                                                                                        11.9%; Score 92; DB 4; Length 1327; 30.4%; Pred. No. 1.3; ive 15; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER REABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage COMPUTER: IBM Compatible OPERATING SYSTEM: Microsoft Windows 95 SOFTWARE: Word Perfect 6.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/864,038A
FILING DATE: MAY 28, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 9-184459
FILING DATE: 15-101/-1996
ATTORNEY/AGENT INFORMATION:
NAME: C. Bruce Hamburg
REGISTRATION NUMBER: 22,389
REFERENCE/DOCKET NUMBER: F-5610
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 89.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mantle epithelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (212)953-7733
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CELL TYPE: mantle fucata Armer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: peptide
LOCATION: from 1 to 738
IDENTIFICATION METHOD: E
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: TSu-city
STATE: Mie-prefecture
COUNTRY: JAPAN
ZIP: 514-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (212) 953-7733
                                                                                                                                                      Query Match
Best Local Similarity 30.45
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
LENGTH: 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein ORIGINAL SOURCE:
                                            LENGTH: 1327
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-972-115A-8
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159 IGLIGSGLIGF-----GGLNSGTGN-----IGLFNSGTGNVGIGNSGTGNWGIGNSG 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 TITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD---ITVGQYD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 NSYNTGFGNSGDANTGFFNSGIANTGVGNAGNYNTGSYNPGNSNTGGFNMGQYN 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
10.8%; Score 83.5; DB 4; Length 943;
Best Local Similarity 25.4%; Pred. No. 6;
Matches 29; Conservative 16; Mismatches 50; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Twardzik, Thomas S.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and not of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contr
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTUMES SYSTEM: PC-DOS/MS-DOS
SOFTUME: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 199, Application US/09072596 Patent No. 6458366 GENERAL INFORMATION:
                        TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 204:
SEQUENCE CHARACTERISTICS:
LENGTH: 943 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
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INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
(206) 622-4900
                                                                                                                                                                         LENGTH: 943 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington
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CITY: Seattle
STATE: Washingt
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TOPOLOGY:
US-09-056-556-204
    TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db
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                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDCMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-18
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32096
LENGTH: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 ALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNS---- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----TLNNYSNPNTASLSNSANNVSGNLG 149
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Batent NO. 6350456

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Steiky, Yasix A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.8%; Score 83.5; DB 4; Length 339; llarity 21.5%; Pred. No. 1.6; Conservative 28; Mismatches 53; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 -DITVGQYDQ----LVTRVVTHEMAHASVMVRQVGFGNNATAN 149
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ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDPPY disk
COMPUTER: IBM PC compatible
CORPUTER: IBM PC compatible
CORPUTER: TEM PC compatible
CORPUTER: TEM PC compatible
COMPUTER: TEM 
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                   US-09-252-991A-32096
; Sequence 32096, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----TSVLQSGYGN----
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US-09-252-991A-32096
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    213 NAFGTRATA 221
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Best Local Similarity
Labes 35; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-056-556-204
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266 IGLTGSGLLGF-----GGLNSGTGN-----IGLFNSGTGNVGIGNSGTGNWGÏGNSG 312
                                                                        RESULT 15
US-09-477-135A-131
US-09-477-135A
Sequence 131, Application US/09477135A
Fatent No. 6572865
Fatent No. 6572865
Fatent No. 6572865
Fatent No. 6572865
Fatent No. 6572865
Fatent No. 6572865
Fatent No. 6572865
Fatent Namo, Francis
FILE REFERENCE: 5288
FATENCE OF INVENTION: immunostimulatory Peptides
FILE REFERENCE: 5288
FATENCE PAPLICATION NUMBER: US/09/477,135A
FATENCE PAPLICATION NUMBER: US/09/477,135A
FATENCE PAPLICATION NUMBER: US/09/477,135A
FATENCE PAPLICATION NUMBER: US/09/1215
FATENCE PAPLICATION NUMBER: 6/000,254
FATENCE PAPLICATION NUMBER: 6/000,254
FATENCE PAPLICATION NUMBER: 6/000,254
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FATENCE PAPLICATION NUMBER: 6/000,254
FATENCE PAPLICATION NUMBER: 6/000,254
FATENCE PAPLICATION NUMBER: 6/000,254
FATENCE PAPLICATION NUMBER: 6/000,0554
FATENCE PAPLICATION NUMBER: 6/000,000,254
FATENCE PAPLICATION NUMBER: 6/000,000,000,000,000
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12 IVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR---KSET 68
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Best Local Similarity 25.4%; Pred. No. 6;
Matches 29; Conservative 16; Mismatches 50; Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 TITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD---ITVGQYD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             313 NSYNTGFGNSGDANTGFFNSGIANTGVGNAGNYNTGSYNPGNSNTGGFNMGQYN 366
                                                                                                                                                                                                                               69 TITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD---ITVGQYD 119
                                                                                                                                                                                                                                                                                           206 NSYNTGFGNSGDANTGFFNSGIANTGVGNAGNYNTGSYNPGNSUTGGFNMGQYN 259
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Job time : 13 secs
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| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/PCT_MEW_PUB_pep:*
| cgn2_6/ptodata/2/pubpaa/PCT_MEW_PUB_pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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| cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	Sequence 4, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 20638, A	Sequence 53421, A	Seguence 245045,	Seguence 49412, A	Sequence 8, Appli	Seguence 10, Appl	Sequence 2, Appli	Seguence 8, Appli	Seguence 4, Appli	Sequence 49960, A	Sequence 147748,
	ΩΙ	US-09-741-873B-4	US-09-741-873B-4	US-09-741-873B-2	US-09-741-873B-2	US-10-369-493-20638	US-10-425-114-53421	US-10-424-599-245046	US-10-282-122A-49412	US-09-841-835-8	US-09-841-835-10	US-09-841-835-2	US-09-972-115A-8	US-10-199-937-4	US-10-425-114-49960	US-10-437-963-147748
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	Query Match Length DB	151	151	131	131	445	210	211	186	673	949	1327	1327	1327	263	145
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	Score	525	525	447	447	104	98	96	95	92	92	92	9	92	90.5	88.5
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US-10-425-114-5604	2 US-10-424-	2 US-10-425-114-5776	US-09-793-306-146	2 US-10-282-122A-5326	2 US-10-282-122A-	US-09-813-214A-9	US-09-712-363-156	4 US-10-080-170-34	S US-10-080-170-348	4 US-10-156-761-876	5 US-10-369-493-2	S US-10-437-963-1222	4 US-10-174-363-56	5 US-10-374-780A-20	4 US-10-156-761-934	4 US-10-156-761-1	19-996-634-131	0 US-09-997-182-13	0 US-09-997-181-13	4 US-10-193-002-19	4 US-10-084-843-20	2 US-10-282-122A-64	2 US-10-425-114-6152	0 US-09-880-748-113	0 US-09-880-748-1	2 US-10-293-418-113	2 US-10-293-418-116	0 US-09-880-748-149	2 US-10-293-418-149	
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### ALIGNMENTS

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Normark, Staffan.
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012089-084
CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT APPLICATION NUMBER: US 08/978,878
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR PILING DATE: 1998-05-04
PRIOR PILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR PILING DATE: 1999-11-06
PRIOR PILING DATE: 1999-1-06-04
PRIOR PILING DATE: 1999-05-04
PRIOR PILING DATE: 1994-01-08
PRIOR PILING DATE: 1994-01-28
PRIOR PELING DATE: 1994-01-28
PRIOR PELING DATE: 1994-01-28
PRIOR PELING DATE: 1994-01-28
PRIOR PILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Version 3.0
SOFTWARE: Patentin Version 3.0
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                                                     ; Sequence 4, Application US/09741873B; Publication No. US20020081722A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Escherichia coli
RESULT 1
US-09-741-873B-4
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| GENERAL INFORMATION:
| JAPPLICANI: NORMER'S, Staffan
| APPLICANI: NORMER'S, Staffan
| APPLICANI: Olsen, Are
| TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
| TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
| TITLE OF INVENTION: 102869-084
| CURRENT APPLICATION NUMBER: US 003-04-04
| PRIOR APPLICATION NUMBER: SE 8801723-1
| PRIOR APPLICATION NUMBER: US 08/978,878
| PRIOR FILING DATE: 1997-11-26
| PRIOR FILING DATE: 1997-11-26
| PRIOR APPLICATION NUMBER: US 07/37,189
| PRIOR FILING DATE: 1991-11-06
| PRIOR APPLICATION NUMBER: US 07/970,846
| PRIOR APPLICATION NUMBER: US 07/970,846
| PRIOR APPLICATION NUMBER: US 08/187,865
| PRIOR APPLICATION NUMBER: US 08/187,865
| PRIOR FILING DATE: 1994-01-28
| PRIOR FILING DATE: 1994-01-05
| NUMBER OF SEQ ID NOS: 10
| SEQ ID NO 2
| TENGTH: 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.7%; Score 447; DB 12;
64.9%; Pred. No. 1.5e-37;
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PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR PILING DATE: 1997-11-26
PRIOR PILING DATE: 1999-05-04
PRIOR PILING DATE: 1999-05-04
PRIOR PILING DATE: 1991-11-06
PRIOR PILING DATE: 1991-11-05
PRIOR PILING DATE: 1994-01-28
PRIOR PILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-01-28
NUMBER: PRIOR FILING DATE: 1994-01-8
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Matches 85; Conservative
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US-09-741-8738-2
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APPLICANT: Olsen, Arne
APPLICANT: Olsen, Arne
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Firenectin Binding Protein As Well As Its Preparation
FILE REPERENCE: 012889-084
CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT APPLICATION NUMBER: US 08/09/8,878
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR FILING DATE: 1999-05-04
PRIOR FILING DATE: 1999-05-04
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1992-11-03
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR FILING DATE: 1992-11-03
PRIOR FILING DATE: 1994-10-05
PRIOR FILING DATE: 1994-10-05
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      Sequence 2, Application US/09741873B
Publication No. US20020081722A1
GENERAL INFORMATION:
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084
CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT FILING DATE: 2003-04-04
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                                                                                                                                                                                                            121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                121 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
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SOFTWARE: PatentIn version 3.0
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ORGANISM: Escherichia coli
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US-09-741-873B-2
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Length 131;

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VS-010-424-599-245046
VS-010-424-599-245046
VS-0240ence 245046, Application US/10424599
Sequence 245046, Application VG-020040031072A1
Publication No. US20040031072A1
Sequence 245046, Application No. US20040031072A1
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRESENCE: 32-21(5223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 245446
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TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 53421
LENGTH: 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.6%; Score 98; DB 12; Length 210; Best Local Similarity 26.7%; Pred. No. 0.08; Matches 36; Conservative 18; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Clone ID: PAT_MRT3847_63306C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: Clone ID: 700839445_FLI.pep US-10-425-114-53421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
US-10-282-122A-49412
; Sequence 49412, Application US/10282122A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 QGHLIVNYQFVDCGN 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 MAHASVMVRQVGFGN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 MAHASVMVRQVGFGN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 QGHLIVNYQFVDCGN 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; UTHER INFORMATION
US-10-424-599-245046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
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Sequence 20638, Application US/10369493

Publication No. US2003023367541

GENERAL INPORMATION:

APPLICANT: Cac, Yongwei

APPLICANT: Gldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Gldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10 (5305.2)

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

SEQ ID NOS: 47374
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CENDIGATION NO. US20040034888A1
CENDIGATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Stou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 GNSNSV-----GRDIQGKQSGAGNSAAIFQEGTGSDVELQQTGTSNGAVPSGWNWTN 129
                                                                                                                                                                                                                                                                                                                                        61 VGQGSDDSSIDLTQRGFGNSATLDQWNGRNSEMTVKQFGGGNGAAVDTASNSVNVTQV 120
                                                                                                                                                                                                                                                                                           81 VGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQLVTRVVTHEMAHASVMVRQV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
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                                                                                                                                         80
                                                                                                                                                                                  21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 AAFAA-----IVVSGSALAGVVPQWGGGG-----NHNGG-----GNSSGPDSTLSIYQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 SDITVGQYDQLVTRVVTHEMAHASVM------VRQVGFGNNATANQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61, Indels
                                                            Indels
                        Pred. No. 1.5e-37;
); Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
13.4%; Score 104; DB 15;
Best Local Similarity 26.6%; Pred. No. 0.051;
Matches 45; Conservative 25; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1)..(445)
OTHER INFORMATION: unsure at all Xaa locations
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ORGANISM: Rhodopseudomonas palustris
64.9%; Fil.
                                                                85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 GFGNNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GFGNNATAHQY 131
                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: unsure LOCATION: (1)..(
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NUMBER OF SEQUENCES:

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50 ----TPADKAITLATVPA-GSLASAGAVAGTSNPTDLQLSLTGCTGTATKAIARFENGPT 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Xu, H.
IITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
WIWHER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/09841835
Patent No. US20020076795A1
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 IDOWNAKNSDITVGOYDQLVTRVVTHEMAHASVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 LALOSDARKSETTITOSGYGNGADVG--QGADNST-IELTQNG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 12; Length 186;
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12.3%; Score 95; DB 12; Length 18
Best Local Similarity 29.9%; Pred. No. 0.14;
Matches 50; Conservative 20; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION INGRER: US/10/282,122A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-06
PRIOR PILING DATE: 2000-05-06
PRIOR PILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PELING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PELING DATE: 2000-12-27
PRIOR PELING DATE: 2000-12-27
PRIOR PELING DATE: 2000-12-27
PRIOR PELING DATE: 2000-12-27
PRIOR PELING DATE: 2001-02-09
PRIOR PELING DATE: 2001-02-09
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ORGANISM: Burkholderia fungorum
                                                              APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ollsen, Rari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
Publication No. US20040029129A1
SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    Robert
                                                                                                                                                                                                                                                                                                              Trawick, John
Carr, Grant
Yamamoto, Rober
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-282-122A-49412
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6 VAAFAA1-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10. Application US/09841835
Facent No. US20020076795A1
GENERAL INFORMATION:
APPLICANT: deliange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: OF USE THEREOF
ITILE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack Avenue, 4th Floor
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

11.9%; Score 92; DB 9; Length 673;
Best Local Similarity 30.4%; Pred. No. 1.4;
Matches 35; Conservative 15; Mismatches 57; Indels
                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
                                                                                                                                                                                                                                                                                                                                                                                                            APLILOG DATE:
FILING DATE:
ATORNEY, AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMERS: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                           STREET: 411 Hackensack Avenue, 4th Floor CITY: Hackensack
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/841,835 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-09-841-835-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                            New Jersey
: USA
                                                                                                                 COUNTRY: UZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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single
linear
                                                                      HYPOTHETICAL: NO US-09-841-835-2
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ORGANISM: Homo sapiens
                   TYPE: amino acid
STRANDEDNESS: sing
TOPOLOGY: linear
MOLECULE TYPE: prote
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US-10-199-937-4
  LENGTH:
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Patent No. US20020076795A1
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                            11.9%; Score 92; DB 9; Length 949; 30.4%; Pred. No. 2.2; tive 15; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTY: UNW DELESY
ZIP: 07601
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REPERENCE/DOCKET UNBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                  600-1-230 CIP1
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMEER: 09/196,387
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMONE: 201-3437-5800
TELEFRAX: 201-343-1684
                                                                09/196,387
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 949 amino acids
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Matches 35; Conservative
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USA
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TOPOLOGY: linear
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99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSPSSPGSBLABSPEAA 157
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                                                                                                                        6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
                                                                 Gaps
                                                                                                                                                                                                                                                                                                     158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
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                                                                 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Publication No US20030032769A1
| Publication No US20030032769A1
| GENERAL INFORMATION:
| APPLICANT: Geron Corporation
| APPLICANT: Gregg, Morin B.
| APPLICANT: Malter, Funk D.
| APPLICANT: Maczyaław, Piatyszek A.
| TITLE OF INVENTION: A Second Mammalian Telomerase
| FILE REFRENCE: 080/003C
| CURRENT APPLICANTON NUMBER: US/09/972,115A
| PRIOR FILING DATE: 2000-10-05
| PRIOR APPLICATION NUMBER: US 60/128,577
| PRIOR FILING DATE: 1999-04-13
| PRIOR FILING DATE: 1999-04-13
| PRIOR FILING DATE: 1999-04-13
| PRIOR FILING DATE: 1999-04-13
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APPLICANT: Goldman, Phyllis S.
APPLICANT: McElligott, David L.
TITLE OF INVENTION: TANKYRASE2 MATERIALS AND METHODS
FILE REPERENCE: 27866/38559
CURRENT APPLICATION NUMBER: US/10/199,937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
11.9%; Score 92; DB 10;
Best Local Similarity 30.4%; Pred. No. 3.3;
Matches 35; Conservative 15; Mismatches 57;
Query Match
11.9%; Score 92; DB 9
Best Local Similarity 30.4%; Pred. No. 3.3;
Matches 35; Conservative 15; Mismatches
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Publication No US20030190739A1
GENERAL INFORMATION:
APPLICANT: Christenson, Erik
APPLICANT: DeMaggio, Anthony J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002-07-22
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Shou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Screen, Steven E
APPLICANT: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 73128
LENGTH: 263
                                                                                                                                                                                                                                                                                                                                                                                                                      84 SSIAG-----GGGGGGGGGTNGGSGSGGGSGTGSSSSTAASGPSGNYADAEGKGAG 138
                                                                                                                                                                                                                                                                                                                                                                                      6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 263;
                                                                                                                                                                                                                                                                                Query Match
11.9%; Score 92; DB 14; Length 1327;
Best Local Similarity 30.4%; Pred. No. 3.3;
Matches 35; Conservative 15; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 -----YGNGA--DVGQGADNSTIEL--TQNGFRNNATID 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 GGMGGGANGAYGSGAGGGGGGKGEGVSGVALAPSSNGYYNGGAAD 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: 700071884_FLI.pep
US-10-425-114-49960
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: AROSA, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 49960, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION WUMBER: 60/141,582
PRIOR FILING DATE: 1999-06-29
NUMBER OF SEQ ID NOS: 178
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1327
                                                                                                                                                                                                  ORGANISM: Homo sapiens
US-10-199-937-4
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Best Local Similarity
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ORGANISM: Zea mays
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US-10-437-963-147748
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US-10-425-114-49960
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Matches
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APPLICANT: Barbazuk, Brad

Harbitachn: Li, Pling

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPERBNCE: 38-21(5321)B

CURRENT APPLICATION WUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 147748

LENGTH: 145

TYPE: PTT

ORGANISM: Oryza sativa

FEATURE

ORGANISM: Oryza sativa

FEATURE

ORGANISM: Oryza sativa

FEATURE

ORGANISM: 014748

Query Match

Best Local Similarity 32.6%; Pred. No. 0.46;

Matches 29; Conservative 11; Mismatches 36; Indels 13; Gaps 5;

Matches 29; Conservative 11; Mismatches 36; Indels 69

OY 8 APALIVYGSSALAGV-VP---QWGGGGNHNGGTAPSAAANGSTTAYDDRGTGGQTAT 69

OY 8 APALIVYGSSALAGV-VP---QWGGGCNHNGGTAPSAAAANGSTTAYDDRGTGGQTAT 69

OY 67 LALOSDARKSETHTTQSGYGNGADVGGA 85

Db 70 PQVQGAQPEETTTE-MGNAAEAATGS 96

Search completed: August 2, 2004, 15:36:09

JOB time: 36.8 secs
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Sequence 12, Appl Sequence 5, Appl Sequence 57, Appl Sequence 30, Appl Sequence 26, Appl

Sequence 3

Sequence Seq Sequence Sequence Sequence Sequence Sequence Sequence Sequence

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OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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GENERAL INFORMATION:
APPLICANT White, Aaron P.
APPLICANT Collinson, S. Karen
APPLICANT COLLInson, S. Karen
APPLICANT KAY, William W.
ITILE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEP
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT APPLICATION NUMBER: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
19 US-09-543-407-14
19 US-09-543-407-12
19 US-09-543-407-24
19 US-09-543-407-24
19 US-09-543-407-26
19 US-09-543-407-26
19 US-09-543-407-28
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ORGANISM: Artificial Sequence
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LENGTH: 151
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104.5
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1 MKLLKVAAFAAIVVSGSALA......HASVMVRQVGFGNNATANQY
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                                               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Minimum DB Maximum DB

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5833, Ap 5833, Ap 86, Ap 20638, Ap 20638, Ap 6, Appli 6, Appli 73421, A 53421, A 53421, A 53421, A 53451, A 54565, Ap

PEPTIDE SEQUENCES

Description

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Score

Result Š. ; ;

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US-08-233-642A-57; Sequence 57, Application US/08233642A; GENERAL INFORMATION: GENERAL APPLICANT: Kay, William W.
                                                                                    LENGTH: 151
TYPE: PRT
ORGANISM: Artificial Seguence
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Best Local Similarity 87.6%;
Matches 141; Conservative
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US-09-543-407-12
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GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Octan, James D.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

CURRENT APPLICATION WHERE: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 24

LENGTH: 151
                                                                                                                                 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                         Gaps
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US-09-543-407-12
US-09-543-407
Sequence 12, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Dozan, James L.
APPLICANT: Callinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-24
                                            Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
92.1%; Score 714; DB 19; Length 151;
Best Local Similarity 91.1%; Pred. No. 2.4e-68;
Matches 144; Conservative 0; Mismatches 0; Indels 1
                                                                                       Indels
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                                        Query Match 100.0%; Score 775; DB 19; Best Local Similarity 100.0%; Pred. No. 6.1e-75; Matches 151; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                       121 LVIRVVTHEMAHASVMVRQVGFGNNATANQY 151
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-09-543-407-24
US-09-543-407-14
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61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQ--- 117
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APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
                                                                                                                                                                                                                           OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                          Length 151;
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0
                                                                                                                                                                                                                                                                                                                                                                       Score 696; DB 19;
Pred. No. 2.1e-66;
0; Mismatches 0;
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Best Local Similarity 90.7%; Pred. No. 4.4e-66;
Matches 137; Conservative 3; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 151
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Gaps

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SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
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APPLICANT Doran, James L.
APPLICANT Collings, S. Karen
APPLICANT Collings, S. Karen
APPLICANT Collings, S. Karen
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REPERENCE: 92043,407
CURRENT FILING DATE: 2000-04-05
SUFFENT FILING DATE: 2000-04-05
SUFFWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 81.9%; Pred. No. 2.1e-62;
Matches 136; Conservative 0; Mismatches 0; Indels 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: Sequence containing the replacement fragmen OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
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US-09-543-407-18
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US-09-543-407-26
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APPLICANT: Collinson, S. Karen
APPLICANT: Clouthier, Sharon C.
APPLICANT: Doran, James L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: BASED VACCINES
NUMBER OF SEQUENCES: 58
NUMBER OF SEQUENCES: -
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                            CITY: Seattle
STATE: Washington
COMPRY: U.S.A.
ZIP: 98104-7092
ZIP: 98104-7092
ZIP: 98104-7092
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE E Floppy disk
COMPUTER: Datentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Datentin Release #1.0, Version #1.25
SOFTWARE: 26-ARR-1994
FLING DATE: 26-ARR-1994
ATTORNEY/AGENT INFORMATION:
NAME: King. Joshum 35,570
REFERENCE/DOCKET NUMBER: 920043.403C3
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-6031
TELEPHONE: (206) 622-6031
TELEPHONE: 372383 & SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57: SEQUENCE CHARACTERISTICS:
LENTH: 1151 mino acids
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6300 Columbia Center, 701 Fifth Avenue
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Pred. No. 5.6e-66;
3; Mismatches 11;
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US-09-543-407-30
Squence 30, Application US/09543407
GENERAL INFORMATION:
APPLICANT White, Aaron P.
APPLICANT:
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEI
TITLE OF INVENTION: PRESENTATION OF HETEROL(
FILE REFERENCE: 920043.406
CURRENT PELLING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOUTHARE: FastSEQ for Windows Version 4.0
LENGTH: 151
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Best Local Similarity 90.7
Matches 137; Conservative
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STREET: 630
CITY: Seatt
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81 VGQGADNSTIELTQNGFRNNATIDQMNAKNSDITVGQYDQLVTRVVTHEMAHASVMVRQV 140
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                                                                                                                                                                                Sequence 31, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: NWINTON: DRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 2000-04-05
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 59
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APPLICANT: White, Toran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Callinson, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 5900-04-05
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
78.2%; Score 606; DB 19; Length 131;
Best Local Similarity 89.3%; Pred. No. 9e-57;
Matches 117; Conservative 3; Mismatches 11; Indels
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121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
                                                121 NNAALVNQTASDSSVMVRQVGFGNNATANOY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Salmonella enteritidis US-09-543-407-31
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Best Local Similarity
Matches 122; Conserv
                                                                                                                                           RESULT 10
US-09-543-407-31
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US-09-543-407-28
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APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: KAY, William W.
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
| LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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78.6%; Score 609; DB 19; Length 151;
Best Local Similarity 81.5%; Pred. No. 5.2e-57;
Matches 123; Conservative 6; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 78.8%; Score 611; DB 19; Length 151; Best Local Similarity 81.5%; Pred. No. 3.2e-57; Matches 123; Conservative 6; Mismatches 22; Indels
                     APPLICANT: KAY, WILLIAM W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
FILE REFERENCE: 920043.466
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SEQ ID NOS: 59
SEQ ID NO 18
LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
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US-09-543-407-20
Sequence 20, Application US/09543407
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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                                                                       SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
                                                                                                                 SDARKSETTITOSGYGNGADYDOLVTRVVTHEMAHAFRNNATIDOWNAKNSDITVGOYGG 120
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Callinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
SOFTWARE: PASTS D NOS: 59
SOFTWARE: FASTS OF OF Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: White, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: COLINSON, S. Karen
APPLICANT: COLINSON, S. Karen
APPLICANT: COLINSON, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 77.7%; Score 602; DB 19; Length 151; Best Local Similarity 81.5%; Pred. No. 3e-56; Matches 123; Conservative 5; Mismatches 23; Indels C
                                                                                                                                                                                           LVTRVVTHEMAHASVMVROVGFGNNATANOY 151
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US-09-543-407-22
Sequence 22, Application US/09543407
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQMNAKNSDITVGQYDQ 120
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GENERAL INFORMARK.
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APPLICANT: NORMARK.
APPLICANT: NORMARK.
FILE APPLICANT: OLSEN, Are
FILE OF INVERTION FIRENDECTIN BINDING PROTEIN AS WELL AS ITS PREPARATION
FILE REPRENCE: 0.12889-0.801
CURRENT APPLICATION NUMBER: US/08/978,878
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: SE 8801723-1
EARLIER FILING DATE: 1988-05-06
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT WILLE, Aaron P.
APPLICANT Collinson, S. Karen
APPLICANT COLLINSON, S. Karen
APPLICANT SAY, William W.
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
CURRENT FILING DATE: 2000-04-05
CURRENT FILING DATE: 2000-04-05
CURRENT FILING DATE: 2000-04-05
SOFTWARE: FESTERO FOR WINDOWS VERSION 4.0
SEQ ID NO 7.
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                                                                                                                                                                                              Gaps
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OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragmer OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                         Length 151;
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                                                                                                                                                                                              Indels
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                                                                                                                                      / Match 74.6%; Score 578; DB 19; 1
Local Similarity 80.8%; Pred. No. 1.2e-53;
les 122; Conservative 6; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT; ORGANISM: Escherichia coli
US-09-543-407-7
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Matches 104; Conservative
     OTHER INFORMATION:
OTHER INFORMATION:
                                                                                     US-09-543-407-16
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US-09-543-407-7
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US-08-978-878-4
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Search completed: August 2, 2004, 15:26:42 Job time : 167.9 secs

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August 2, 2004, 14:49:38 ; Search time 17.8 Seconds (without alignments) 888.146 Million cell updates/sec
                                                                                                                                                                                                            US-09-543-407-14
775
1 MKLLKVAAFAAIVVSGSALA.......HASVMVRQVGFGNNATANQY
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Pending Patents AA New:\*

(cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep:\*

(cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep:\*

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(cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep:\*

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Database :

# SUMMARIES

	Description	Sequence 4, Appli	Sequence 2, Appli			49,		Seguence 301334,	Seguence 312468,	Sequence 21, Appl	Seguence 348, App	Seguence 346132,	Sequence 2086, Ap									Sequence 11109, A	11109		34252		Seguence 17306, A
	ΩI	US-09-741-873C-4	US-09-741-873C-2	9 6 US-10-170-205E-35751	US-10-170-205E-741	PCT-US04-02338-49	US-10-425-115-300390	US-10-425-115-301334	US-10-425-115-312468	US-10-479-638-21	US-10-468-356-348	US-10-425-115-346132	PCT-US04-05654-2086	PCT-US04-21492-88	US-60-565-632-9194	US-60-579-062-9194	PCT-US03-24982A-273	US-10-745-237-96	US-10-491-733-2	US-10-425-115-285216	US-10-425-115-285214	US-60-565-632-11109	US-60-579-062-11109	US-10-425-115-309662	-425	US-10-854-439-511	US-09-248-796A-17306
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æ	Query Match	67.7	57.7	11.9	11.9	11.9	11.7	11.5	11.5	11.4	11.2	11.1	11.0	10.6	10.6	10.6	10.6	10.6	10.5	10.5	10.5	10.5	10.5	10.5	10.5	10.4	10.4
	Score	525	447	92	92	92	90.5	89.5	89	88	86.5	98	85.5	82.5	82	82	82	82	81,5	81.5	81.5	81	81	81	81	80.5	0
	Result No.	-	~	m	4	ιΩ	φ	7	60	Ø	10	11	12	13	14	15	16	17	18	19	20.	21	22	23	24	25	26

13,	equence 13,	equence 13,	Sequence 5, Appli		Ŋ		Sequence 317, App	3092	7907	79		4,	'n	Sequence 198, App	Sequence 193207,	Sequence 254355,		e 19018
-09-952-267	-10-872-768	US-10-872-769-13	US-09-952-267B-5	US-10-872-768-5	US-10-872-769-5	US-10-425-115-351875	PCT-US03-24982A-317	US-10-100-683-7608	US-60-565-632-7907	US-60-579-062-7907	PCT-US04-09385-4	US-10-809-790-4	PCT-US04-12070-2	PCT-US04-21492-198	US-10-425-115-193207	US-10-425-115-254355	9	US-10-425-115-190187
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27	78	59	30	31	32	33	34	35	36	37	38	<u>წ</u>	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 US-09-741-873C-4	.873C-4
; Sequence ; GENERAL ; APPLICA	A / PA
, APPLICA	ANT: Olsen, Arne OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
; FILE RE	FILE REFERENCE: 012889-084 CTEDENT ADDITION NIMBER: 118/09/741 873C
; CURRENT	CURRENT FILING DATE: 2000-12-22
PRIOR A	APPLICATION NUMBER: SE 8801723-1 FTITMG DATE: 1998-05-06
	APPLICATION NUMBER: US 08/978,878
	FILING DATE: 1997-11-26
PRIOR F	AFFLICALION NUMBER: US 0//34/,109 FILING DATE: 1989-05-04
	APPLICATION NUMBER: US 07/789,437
PRIOR F	FILING DATE: 1991-11-06 abbitcattom attabab: 119 07/970 846
	FILING DATE: 1992-11-03
	APPLICATION NUMBER: US 08/187,865
	-28
	APPLICATION NUMBER: US_08/318,519
, PRIOR FIL.	FILING DATE: 1994-10-05
; SOFTWARE:	٠.٠
; SEQ ID NO	O ID NO 4 LENGTH: 151
, TYPE: PRT	PRT
, ORGANISM: ES US-09-741-873C-4	ISM: Escherichia coli -873C-4
Query Match Best Local	Query Match 67.7%; Score 525; DB 5; Length 151; Best Local Similarity 69.2%; Pred. No. 2.3e-38; Marches 103. Conservative 21: Mismarches 27; Indels 0; Gaps 0;
	0 O LA LA SANATA CONTRACTOR A CONTRACTOR CON
Š	MKLLKVAARAAA VVOGGALLAGOVA VANGGAGGARAA GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
DP	1 MKLLKVAAIAAIVFSGSAVAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ 60
٥y	61 SDARKSETIITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQMNAKNSDITVGQYDQ 120
Db	ISSO
QY	121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
qq	121 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151

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GENERAL INCURVATION:

GENERAL INCURVATION:

TITLE OF INVENTION: MAPCAKS AS MODIFIERS OF THE APC AND AXIN PATHWAYS AND METHODS OF

TITLE OF INVENTION: USE

FILE REPERBRICE: EXO4-003C-PC

CURRENT APPLICATION NUMBER: PCT/US04/02338

CURRENT APPLICATION NUMBER: PCT/US04/02338

PRIOR PLING DATE: 2004-01-28

PRIOR PLING DATE: 2003-01-29

PRIOR FILING DATE: 2003-02-11

PRIOR FILING DATE: 2003-02-11

PRIOR FILING DATE: 2003-04-10

PRIOR FILING DATE: 2003-04-10

PRIOR PLING DATE: 2003-05-14

PRIOR FILING DATE: 2003-05-14
                                                                                                                                                                                                                                            RESULT 4

US-10-170-205E-741

US-10-170-205E-741

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ADAMS, Mark
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE REFERENCE: CLOAL381

CURRENT APPLICATION WUMBER: US/10/170,205E

CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312

SOFTWARE: Patentin version 3.2

SOFTWARE: Patentin version 3.2
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99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA
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                                                                                                                                      .58 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Gaps
                                                                   65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.9%; Score 92; DB 1; Length 1327; llarity 30.4%; Pred. No. 12; Conservative 15; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-USO4-02338-49; Sequence 49, Application PC/TUSO402338; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 35; Conserv
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TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE REPERENCE: CLO01381
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT PILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFFWARE: Patentin version 3.2
SEQ ID NO 35751
LENGTH: 299
                                                                                                                                                             APPLICANT: Olsen, Arne
ITTLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
ITTLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
ITTLE OF INVENTION: 01289-084
CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 1998-05-08
FRIOR APPLICATION NUMBER: US 08/978,878
FRIOR APPLICATION NUMBER: US 07/347,189
FRIOR APPLICATION NUMBER: US 07/347,189
FRIOR APPLICATION NUMBER: US 07/789,437
FRIOR APPLICATION NUMBER: US 07/789,437
FRIOR FILING DATE: 1991-11-06
FRIOR PELING DATE: 1992-11-03
FRIOR APPLICATION NUMBER: US 08/187,865
FRIOR APPLICATION NUMBER: US 08/187,865
FRIOR APPLICATION NUMBER: US 08/187,865
FRIOR APPLICATION NUMBER: US 08/187,865
FRIOR APPLICATION NUMBER: US 08/187,865
FRIOR APPLICATION NUMBER: US 08/187,865
FRIOR APPLICATION NUMBER: US 08/187,865
FRIOR FILING DATE: 1994-01-05
NUMBER OF SEQ ID NOS: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GVVPQYGGGGNHGGGGNNSGPNSELNTYQYGGGNSALALQTDARNSDLTITQHGGGNGAD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 57.7%; Score 447; DB 5; Length 131; Best Local Similarity 64.9%; Pred. No. 1.2e-31; Matches 85; Conservative 20; Mismatches 26; Indels
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Best Local Similarity 30.4%; Pred. No. 2.2;
Matches 35; Conservative 15; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 35751, Application US/10170205E GENERAL INFORMATION:
                                                           Sequence 2, Application US/09741873C GENERAL INFORMATION:
                                                                                                                                      APPLICANT: Normark, Staffan APPLICANT: Olsen, Arne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Escherichia coli
US-09-741-873C-2
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US-10-170-205E-35751
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US-10-170-205E-35751
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US-10-425-115-312468
) Sequence 312468, Application US/10425115
| Sequence 312468, Application US/10425115
| GENERAL INFORMATION: Thomas J.
| APPLICANT: Kovalic, David K.
| APPLICANT: Kovalic, David K.
| APPLICANT: Cao, Yongwei
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Datass
| FILE REPERENCE: 38-21(5322)B
| CURRENT APPLICATION NUMBER: US/10/425,115
| CURRENT APPLICATION NUMBER: US/10/425,115
| NUMBER OF SEQ ID NOS: 369326
| SEQ ID NO 312468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21, Application US/10479638
GENERAL INFORMATION:
APPLICANT: Don A. REAL
TAPLICANT: Randolph V. Lewis
APPLICANT: Randolph V. Lewis
APPLICANT: The University of Wyoming
TITLE OF INVENTION: Expression of Spider Silk Proteins in Higher Plants
FILE REPERENCE: WVO. 02-00040S
CURRENT FILING DATE: 2003-12-03
PRIOR APPLICATION NUMBER: US/10/479,638
PRIOR PLING DATE: 2002-06-06
PRIOR PLING DATE: 2002-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
SPINGREN FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 54
NUMBER OF SEQ ID NOS: 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSET-TITQS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 35.1%; Pred. No. 3.9;
Matches 33; Conservative 10; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6; Length 520; 9.2;
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                                                                                                                 134 GGMGGGADGAYGSGAGGGVGKGQGESGVALAPSSDGYYNGGAAD 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:;
; CTHER INFORMATION: Clone ID: MRT4577_48027C.1.pep
[0S-10-422-115-312468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 NNLSSGYNSNGRYN--TIG-----SSDGNTGGYN 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 DNSTIELTQNGFRNNATIDQWNAKNSDITVGQYD 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , TYPE: PRT
, ORGANISM: Argiope trifasciata
US-10-479-638-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 21.2%;
Matches 36; Conservative
                                                           73 SGYGNGAD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-479-638-21
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                                                                                                                                                                                                                                                                  APPLICANT: La Rosa, Thomas J.
APPLICANT: Expedit bavid K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
ITILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
ITILE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: 18-21 (33.22) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 30390
LENGTH: 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 301334, Application US/10425115
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Scoul, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
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APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: 200, Yought Sould Molecules and Other Molecules Associated With
FILE OF INVENTION: Plants
FILE OF INVENTION WHERE: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 301334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 SSIÅG-----GGGGGGGGGGGTNGGSGSGGGGGGGGSGSSTAASGPSSGNYADAEGKGAG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 SALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSG-- 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 SALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDA----RKSETTITQ 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
11.7%; Score 90.5; DB 6; Length 25%;
Best Local Similarity 27.9%; Pred. No. 2.5;
Matches 29; Conservative 15; Mismatches 39; Indels 21; Gaps
                               65 KSETTIT----OSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                        158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
11.5%; Score 89.5; DB 6; Length 2:
Best Local Similarity 27.9%; Pred. No. 3;
Matches 29; Conservative 14; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 -----TQNGA--DVGQGADNSTIEL--TQNGFRNNATID 104
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US-10-425-115-301334
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US-10-425-115-300390
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OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                RESULT 6
US-10-425-115-300390
US-10-425-115-300390, Application US/10425115
GENERAL INFORMATION:
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ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
US-10-425-115-301334
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NAME/KEY: unsure
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PCT-US04-05654-2086
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32;
  Matches
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GENERAL INFORMATION:
Sequence 346132, Application US/10425115
GENERAL INFORMATION:
APPLICANT: Evosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: APPLICANT: And Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 346132
LENGTH: 179
                                                                                                                                                                                                                                                     TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENEOMICS AS A TOOL FOR TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENEOMICS AS A TOOL FOR TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR FILLE REPRENCE: 05394.0019
CURRENT APPLICATION NUMBER: US/10/468,356
CURRENT PRIOR DATE: 2003-08-19
PRIOR PEPLICATION NUMBER: 10/080,170
PRIOR FILING DATE: 2002-02-2
PRIOR PELICATION NUMBER: 60/270,123
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 655
SOOTHWARE: PATENTIN Ver. 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -- 113
                                       403 GYGAGAAAGAGAGAAAGAGSYSGSISRLSSAEAVNRVSSNIGAVASGGASALPGVISNIF 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                387 GYAPQGGGYAEPAGRDYDYGQSGAPDYGQPAPGGYSGYGQGGYGSAGTSVTLQLDDGSGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -STLSIYQYGSANAALALQSDARKSE
                                                                                114 ----TVGQYDQLVTR-----VVTHEMAHASV-MVRQVGFGNNATANQ 150
                                                                                                            463 SGVSSSAGSYBEAVIQSLLEVLSVLLHILSNSSIGYVGAEGLGDSLAVVQ 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 527;
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  74 GYGNGADVGQGADNSTIELTQNG-FRNNATIDQWNAKNSDI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_78839C.1.pep
US-10-425-115-346132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.2%; Score 86.5; Dilarity 22.9%; Pred. No. 13; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 GVVPQWGG----GGNHNGGGNSSGPD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Mycobacterium tuberculosis US-10-468-356-348
                                                                                                                                                                                                      US-10-468-356-348
; Sequence 348, Application US/10468356
; GENERAL INFORMATION:
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -10-425-115-346132
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LENGTH: 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 BQLSVEQGAPSQAIQPIPSSSKAFKFPMRPGKGQSGKRCIVKANHFFAELPDKDLHHYDV 213
                                               ---NHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTI 70
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24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: PIJGTH, MAYEAL L
TITLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 PCTT-0047 PCT
CURRENT APPLICATION NUMBER: PCT/US04/05654
CURRENT FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: 10/374, 780
PRIOR FILING DATE: 2003-02-25
PRIOR FILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 2950
SOFTWARE: Patentin version 3.2
SEQ ID NO 2086
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                                                                                                                                             71 TOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQ 117
                                                                                                                                                                                       117 EESGNNQNAGAGAGA-----ENGAANNGT-EAAGAENAAAGNGQ 154
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
  40;
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Best Local Similarity 25.7%; Pred. No. 34;
Matches 36; Conservative 17; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: G1152 Paralogous to G1146
Mismatches
                                                                                                                                                                                                                                                                                                                   Sequence 2086, Application PC/TUS0405654
GENERAL INFORMATION:
APPLICANT: Sherman, Bradley K
APPLICANT: Riechann, Jose Luis
APPLICANT: Jiang, Cai. Zhong
APPLICANT: Heard, Jacqueline E
APPLICANT: Heard, Volker
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214 TITPEVISRGVNRAVMKQLV 233
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Keddie, James
Dubell III, Arnold N
Pineda, Omaira
11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Creelman, Robert A
Ratcliffe, Oliver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 NGADVGQGADNSTIE---
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  Conservative
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Yu, Guo-Liang
                                               19 LAGVVPQWGGGG---
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APPLICANT: Larosa, ....
APPLICANT: Lu, Maclong
APPLICANT: Lu, Maclong
APPLICANT: Lu, Maclong
APPLICANT: Munyikwa, Tichifa R. I.
APPLICANT: Roberts, James K
APPLICANT: Roberts, James K
APPLICANT: Roberts, Campositions thereof
ITILE OF INVENTION: Compositions thereof
ITILE OF INVENTION: Cappositions thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
   77 GHENNGHGYGSSSTKTQTITQTSSSS-----SQGGNLEQTIL-NGHGNNG-IGYGSGSK 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 VIE------GYGGNNEKHLGGKLDQVV--LTGHENNGH-------GYGGSST 169
                                                                                                                               129 VIE------TTVTKHLGGNNEKHLGKLDQVV--LTGHENNGH-------GYGSSST 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 GHENNGHGYGSSSTKTQTITQTSSSS-----SQGGNLEQTÍL-NGHGNNG-IGYGSGSK 128
                                                                                             TIELTQNGFRNNATIDQWNAKNSDITVGQYDQLVTRVVTHE-MAHASVMVRQVGFGNNAT 147
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9194, Application US/60579062 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baum, James A
Kovalic, David K
Larosa, Thômas J
Lu, Maolong
Munyikwa, Tichifa R
Roberts, James K
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Best Local Similarity 26.8%
Matches 33; Conservative
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APPLICANT: Rovalic, David K.
APPLICANT: Larosa, Thomas J.
APPLICANT: Larosa, Thomas J.
APPLICANT: Larosa, Thomas J.
APPLICANT: Nunyikwa, Tichifa R. I.
APPLICANT: Roberts, James K.
APPLICANT: Roberts, James K.
APPLICANT: Roberts, James K.
APPLICANT: Wu, Wei
TITLE OF INVENTION: Compositions Thereof
FILE PEREBRENCE: 38-21(53403) B
CURRENT APPLICATION NUMBER: US/60/565,632
CURRENT APPLICATION NUMBER: US/60/565,632
CURRENT APPLICATION NUMBER: US/60/565,632
SOFTWARE: Patentin Version 3.2
SEQ ID NOS : 15449
SOFTWARE: Patentin version 3.2
LENGTH: 758
APPLICANT: Diversa Corporation
APPLICANT: Steer, Brian
APPLICANT: Steer, Brian
APPLICANT: Callen, Walter
APPLICANT: Callen, Walter
APPLICANT: Healey, Shaun
APPLICANT: Healey, Shaun
APPLICANT: Pulliam, Derrick
TITLE OF INVENTION: GUUCANASES, NUCLEIC ACIDS ENCODING THEM AND METHODS FOR MAKING AN
TITLE OF INVENTION: THEM
FILE REFRENCE: 564462009540
CURRENT FILING DATE: 2004-07-20
PRIOR PILING DATE: 2004-07-20
PRIOR PILING DATE: 2003-07-02
NUMBER OF SEQ ID NOS: 518
SOFWWARE: Patent In version 3.1
SEQ ID NO 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 IVVNGQTRQAENQSVNTGVWANNQCGGSGNSEWLHCNGYISFGNVSGSSSSSSSSSSSSS 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 NAALALQSDARKSETTITQ-----SGYGNGADVGQGADNSTIELT-QNGFRNNATIDQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 IVVSG-----SALAGVVP--QWGGGGN----HNGG----GNSSGPDSTLSIYQYGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
10.6%; Score 82.5; DB 1; Length 535;
Best Local Similarity 26.2%; Pred. No. 29;
Matches 38; Conservative 18; Mismatches 58; Indels 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Obtained from an environmental sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 WNAKN----SDITVGQYDQLVTRV 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9194, Application US/6056532
GENERAL INFORMATION:
APPLICANT: Baum, James A.
APPLICANT: Rovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Larcsa, Thomas J.
APPLICANT: Lu, Maolong
APPLICANT: Lu, Maolong
APPLICANT: Www. Tichifa R. I.
APPLICANT: Why Kwa, Tichifa R. I.
APPLICANT: Wu, Weif, James K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WGVSNFTGRTISVTVNGSGTAVTTI 505
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US-60-565-632-9194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (1)...(27) PCT-US04-21492-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
US-60-565-632-9194
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29 GGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNS

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OM protein - protein search, using sw model

Run on:

August 2, 2004, 14:39:53; Search time 9.4 Seconds (without alignments) 1545:204 Million cell updates/sec

US-09-543-407-14 775 1 MKLLKVAAFAAIVVSGSALA........HASVMVRQVGFGNNATANQY 151 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:\*
1: Dir1:\*
2: Dir2:\*
3: Pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMAKIES	DB ID Descri	2 JOSO39	2 AI0635 major cu	788 curlin protei	2 D90806 curlin major subu	2 H85665 hypothetical	2 S70787 curlin nuclea	2 C90806 minor curlin	2 G85665	2 JC6040	2 D70604	2 T51024	748 2 S42136 cnjB protein	174 2 E95965 hypothetical	2 B84533 hypotheti	028 2 A56038 DNA-binding p	213 2 S16356 ovo protein	2 AD3143	2 H98144	2 AH0635	2 JN0891	2 T03371 glycine-rich pr	2 S00275 tail fiber pr	2 C86266	2 A38307	2 E70946	1 \$19916	2 A70762 p	
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οN	Query Match Length	9.4	4.6	68.1	5.4	5.4	3.5	3.5	٠. ت	٠.	ĸ.	4.	.3	.0	۲.	.7	.7	.7	٠.	.7	9.	'n.	'n	ď.	4.	.2	.2	11.2 6	•
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PPE pr	rn.	leishmanolysin (EC	protein kinase sgg	merozoite 45K surf	hypothetical prote	probable sugar ABC	hypothetical prote	leishmanolysin (EC	Ξ.		hypothetical prote	hypothetical prote	protein kinase sgg	probable PPE prote
F70825	G84687 B42049	A44951	835327	B39112 ·	S66852	AD1539	T21956	A45621	PL0221	H84219	A83401	T15352	S35423	D70575
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645	599 599	599	575	347	967	440	407	590	602	285	340	440	1067	3300
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رم 9 8	φ.φ ∞.α	9.	85.5	8	82		9.4	m.	.eo	83.5	٠. ص	83.5	m.	m.
30	H 62	33	34	32	36	37	38	ტ ტ	40	41	42	43	44	45

### ALIGNMENTS

RESULT 1 JC6039 JC6039 JC6039 JC6039 JC6030
C;Function: } A;Description: major component of thin aggregative fimbriae A;Description: major component of plasminogen, tissue plasminogen activator C;Reywords: fimbria F;1-20/Domaiñ: signal sequence #status predicted <sig>F;21-151/Product: fimbrin protein agfa #status experimental <wat></wat></sig>
 Query Match Best Local Similarity 90.7%; Pred. No. 5e-52; Matches 137; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
 OY 1 MKLLKVAAFAAIVVSGSALAGVVPOWGGGGNHNGGGNSGPDSTLSIYOYGSANAALALO 60 
QY 61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120 

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CSG

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A) Description: major component of wild-type curli; interaction between CsgA and CsgB tr: A;Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli that and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers L-20, Domain: signal sequence #status predicted <SIG>F;21-151/Product: curlin #status experimental <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: D90806
B;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
A;Reference number: A99629; MUID:21156231; PMID:11258796
A,Title: The RpoS sigma factor relieves H-NS-mediated transcriptional repression of A,Reference number: S31202, MUID:93211294; PMID:8459772
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A;Residues: 1-152 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34843.1; PID:g13360880; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYD 119
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                                                                                                                               A/Molecule type: DNA
A/Residues: 1-6, 7', 8-151 < OLS1>
A/Accession: S34560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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ilarity 67.1%; Pred. No. 3.6e-36;
Conservative 21; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 528; DB 2;
; Pred. No. 5.4e-38;
20; Mismatches 27.
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| GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
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68.9%;
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Best Local Similarity
Matches 102; Conserv
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                                                                                                   A, Accession: S31202
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Matches 104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Function:
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N.Alternate names: csgA protein; major curlin protein
C.Species: Bacherichia coli
C.Species: Bacherichia coli
C.Species: Bacherichia coli
C.Species: Bacherichia coli
C.Species: Bacherichia coli
C.Species: Bacherichia coli
C.Species: Bacherichia coli
C.Species: S70788; G64846; S31202; S34560; S34559
R.Hammar, M.; Arnqvist, A.; Blan, Z.; Olsen, A.; Normark, S.
M.I. Microbiol. 18, G6140, 1995
A.Title: Expression of two csg operons is required for production of fibronectin- and C.
A.Reference number: S70783; MUID:96414468; PMID:8817489
A.Reference number: S70783; MUID:96414468; PMID:8817489
A.Status: nucleic acid sequence not shown; translation not shown
A.Residues: 1-151 c-HAM>
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A.Residues: 1-151 c-HAM>
A.Residues: 1-151 c-HAM
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A;Note: this species has also been called Salmonella typhi
C;Dacession: Al0635
C;Accession: Al0635
A;Status: preliminary
C; Countrior Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Status: preliminary
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R;Olsen, A.; Arngvist, A.; Hammar, M.; Sukupolvi, S.; Normark, S. Moltoni, T.; 523-536, 1993
                                                                                                                                                                                                                                       subsp. enterica serovar
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A;Residues: CB:AL513382; PIDN:CAD08268.1; PID:g16502315; GSPDB:GN00176
C;Genetics: A;Gene: STY1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
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Pred. No. 5e-52;
3; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
         NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                  curlin chain precursor [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.4%;
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Matches 137; Conservative
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A;Residues: 1-151 <BLAT>
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GjGenetics:
Ajdene: csgB
AjMap position: 23.15
CjFunction:
AjMap position: minor component of wild-type curli; interaction between CsgA and CsgB tr
AjMosecription: minor component of wild-type curli; interaction between CsgA and CsgB tr
AjMosecription: minor component of wild-type curli; interaction between CsgA and CsgB tr
AjMosecription: minor component of CsgA, CsgB can self-assemble into polymers
Fj1-21/Domain: signal sequence #status predicted <MGT>
Fj22-151/Product: minor curlin chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gurlin minor chain precursor, CsgA homolog [imported] - Escherichia coli (strain O157:H curlin minor chain precursor, CsgA homolog [imported] - Escherichia coli (strain O157:H C;Species: Escherichia coli (c;Species: Escherichia coli (c;Accesion: Gs666 Escherichia coli (d; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayher R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayher Hiler, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:111206551
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A;Molecule type: DNA
A;Residues: 1-151 <STO>
A;Cross-references: GB:AE005174; NID:g12514573; PIDN:AAG55787.1; GSPDB:GN00145; UWGP:Z1
A;Cross-references: GB:AE005174; NID:g12514573; PIDN:AAG55787.1; GSPDB:GN00145; UWGP:Z1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            minor curlin subunit precursor CsgB [imported] - Escherichia coli (strain O157:H7, s
Cj980des Escherichia coll
Cj98cdes: Bscherichia coll
Cjpacies: Bscherichia coll
Cjaccesion: C90806
R;Haysahi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: C90806
A;Status: preliminary
A;Molecule type: DMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 SETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQLVTRV 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-151 <HAY>
A;Residues: 1-151 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34842.1; PID:g13360879; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | :| |: | | :
| | SAVNELSKSSFNQAAII---GQAGTNNSAQLRQGGSKLLAVVAQEGSSNRA-KIDQTGDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 FAAIVVSGSAL--AGVVPQWGGGGNHNGGGNSSGPDSTLSIY-QYGSANAALALQSDARK
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                                                                                                                                                                                                                                                                                                                                                                                               Length 151;
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   source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                           ; Score 104.5; DB
; Pred, No. 0.054;
19; Mismatches 5
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                                                                                                                                                                                                                                                                                                                                                                                           13.5%;
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Best Local Similarity 29.28
Matches 35; Conservative
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nes 35; Conserv
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       A; Experimental
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Matches
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NiAlternate names: csgB procein; curlin nucleation component; minor curlin protein
C;Speciess: Escherichia coli
C;Speciess: Escherichia coli
C;Speciess: Escherichia coli
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 01-Mar-2002
C;Accession: S70787; F64846

A;Riammar, M; Arnqvist, A; Bian, Z; Olsen, A; Normark, S.
Mol. Microbiol. 18, 661-670, 1995
A;Ritle: Expression of two csg operons is required for production of fibronectin- and Cc
A;Reference number: S70783; MULD:96414468; PMID:8817489
A;Reference number: S70787
A;Reference number: S70783; MULD:96414468; PMID:8817489
A;Residues: 1-151 c4AM
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A;Residues: 1-151 c4AM
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A;Residues: 1-151 c4AM
A;Residues: 1-151 c
                                                                                                                                                                                                                                                                                                                                         hypothetical protein csqA [imported] - Escherichia coli (strain O157:H7, substrain EDL93 C; Species: Escherichia coli C; Species: Escherichia coli C; Species: L6-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C; Accession: H8565 H8565 C; Plunkett III, G; Burland, V; Mau, B; Glasner, J.D; Rose, D.J; Mayhen, Iller, L.; Grobbeck, E.J; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001 A; H1tle: Genome sequence of enterohemorrhagic Escherichia coli O157:H7. Apodaca, Nature 409, Especies: Ascession: H8565 A; Reference number: A85480; MUID:21074935; PMID:11206551 A; Reference number: DNA A; Residues: DNA A; Residues: L152 csTO> A; Residues: L152 csTO> A; Cross_references: GB:ABO05174; NID:g12514574; PIDN:AAG55788.1; GSPDB:GN00145; UWGP:216 A; Cross_references: Strain O157:H7, substrain EDL933 C; Genetics: A; Gene: csgA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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A,Residues: 1-151 <BLAT>
A,Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74125.1; PID:g1787278,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 QADARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKDSHMTVKOFG 120
S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKLLKVAAFAAIVVSGSALAGVVPQW-GGGGNHNGGGNSSGPDSTLSIYQYGSANAALAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.4%; Score 506.5; DB 2; 67.1%; Pred. No. 3.6e-36; ive 21; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGNGAAVDQTASNSTVNVTQVGFGNNATAHQY 152
                                                                                                                                                           GGNGAAVDQTASNSTVNVTQVGFGNNATAHQY 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 QLVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
                                                                                                             120 QLVTRVVTHEMAHASVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 67.1:
Matches 102; Conservative
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related to C2H2 zinc finger transcription factor D-Spl [imported] - Neurospora crassa N, Alternate names: protein B7F21.50 C. Species: Neurospora crassa C. Species: Neurospora crassa C. Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000 C. Accession: T51024 A. A. A. A. Hoheisel, J., Brandt, P., Fartmann, B.; Holland, R.; Nyakatura, Submitted to the Protein Sequence Database, July 2000 A. Reference number: 225286
                                                       A; Cross-references: GB:292774, GB:AL123456; NID:g3261729; PIDN:CAB07133.1; PID:g1877289
A; Experimental source: strain H37Rv
C; Genetios:
A; Gene: PPE
C; Superfamily: Phaseolus glycine-rich cell wall protein 1.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cnjB protein - Tetrahymena thermophila
Cispecies: Tetrahymena thermophila
Cipate: 19-Mar.1997 #sequence
Cipate: 19-Mar.1997 #sequence
Cipate: 19-Mar.1997 #sequence
Cipate: 19-Mar.1997 #sequence
Rigaylor, P.M.; Martindale, D.W.
Submitted to the EMBL Data Library, October 1992
A;Reference number: 842136
                                                                                                                                                                                                                                                                                                                                                                                                                      15 SGSALAGV-----VPQWGGGGNHNGGGNSSGPD---STLSIYQYGSANAALALQSDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          353 SGSGNIGVFNTGANTLVP---GDLNNLGVGNSGNANIGFGNAGVLNTGFGNASILNTGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 RKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 NAGE --- LINTGFGWAGFVNTGFDWSGNVNTGWGNSGNINTGSWWAGNVNTGFG----
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                                                                                                                                                                                                                                                                                                                                                   31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32; Gaps
                                                                                                                                                                                                                                                                         12.5%; Score 96.5; DB 2; Length 552; 28.5%; Pred. No. 1.1; ive 10; Mismatches 62; Indels 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Accession: T51024
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-70 < < SCH>
A,CESIA < CARP
A,CTOSS-references: EMBL:AL389901; GSPDB:GN00116; NCSP:B7F21.50
A,CTOSS-references: BAC clone B7F21; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 770;
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12.4%; Score 96; DB 2
Best Local Similarity 22.8%; Pred. No. 1.8;
Matches 31; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 RVVTHEMAHASVMVRQVGFGNNAT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -IIIDSGLINS-----GFGNTGT 476
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                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 28.55
Matches 41; Conservative
   A;Molecule type: DNA
A;Residues: 1-552 <COL>
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A,Gene: NCSP:B7F21.50
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A;Introns: 117/1
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: D70664
E;Cole, S.T.; Brosch, R.; Perkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentler, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
A;Authors: Sqares, S.
A;Authors: Organis the biology of Mycobacterium tuberculosis from the complete genome A;Accession: D70664
A;Accession: D70664
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C, pages 11-10c-11990 #sequence_tevision_1-1-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-10c-1-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 ITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQLVTRVVTHE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----AIIQKGSGNKANİTQYGTQK------TAVVVQK 140
                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                           88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fimbrin protein agfB precursor - Salmonella enteritidis
C;Species: Salmonella enteritidis
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                             | | | : | | : | | : | | : | | EAVNELSKSSFNQAAII---GQAGTNNSAQLRQGGSKLLAVVAQEGSSNRA-KIDQTGDY
                                                                                                                                                                                                                                                                                                                                                                                                                          66 SETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQLVTRV
                                                                                                                                                                                                                                                                                    9 FAAIVVSGSAL--AGVVPQWGGGGNHNGGGNSSGPDSTLSIY-QYGSANAALALQSDARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 AAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETT
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37;
                                                                                                                                             Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.7%; Score 98.5; DB 2; Length 151; 26.2%; Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                 Indels
   strain 0157:H7, substrain EDL933
                                                                                                                                      ;; Score 104.5; DB 2;
;; Pred. No. 0.054;
19; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34; Conservative 17; Mismatches
                                                                                                                                          13.5%;
llarity 29.2%;
Conservative 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 OSHMAIRVTO 150
                                                                                                                                      Query Match
Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
A,Experimental source:
C,Genetics:
A,Gene: csgB
                                                                                                                                                                                                                                                                                                                                                           33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58
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us-09-543-407-14.rpr

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Mypothetical protein At2g15770 [imported] - Arabidopsis thaliana C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Accession: B84533
R'idin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffet, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L. Nature 402, 761-768, 1999
Ayītile: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: B84533
A;Accession: B84534
A;Accession: Preliminary
A;Accession: Speciminary
A;Accession: Speciminary
A;Residues: 1-301 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaste
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 TITQSGYGNGADVG-QGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQLVTRVVT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 SGSGLGSNSNNGSGWGWGTGSNRGSGSGSTNPDGSRRSWWW----SLKSGWSWSWG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Cross-references: GB: AE002093; NID: g5306254; PIDN: AAD41987.1; GSPDB: GN00139 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA-binding protein ovo - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Dacession: A56038
R;Garfinkel, M.D.; Wang, J.; Liang, Y.; Mahowald, A.P.
Mol. Cell. Biol. 14, 6809-6818, 1994
A;Fitle: Multiple products from the shavenbaby-ovo gene region of Drosophila A;Reference number: A56038; MUID:95021209; PMID:7935398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGSALA----GVVPOWGGGGNH-NGGGNSSGPDSTLSIYQYGSANAALALQSDARKSET
                                                                                                                                                                                         11 AIVVSGSALAGVVPQ--WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Molecule type: mRNA
A,Residues: 1-1028 <GAR>
A,Cross-references: GB:U11383; NID:g520526; PIDN:AAB60216.1; PID:g520527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                       64;
                                                                                                                                                                                                                                                 693 AIATAGAGAVGILAQSIGGGGGN---GGNATGGDAGFGSFQIGGGGGG----
                                                                            Length 2174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51; Indels
                                                                                                                                       Indels
                                                                                                                                    32;
                                                                            ; Score 93; DB 2;
; Pred. No. 11;
15; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 91; DB 2;
Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    HEMAHASVMVRQV --- GFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---SHAAGIVAQSVGGGGGTGGTASSY 781
                                                                                                                                                                                                                                                                                                                                                            ----GGYANTANVGFKG-----LTLTTQG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.7%;
26.4%;
                                                                                  12.0%;
24.5%;
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                                                                                                                                       36; Conservative
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Best Local Similarity
                                                                                  Query Match
Best Local Similarity
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A;Gene: SMb21548
A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Gene: At2g15770
A,Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                       128
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                                                                                                                                                                                                                                                                                                                                                               738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical glycine-rich protein [imported] - Sinorhizobium meliloti (strain 1021) maga C; Species: Sinorhizobium meliloti
C; Species: Sinorhizobium meliloti
C; Accession: E95965
R; Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. Us.A. 98, 9889-9894, 2001
A; Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endc A; Reference number: A95842; MUID:21396508; PMID:11481431
A; Reference number: A95842; MUID:21396508; PMID:11481431
A; Recasion: E95965
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-2174 «KUR»
A; Residues: 1-2174 «KUR»
A; Residues: 1-2174 «KUR»
A; Residues: DNA
A; Residues: D: Chain, P.; Cowie, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P; Bilbert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Pelalue, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A; Contents: annotation
C; Genetics: annotation
C; Genetics:
                                                                                                                                                                                                                                   A;Gene: cnjB
A;Gene: cnjB
A;Genetic code: SGC5
A;Intrones: 85/3; 157/3; 201/2; 290/2; 327/3; 499/1; 573/2; 607/3; 708/3; 777/3;
C;Keywords: zinc finger
F;1164-1450/Region: glycine-rich
F;1478-1491/Region: zinc finger CCHC motif
F;1478-1491/Region: zinc finger CCHC motif
F;1501-1514/Region: zinc finger CCHC motif
F;1501-1514/Region: zinc finger CCHC motif
F;1579-1592/Region: zinc finger CCHC motif
F;1579-1592/Region: zinc finger CCHC motif
F;1678-148/Region: zinc finger CCHC motif
F;1602-1615/Region: glycine-rich
                                                                                                                                          repeats in a protein encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1640 QFGGGGNSNGGQSWGTSSGSDWN-------CQSNVQESTTTSSGGWGSSGSGN 1685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QWGGGGNHNGG----GNSSGPDSTLSIYQYGSANAALALQSDARKSETTIT-----QSGYGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1748;
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                    A, Residues: 1-1748 <TAY>
A, Cross-references: EMBL:L03710; NID:g161751; PID:g161752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QTGGGWGSNDN-----QQQQNENTGGGGWGSSNSNQT 1717
                                                                            R;Taylor, F.M.; Martindale, D.W.
Nucleic Acids Res. 21, 4610-4614, 1993
A;Title: Retroviral-type zinc fingers and glycine-rich xA;Reference number: 542135; MUID:94051569; PMID:8233798
A;Accession: 842135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 GADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDIT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: 236-250, 17, 252-255, N7, 257-773 < MAR> A; Cross-references: EMBL:X06462 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.3%; Score 95; DB 2
32.0%; Pred. No. 5.6;
tive 11; Mismatches
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Best Local Similarity 32.00
Matches 31; Conservative
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C.Genetics:
A;Gene: ovo
A;Cross-references: FlyBase:FBgn0003028
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		4,	62
		Gaps	LALQSD
		26;	SANAA
ngth 1028		Indels	STLSIYOYG
. Le		41;	SSGPD
Score 91; DB 2	Pred. No. 6.7;	8; Mismatches	VVPQWGGGGNHNGGGN
11.78;	Best Local Similarity 31.2%; Pred. No. 6.7;	Matches 34; Conservative 8; Mismatches 41; Indels 26; Gaps 4;	3 LLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD 62
Query Match	Best Local	Matches 3	3

Search completed: August 2, 2004, 14:56:21 Job time: 9.4 secs

us-09-543-407-14.rsp

42

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August 2, 2004, 14:36:12; Search time 5.3 Seconds (without alignments) 1483.508 Million cell updates/sec
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775
I MKLLKVAAFAAIVVSGSALA.......HASVMVRQVGFGNNATANQY 151
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SwissProt\_42:\*

Database :

SUMMARIES

Description	P55225 salmonella	Ø	(D)	a)	P55226 salmonella	homo sapi	drosophil	salmonell		bacteri			Q10778 mycobacteri		004379 arabidopsis	Q03646 plasmodium	P23223 leishmania	P08148 leishmania			Q50367 mycoplasma		drosop	homo sa	oryza s		pepper	Φ	arthrobac	•		Ψ	P02877 hevea brasi
QI	CSGA SALTY	CSGA_ECOLI	CSGA_ECO57	CSGB_ECOLI	CSGB_SALTY	TNK1 HUMAN	OVO DROME	CSGB_SALTI	PER_DROWI	VG38 BPT2	PRTC_ERWCH	GP63_LEIME	YF48 MYCTU	GP63_LEICH	AGO1_ARATH	MSA2 PLAF2	GP63_LEIDO	GP63_LEIMA	PDA6_CAEEL	SGG DROME	P35 MYCPE	OMPB RICJA	HDC DROME	HME1 HUMAN	GRP1_ORYSA	RRPO_PMMVJ	RRPO PMMVS	PRTB_ERWCH		PER DRONE	YK98 MYCTU	CEAK_ECOLI	HEVE_HEVBR
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P91698 drosophila Q8ixf0 homo sapien	P18127 xanthomonas P30688 neisseria m	Q24180 drosophila	P34291 caenorhabdi	P34308 caenorhabdi	P52302 drosophila	Q12756 homo sapien	P06997 escherichia	P55004 pharbitis n
PER_DROPV NPA3_HUMAN	ICEN_XANCT OMB2_NEIMB	DEAF_DROME	YKO3 CABEL	YKR2_CAEEL	MBN_DROME	KF1A_HUMAN	SUBI_ECOTI	PHYE_PHANI
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# ALIGNMENTS

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This SWISS-PROW entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstainnthe between the Swiss institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 21-33.

SPECIES=S.enteritidis, STRAIN=27655-3B;

MEDLINE=91310586; PubMed=1677357;

Collinson S.K., Emcedy L., Mueller K.-M., Trust T.J., Kay W.W.;

Collinson and characterization of thin, aggregative fimbriae from Salmonella enteritidis.";

J. Bacteriol. 173:4773-4781(1991).

-! FUNCTION: CURLIN IS THE STRUCTUREL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                   SPECIESS. enteritidis. STRAIN=27655-3B;
MEDLINE=94013373; PubMed=8104955;
Doran J.L., Collinson S.K., Burian J., Sarlos G., Todd B.C.D.,
Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., Kay W.W.;
"DNA-based diagnostic tests for Salmonella species targeting agfA, the structural gene for thin, aggregative fimbriae.";
J. Clin. Microbiol. 31:2263-2273(1993).
                                                                           SEQUENCE FROM N.A.
SPECIES-S.-encretitidis; STRAIN=27655-3B;
MEDLINE=96146512; Pubmed=8550497;
Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W.W. "Salmonella enteritidis agf8AC operon encoding thin, aggregative fimbriae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVMVRQVGFGNNATANQY -> DSYTQVAS (IN
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Pred. No. 4.9e-53;
3; Mismatches 11;
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SIGNAL
                                     Bacteriol. 185:2330-2337(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REF.
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EMBL; AL67269; CAD08268.1; -
EMBL; AE016840; AA069399.1; -
EMBL; U43280; AA43599.1; -
PIR; UG089; AG0389.1; -
Stygene; SG10608; csgA.
                                                                                                                                                                                              Bacteriol. 178:662-667(1996)
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Best Local Similarity 90.7%;
Matches 137; Conservative
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                                                                                                                                                                                                                                    SEQUENCE OF 21-151
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SEQUENCE OF 21-31.

MEDLINEs-9110/586; PubMed=1677357;

MEDLINEs-9110/586; PubMed=1677357;

MEDLINEs-9110/586; PubMed=1677357;

MEDLINEs-9110/586; PubMed=1677357;

"Purification and characterization of thin, aggregative fimbriae from Salmonella enteritidis.";

J. Bacteriol. 173:4773-4773 (1991).

I. PONCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES TRAT ASSEMBLE PREFERENTALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=66414468; PubMed=8817489; Hammar M., Arnqvist A., Bian Z., Olsen A., Normark S.; Expression of two csg operons is required for production of fibronectin- and congo red-binding curli polymers in Escherichia coli
                                                                                                                                                                                                                           MEDLINE 7061202; PubMed=8905212;
Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Oshima T., Alba H., Baba T., Fujita K., Kanai K., Kashimoto K.,
Ilada T., Ilada T., Kajhara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Moromura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
A. 718-kb DNA sequence of the Escherichia coli K-12 genome
Corresponding to the 12.7-28.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MICHAEL / MG1655,
MEDLINE=97422 / MG1655,
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Biattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arnqvist A., Olsen A., Pfeifer J., Russell D.G., Normark S.; "The Cr! protein activates cryptic genes for curli formation and fibronectin binding in Escherichia coli HB101."; Mol. Microbiol. 6:2443-2452(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of Bscherichia coli K-12."; Science 277:1453-1474(1997).
                               01.DEC-1992 (Rel. 24, Created)
01-007-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Major curlin subunit precursor.
151 AA.
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SEQUENCE OF 21-40.
STRAIN-K12 / YMEL;
MEDLINE-93023873; PubMed-1357528;
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                                                                                                                                                                                                                                                                                                                 Escherichia coli.";
Mol. Microbiol. 7:523-536(1993)
STANDARD;
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                                                                                                                    Escherichia coli
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Mau B., Shao Y.;
                                                                                                                                                                          NCBI_TaxID=562;
                                                                                                     CSGA OR B1042
ECOLI
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65.4%; Score 506.5;
67.1%; Pred. No. 5.6e
:ive 21; Mismatches
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01-CT-1996 (Rel. 34, Last sequence up. 28-FEB-2003 (Rel. 41, Last annotation Minor curlin subunit precursor.
CSGB OR B1041 OR Z1675 OR ECS1419.
                                                                                                                                                                                                                                                                                                                              EMBL, AP275733; AAK53212.1; -.
EMBL; ABC05315; AAG55788.1; -.
EMBL; APC05254; BAB34843.1; -.
PIR, D90806; D90806.
PIR, H85665; H85665.
Fimbria; Signal; Complete proteome.
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NCBI_TaxID=562, 83334;
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Best Local Similarity 67.1<sup>5</sup>
Matches 102, Conservative
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                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=21218556; PubMed=11319125;
Uhlich G.A., Keen J.E., Elder R.O.;
"Mutations in the csgD promoter associated with variations in curli
expression in certain strains of Escherichia coli 0157:H7.";
Appl. Environ. Microbiol. 67:2367-2370(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0157:H7.";
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Fosfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.,
                                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                         Length 151;
                                                                                                                                                                                                                                                                                            68.1%; Score 528; DB 1; Length 15:
68.9%; Pred; No. 7.9e-39;
Mismatches 27; Indels
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Nature 409:529-533(2001)
                                                                                                                                                                                                                                                                A -> E (IN REF. 1).
C003470D208D395F CRC64;
                                                                                                                                                                                                                                                     MAJOR CURLIN SUBUNIT.
 -!- SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                           Fimbria, Signal, Complete proteome.
SIGNAL
                                                                                                                              EMBL, L04979, AAR23616.1; -.
EMBL, S07074; CA662282.1; -.
EMBL, AE000205, AAC74126.1; -.
EMBL, D90741; BAA35832.1; -.
PIR, S707788; S707788.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last seque
28-FEB-2003 (Rel. 41, Last annot
Major curlin subunit precursor.
CSGA OR Z1676 OR ECS1420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterobacteriaceae; Escherichia
                                                                                                                                                                                                                                                                              151 AA; 15049 MW;
                                                                                                                                                                                                                                                                                                                                  104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                     Similarity
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Q93U24;
                                                                                                                                                                                                                                                                 CONFLICT
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DEGLEMENT N. H. STRING 0509952;

MEDLINE=21156231; PubMed=11258796;

MEDLINE=21156231; PubMed=11258796;

MEDLINE=21156231; PubMed=11258796;

Han C.-G., Ohtsubo E., Nakama K., Murata T., Tanaka M., Tobe T.,

Iida T.; Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

Kuhara S., Shiba T., Hattori M., Shinaqawa H.,

"Complete genome sequence of enterchemorrhagic Escherichia coli

O157:H7 and genomic comparison with a laboratory strain K-12.";

DNA RES: 8:11-22(2001).

-: FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE

COLLED SURRACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH

TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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STRAIN=K12 / MC4100;
MEDLINE=96414468; PubMed=8817489;
Hammar M., Almqvist A., Bian Z., Olsen A., Normark S.;
Hammar M., Armqvist A., Bian Z., Olsen A., Normark S.;
Hammar M., Armqvist Operons is required for production of the fibronectin- and congo red-binding curli polymers in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gammaproteobacteria; Enterobacteriales;
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MAJOR CURLIN SUBUNIT.
EE2D2D94DDE91243 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
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EMBL, AE000205, AAC74125.1; --
EMBL, D90741, BAA35831.1; --
EMBL, AP005315, AAG55787.1; --
EMBL, AP00254; BAB34842.1; --
PIR, C90806, C90806.
PIR, G9665; G95665.
PIR, S70787, S70787.
ECGGene, EG12621, CsgB.
Fimbria; Signal; Complete protecome.
Fimbria; Signal; Complete Protecome.
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                                                                                                                                                                                                                                                                                                                                                    22 1
151 AA;
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Best Local Similarity
Matches 35; Conserv
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MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12:";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oshima T., Aiba H., Babilta K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95157246; PubMed=7854117;
Arnqvist A., Olsen A., Normark S.;
Arnqvist A., Olsen A., Normark S.;
"Sigma S-dependent growth-phase induction of the csgBA promoter in
Scherichia coli can be achieved in vivo by sigma 70 in the absence
of the nucleoid-associated protein H-NS.";
Mol. Microbiol. 13:1021-1032 (1994).
-!- FUNCTION: CURLIN IS THE STRUCTUBAL SUBUNIT OF THE CURLI. CURLI AR.
COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH
TEMPRERAVURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
CURLIN MONOMERS.
                                                                                                                        SECURIOLENCE TO MIGHES STRAIDENCE TO MIGHES STRAIDENCE TO MEDLINE=97426617; PubMed=9278503; MEDLINE=97426617; PubMedt G. III, Bloch C.A., Perna N.T., Burland V., Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=21074935, PubMed=11206551,
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Dautin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12,7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97061202; PubMed=8905232;
                                        Mol. Microbiol. 18:661-670(1995).
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EMBL; X90754; CAA62281.1; -.

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66 SETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQLVTRV 125
                                                                                                                                                                                                                                                                            9 FAAIVVSGSAL--AGVVVPQWGGGGNHNGGGNSSGPDSTLSIY-QYGSANAALALQSDARK 65
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J. Bacteriol. 178:662-667(1996).
J. Bacteriol. 178:662-667(1996).
J. Bacteriol. CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE
COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTTALLY AT GROWTH
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=S.typhimurium, STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Materston R., Wilson R.K.;
                                                                                                                                                                                                         33 FAVNELSKSSFNQAAII---GQAGTNNSAQLRQGGSKLLAVVAQEGSSNRA-KIDQTGDY
                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=S.typhimurium; STRAIN=SR-11;
MEDLINE=98117058; PubMed=9457880;
Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;
"Curli fibers are highly conserved between Salmonella typhimurium an
Escherichia coli with respect to operon structure and regulation.";
J. Bacteriol. 180:722-731(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Banser P.A., Kay W.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FBE-2003 (Rel. 41, Last annotation update)
Minor cutlin subunit precursor (Fimbrin SEF17 minor subunit).
CSGB OR AGFB OR STM1143.
                                                                                Length 151;
                                                                                                                        Indels
             151 MINOR CURLIN SUBUNIT.
15882 MW, B18D266B964014B8 CRC64;
                                                                                DB 1;
                                                                                                                        59;
                                                                                13.5%; Score 104.5; DB 29.2%; Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                     151 AA
                                                                                                                        19; Mismatches
POTENTIAL.
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FUNCTION,
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its modified and this statement is as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARVRQEGSKLLSVISQ--EGGNNRAKVDQAGNYNFAYIEQIGNAN-------DAS 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 ITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQLVTRVVTHE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----AIIOKGSGNKANITOYGTOK------TAVVVOK 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 AAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20556282; PubMed=10988299;
Chi N.-W., Lodish H.F.;
Tankyrase is a Golgi-associated mitogen-activated protein kinase
substrate that interacts with IRAP in GLUT4 vesicles.";
J. Biol. Chem. 275:38437-38444 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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"Tankyrase, a poly(ADP-ribose) polymerase at human telomeres.";
Science 282:1484-1487(1998).
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                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 151;
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COFC5430E6DD361D CRC64;
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-007-2003 (Rel. 42, Last annotation update)
11-007-2003 (Rel. 41, Last annotation update)
11-007-2003 (Rel. 41, Last annotation update)
11-007-2003 (Rel. 41, Last annotation update)
11-007-2003 (Rel. 41, Last annotation update)
11-007-2003 (Rel. 41, Last annotation update)
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11-007-2003 (Rel. 41, Last annotation update)
11-007-2003 (Rel. 41, Last annotation update)
11-007-2
  SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1327 AA.
                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 0.07
                                                                                                                                                                                                                                                                                                                                                                                                Score 98.5;
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EMBL, AE008749; AAL20073.1; -.
EMBL; U43280; AAC43598.1; -.
EMPL; JC6040; JC6040.
StyGene; SG10609; csgB.
Fimbria; Signal; Complete protecome.
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MEDLINE=99040105; PubMed=9822378;
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                                                                                                                                                                                                                                                                                                                                                                                            12.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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Thuman telacemene yoly (AULF-KIDOSE) polymerases tankyrase I and 2

AL Monagi telomeres.";

Mol. Cell. Biol. 22:33-342 (2002).

-!- FUNCTION: May regulate vesicle trafficking and modulate the subjectifular distribution of SLC2A4/GLUT4-vesicles. Has PARP activity and can modify TRT, and thereby contribute to the regulation of telomere length.

-!- CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribosyl} (N) -acceptor = nicctinamide + {ADP-ribosyl} (N+1) -acceptor.

-!- SUBUNIT: Oligomerizes and associates with TNKS2. Interacts with the cytoplasmic domain of LAPBP/Otase in SLC2A4/GLUT4-vesicles.

-!- SUBUNIT: Oligomerizes and associated with the Golgi and with juxtanuclear SLC2A4/GLUT4-vesicles.

-!- SUBCELLULAR LOCATION: Cytoplasmic, associated with the Golgi and with juxtanuclear SLC2A4/GLUT4-vesicles. A minor proportion is also found at nuclear pore complexes and around the pericentriolar matrix of mitotic centromeres. During interphase, a small fraction of TNKS is found in the nucleus, associated with TRF1.

-!- ALTERNATIVE PRODUCTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isoid=095271-2; Sequence=VSP_004538, VSP_004539;
Note=No experimental confirmation available;
TISOE SPECIFICITY: Ubiquitous; highest levels in testis.
PTM: Upon insulin-stimulation, phosphorylated on serine residues by MAPK kinases.
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R MIN; 603031;

R GO; 60:0000781; C:chromosome, telomeric region; IDA.

GO; GO:0000781; C:chromosome, telomeric region; IDA.

GO; GO:0000781; F:Drotein binding; IPI.

R GO; GO:0007004; P:telomerase-dependent telomere maintenance; NAS.

R InterPro; IPR002110; ANK.

R InterPro; IPR002110; ANK.

R Pfam; PF00023; ANY: 1.

R Pfam; PF00023; ANY: 1.

R PRINTS; PR01415; ANXXIN.

R SMART; SM00248; ANK; 1.
                                                                      ak G., Smith S.;
polymerases tankyrase 1 and
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PROSITE; PS50297; ANK REP REGION; 1.
PROSITE; PS50105; SAM_DOWAIN; 1.
Transferase; Glycosyltransferase; NAD; Golgi stack; Telomere;
Muclear protein; Repeat; ANK repeat; ADF-ribosylation;
Phosphorylation; Alternative splicing.
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SIMILARITY: Belongs to the PARP family.
SIMILARITY: Contains 15 ANK repeats.
SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
AND MUTAGENESIS OF HIS-1184 AND GLU-1291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=2;
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                                                                          Shostak
                                       MEDLINE=21602874, PubMed=11739745,
Cook B.D., Dynek J.N., Chang W., Shosta
"Role for the related poly(ADP-Ribose)
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EMBL; AF082557; AAC79842.1; --
EMBL; AF082559; AAC79843.1; --
EMBL; AF082559; AAC79844.1; --
HSSP; Q00420; LAWC.
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                                                                                                                                                                                                                                                                                               SMART; SM00355; ZnF C2H2; 4.
PROSITE; PS00028; ZINC FINGER C2H2_1; 3.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
Zinc-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein;
      ITS CONTINUED
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; D7068BB2BC0F6F77 CRC64;
BUT IS RAPIDLY LOST IN THE EMBRYOS EXCEPT FOR I PRESENCE IN THE GERM LINE PRECURSOR POLE CELLS. SIMILARITY: Contains 4 C2H2-type zinc fingers.
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8; Mismatches
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C2H2-TYPE 2.
C2H2-TYPE 3.
C2H2-TYPE 4.
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EMBL; X59772; CAB36921.1; ALT_SEQ.
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InterPro; IPR007087; Znf C2H2.
Pfam; PF00096; zf-C2H2; 3.
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CSGB SALTI
ID CSGES SALTI STANDARD;
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CSGTM3;
DT 28-FEB-2003 (Rel. 41, Created)
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Best Local Similarity 31.2%;
Matches 34; Conservative
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HSSP, P07248, 2ADR.
IRANSFAC, T00669; -.
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                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                        /FTIG=VSP_004538.
Missing (In isoform 2).
/FTIG=VSP_004539.
H->A: LOSE OF ACTIVITY, WHEN ASSOCIATED WITH A-1291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSZUB-OVARTY:

MEDIAINE-9502120; PubMed=7935398;

Garfinkel M.D., Wang J., Liang Y., Mahowald A.P.;

Garfinkel M.D., Wang J., Liang Y., Mahowald A.P.;

"Multiple products from the shavenbaby-ovo gene region of Drosophila
"Multiple products from the shavenbaby-ovo gene region of Drosophila
mol. Cell. Biol. 14:6809.6618(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212
                                                                                                                                                                                                                                                                                                                  E->A: LOSS OF ACTIVITY; WHEN ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM
                                                                                                                                                                                                                                                                                                                                                                                                          8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).

Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                          ; Score 92; DB 1; Length 1327;
; Pred. No. 3.3;
15; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                WITH A-1184.
W; E14DE985C710B957 CRC64;
                                                                                                                                                                                                                        EST -> GHS (in isoform 2).
/FTId=VSP_004538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OVO DROWE STANDARD; PRT; 1028 AA. P51521; Q9XZU4; 01-0CT-1996 (Rel. 34, Last sequence update) 01-0CT-2003 (Rel. 42, Last sequence update) Ovo protein (Shaven baby protein).
    ANK 7.

ANK 8.

ANK 9.

ANK 10.

ANK 11.

ANK 11.

ANK 12.

ANK 13.

ANK 14.

PARP

PARP

POLY-PRO.

POLY-PRO.
                                                                                                                                                                                                               POLY-SER
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30.4%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                  1291
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VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 ARVRQEGSKILLSVISQ--EGENNRAKVDQAGNYNFAYIEQTGNAN------DAS 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 ITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQLVTRVVTHE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----AIIQKGSGNKANITQYGTQK------TAVVVQK 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69
                                                                                                                                                     Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Basch S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Chillingworth T., Parrar J., Feltwell T., Handin N., Haque A., Hien T.T., Holroyd S., Jagels K., Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIR=TY2 / ATCC 700931;
STRAIR=TY2 / ATCC 700931;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 AAIVVSGSALAGVVPQWGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETT
                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI AN COLLED SURFACE STRUCTURES THAT ASSENBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                 Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MINOR CURLIN SUBUNIT.
161C54326E573495 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY
28-FEB-2003. (Rel. 41, last sequence update) 10-0cT-2003 (Rel. 42, Last annotation update) Minor curlin subunit precursor. CSGB OR STY1180 OR T1777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.4%; Pred. No. 0.36 iive 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 90.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AL627269; CAD08267.1; -.
EMBL, AE016840; AA069400.1; -.
Fimbria; Signal; Complete proteome.
                                                                                                                               STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol. 185:2330-2337(2003).-!- FUNCTION: CURLIN IS THE STRUCT
                                                                            Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 AA; 16254 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33; Conservative
                                                                                                                                                                                                                                                                                          Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OSHMAIRVTO 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURLIN MONOMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                    SEQUENCE FROM N.A.
                                                       Salmonella typhi
                                                                                        NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141
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Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila.";
Mol. Biol. Evol. 10:127-139(1993).
-!- FUNCTION: Essential for biological clock functions. Determines the
                                                                                                                                                                                                                                                                                                                                              of the period locus in
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE$93196482; PubMed=8450754;
Peixoto;A.A., Campesan S., Costa R.H., Kyriacou C.P.;
"Molecular evolution of a repetitive region within the per gene of
                                                                                                                                        Drosophila willistoni (Fruit fly).
Bukaryoča; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydrosidea; Drosophilidae; Drosophila.
NCBI_TaxID=7260;
                                                                                                                                                                                                                                                                                                                      Gleason J.M., Powell J.R.;
"Interspecific and intraspecific comparisons the Drosophila willistoni sibling species.";
Mol. Biol. Evol. 14:741-753 (1997).
                                                                                  annotation update)
PER DROWI STANDARD; PRT; 1093 AA. 003297; 0018421; 0018422; P91721; P91722; 01-0CT-1993 [Rel. 27, Created) 15-UUL-1998 [Rel. 36, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update Period circadian protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                      STRAIN=Various strains;
MEDLINE=97357421; PubMed=9214747;
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCÈ OF 579-646 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; US1055; AAB41360.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB41361.1; -.
AAB41362.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB41363.1; -. AAB41364.1; -.
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                                                                                                                                                                                                                                                              SEQUENCE
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EMBL;
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EMBL;
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RESULT 9 PER\_DROWI

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Bacteriophage T2.
Viruses; dsDNA viruses, T4-like viruses.
MCBI_TAXID=10664;
                                                                                                                                                                                                                                                                  Local Similarity
hes 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM N.A.
                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROSTRAIN=B374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86
                                                                                                                                                                                                                                  FOLLYMAN (10 STRAIN 0811.4).
S -> F (IN STRAIN 0811.4).
G -> V (IN STRAIN GUANA).
G -> A (IN STRAIN MANAUS 2).
G -> S (IN STRAIN PANTA MARIA).
MISSING (IN STRAIN PORTO ALEGRE 3).
MISSING (IN STRAIN PORTO ALEGRE 4).
MISSING (IN STRAIN PARANS I AND MANAUS
                                                                                                                                                                                                                                                                                                                                                             MISSING (IN STRAINS MANAUS 4, PORTO
ALEGRE 1 AND PORTO ALEGRE 2).
S - A (IN STRAINS GUADELOUPE AND GUANA).
MISSING (IN STRAIN MANAUS 3).
A -> T (IN STRAIN 0811.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 GGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGAD
                                                                                                                                           NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                              MISSING (IN STRAINS LIMA B, L'HABITATUE
                                                                                                                                                                                                                                                                                                                                      MISSING (IN STRAINS GUADELOUPE, MANAUS PORTO ALEGRE 2, PORTO ALEGRE 1 AND
                                                                                                                                                                                                                                                                                                                             -> V (IN STRAIN PORTO ALEGRE 4)
                                                                                                                   Biological rhythms; Repeat; Nuclear protein; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                               11.6%; Score 90; DB 1; Length 1093; 27.7%; Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                115896 MW; AB6DE050267EC187 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----SCSGLGGNGNVGSGNGNNSQPSTNQYTQ 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87 NSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-AUG-1990 (Rel. 15, Last annotation update)
Receptor recognizing protein (Protein Gp38).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262 AA
                                                                                                                                                                                                                                                                                                                      AND CANO MORA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Mismatches
                                                                                                                                                                           POLY-LYS.
POLY-GLY.
POLY-GLY.
POLY-SER.
POLY-GLY.
POLY-ALA.
POLY-ALA.
                                                                 EMBL, L06342; AAA28765.1; --
FlyBase; FBgn0013161; Dwil\per.
InterPro; IPR000014; PAS_domain.
                                 U51069; AAB41374.1; -. U51070; AAB41375.1; -. U51071; AAB41376.1; -.
                US1067; AAB41372.1; -. US1068; AAB41373.1; -.
                                                          US1072; AAB41377.1; -.
 AAB41370.1;
          AAB41371.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                           PROSITE; PS50112; PAS;
                                                                                                                                    766
886
1093
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                                                                                         PF00989; PAS; 2.
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                                                                                                    PAS;
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Matches 26; Conserv
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 US1065;
                                                                                                                           Polymorphism.
NON_TER
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P07875;
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VARIANT
NON TER
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VARIANT
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EMBL;
EMBL;
EMBL;
EMBL;
 EMBL;
                                                          EMBL;
                                                                                            Pfam;
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VG38 BPT2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGGRPFGVGGKIGSDSILS----GSNASL---TDAGTGGTTF-OYGAGNGGNVGAGGG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 GCCGNHNGGCNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGAD 86
                                                                                                                                                                                                                           Riede I., Drexler K., Eschbezch M.L., Henning U.;
"DNA sequence of genes 38 encoding a receptor-recognizing protein of
"DNA sequence of genes 38 encoding a receptor-recognizing protein of
Dacteriophages T2, K3 and of K3 host range mutants.";
J. Mol. Biol. 194:31-39(1987).
-!- FUNCTION: Vg38 is at the tip of the long tail fibers and serves as
the phage recognition site for the cellular receptor.
-!- MISCELLANBOUS: THIS PHAGE USE OUTER MEMBRANE PROTEINS OMPF AND TTR
AS RECEPTORS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pectobacterium.
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no RNA stage; Caudovirales; Myoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.5%; Score 89.5; DB 1; Length 262; 34.1%; Pred. No. 0.83;
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PIR; S00275; S00275.
InterPro; IPR07932; Tail_fibre_GP38.
Fifam, PF05268; GP38; recognition.
Sequence to the phage recognition.
SEQUENCE 262 AA; 25801 MW; 0567366918F6C745 CRC64;
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01-NOV-1991 (Rel. 20, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Secreted protease C precursor (EC 3.4.24.-) (ProC).
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                                                                                                                                                                                                          MEDLINE=87283911; PubMed=3302276;
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synthesized and secreted as zymogens without a signal peptide.";
J. Bicl. Chem. 264:9083-9089(1989).
-!- COFACTOR: Binds 1 zinc ion and 7 calcium ions per subunit (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- DOWAIN: THE GLY-RICH REPEATS MAY BE IMPORTANT IN THE EXTRACELLULAR SECRETRON OF THIS METALLOROTEASE.
-!- SIMILARITY: Belongs to peptidase family M10B.
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CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
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CALCIUM 3 (VIA CARBONYL OXYGEN) (6
SIMILARITY).
CALCIUM 3 (BY SIMILARITY).
CALCIUM 4 (VIA CARBONYL OXYGEN) (6
CALCIUM 4 (VIA CARBONYL OXYGEN) (7
SIMILARITY).
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CALCIUM 3 (VIA CARBONYL OXYGEN)
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CALCIUM 1 (V
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SIMILARITY).  CALCIUM 3 (VIA CARBONYL OXYGEN) (BY SIMILARITY).  SIMILARITY).  CALCIUM 3 AND 5 (BY SIMILARITY).  CALCIUM 4 (VIA CARBONYL OXYGEN) (BY SIMILARITY).  CALCIUM 6 (VIA CARBONYL OXYGEN) (BY SIMILARITY).  CALCIUM 6 (VIA CARBONYL OXYGEN) (BY SIMILARITY).  CALCIUM 6 (VIA CARBONYL OXYGEN) (BY SIMILARITY).  CALCIUM 7 (VIA CARBONYL OXYGEN) (BY SIMILARITY).  CALCIUM 5 (VIA CARBONYL OXYGEN) (BY SIMILARITY).  CALCIUM 5 (VIA CARBONYL OXYGEN) (BY SIMILARITY).  CALCIUM 5 (VIA CARBONYL OXYGEN) (BY SIMILARITY).  CALCIUM 7 (VIA CARBONYL OXYGEN) (BY SIMILARITY).  CALCIUM 7 (VIA CARBONYL OXYGEN) (BY SIMILARITY).  CALCIUM 6 (BY SIMILARITY).  CALCIUM 6 (BY SIMILARITY).  CALCIUM 6 (BY SIMILARITY).  CALCIUM 6 (BY SIMILARITY).	Score 88.5; DB 1; Length 479;   Pred. No. 2;   Dr. 2;   Indels 37; Gaps 9;   LSIYQYGSANALALQSDARKSETTITQSGYGNG 78	reated) ast sequence update) ast annotation update) ast annotation update) ast annotation update) ast annotation update) ast annotation update) ast annotation update) ast annotation update) ast annotation update) ast annotation update) ast annotation update) ast annotation update) ast annotation (Promastigote surface tein) (GP63 protein) (Promastigote surface ast ast annotation (Bost annotation) ast annotation and ast annotation of macrophages ast ast and pair and the promastigote and the
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MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Bisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Bisen J.A., Ernolaeva M., Haft D., Hickey E.,
Folonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishal W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40; Indels 46; Gaps
                                          Harris
MEDLINE=9829597; PubMed=9634210;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.T., Brosch R., Parkhill J., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Seger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitchead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.2%; Score 87; DB 1; Length 678; 26.2%; Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Bacteriol. 184:5479-5490(2002).
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14 34 POTENTIAL.

180 200 POTENTIAL.

258 258 D -> G (IN REF. 2).

678 AA; 66736 MW; 209F1593D52533A2 CRC64;
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GP63_LEICH
ID GR63_LEICH
AC P15706,
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
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InterPro; IPR002899; Mycobac_Dencapep.
Pfam; PF01469; Pentapeptide_2; 11.
Pfam; PF00823; PPE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE007026; AAK45866.1; ALT_INIT
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Tuberculist; Rv1548c; -
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                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=92112918; PubMed=1370484;
Ramamoorthy R., Donelson J.E., Paetz K.E., Maybodi M., Roberts S.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEISHMANOLYSIN.
REMOVED IN MATURE FORM (BY SIMILARITY).
                                                    Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Leishmania
NCBI_TaxID=44271;
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GPI-anchor amidated asparagine (By
                                                                                        MEDINE=90205976; PubMed=2320059;
MIJLAR K., RedG S.G., Parsons M.;
"Leishmania gp63 molecule implicated in cellular adhesion lacks an Arg-Cly-Asp sequence.";
       Leishmanolysin precursor (EC 3.4.24.36) (Cell surface protease) (Major surface glycoprotein) (GP63 protein) (Promastigote surface
                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR00625; Pept M Zn BS.
InterPro; IPR006277; Peptidase_M8.
Pfam; PP01477; Peptidase M8; 1.
PRINTS; PR01427; Peptidase M8; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PHYdrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc; Zymogen; Signal; Cell adhesion; GPT-anchor; Lipoprotein.
Signal: 1 39 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTIVATION PEPTIDE.
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                    ily-Asp sequence.";
Biochem. Parasitol. 39:267-274(1990).
                                                                                                                                                                                                                                                                                                                                                                               EMBL; M80672; AAA29238.1; -.
EMBL; M28827; AAA29235.1; -.
PIR; A44951; A44951.
HSSP; P08148; 1LML.
MEROPS; M08.001; -.
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152
                                                                               SEQUENCE FROM N.A.
                                             Leishmania chagasi
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                           endopeptidase)
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SEQUENCE FROM N.A.

STRAIN=C. Columbias,
MISTAIN=C. Columbias,
MEDLINE=21016719; PubMed=11130712;
MEDLINE=21016719; PubMed=11130712;
MEDLINE=21016719; PubMed=11130712;
MEDLINE=21016719; PubMed=11130712;
MEDLINE=21016719; PubMed=11130712;
MEDLINE=21016719; PubMed=11130712;
MEDLINE=21016719; PubMed=11130712;
MEDLINE=21016719; Conway A.B., Chenhan C.L., Brooks S.Y.,
MEDLINE O.L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
MINTER C.J., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
MINTER C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
Langin-Hooper S., Lee A., Lee J.M., Linz C.A., Li J.H., Li Y.-P.,
MISTAIN C.J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
Milstcher J., Miranda M., Nguyen M., Roney T., Rowley D.,
M. Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
M. D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
M. D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
M. D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
M. D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
M. D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
M. D., Xu G., Fraser C.M., Venter J.C., Davis R.W.,
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C STRAIN=cv. Columbia;

MEDLINE=2954850; Pubmed=14593172;

A REDLINE=2954860; Pubmed=14593172;

A Karlin-Newmann G., Liu G., Niu B., Sakano H., Wham P.K., Cheuk R.F.,

A Karlin-Newmann G., Liu S.K., Lam B., Sakano H., Wu T., Yu G.,

A Miranda M., Tang C.C., Cnodera C.S., Deng J.M., Tang M., Ansari Y.,

A Arakawa T., Banno F., Bowser L., Brooks S.Y., Carninci P.,

A Arakawa T., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,

Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,

Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,

Kamiya A., Meyers C., Nakajima M., Narusaka M., Sakin., Sakurai T.,

A Satou M., Tanse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,

A Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=cv. Columbia; TISSUE=Leaf;
MEDINE=S8090460; PubMed=9427751;
Bobmert, K., Camus I., Bellini C., Bouchez D., Caboche M., Benning C.;
"AGOI défines a novel locus of Arabidopsis controlling leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Argonaute protein.
AGOI OR ATIGAGALO OR FILAL7.3 OR TINIS.2.
AGOI OR ATIGAGALO ON FILAL7.3 OR TINIS.2.
Bukaryota; thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                            Gaps
                                                                                                                                                            .,
                                                                                  Length 599;
                                                                                                                                                            6; Indels
746730AE8E2A2E7C CRC64;
                                                                              Score 86; DB 1;
Pred. No. 4.3;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              AGO1_ARATH
ID AGO1_ARATH
STANDARD;
PRT; 1048 AA.
AC 004379; 2021P83;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                              117 OYDOLVTRVVTHEMAHASVMVRQVGFGNNA 146
                                                                                                                                                                                                                                                                                                                        250 RYDOLVTRVVTHEMAHA--LGFSVGFFEGA 277
63848 MW;
                                                                                  Query Match
Best Local Similarity 66.7%;
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBO J. 17:170-180(1998).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the between bloinformatics Institute. There are one restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 GGYGGGRGGGPSSGPPQRQSVPELHQATSPTYQAVSSQPTLSEVSPTQVPEPTVLAQQF- 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 NGADVGQGADNSTIE------LIQNGFRNNATIDQWNAKNSDITVGQYDQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 GGGGNHNGGGNSSGPDSTLSI-----YQYGSANAALALQSDARKSETTITQSGYG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the argonaute family.
-!- SIMILARITY: Contains 1 PAZ domain.
-!- SIMILARITY: Contains 1 PAZ domain.
-!- SMILARITY: Contains 1 Piwi domain.
-!- CAUTION: Ref. 2 (AAFT)18) sequence differs from that shown due to erroneous gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27; Gaps
                                                                Science 302:842-846(2003).
-!- FUNCTION: Essential for proper development of leaves and floral organs, and formation of axillary meristems.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=1;
Comment=A number of isoforms are produced. According to EST
"Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                             Isold=004379-1; Sequence=Displayed;
TISSUE SPECIFICITY: Widely expressed at low levels.
DEVELOPMENTAL STAGE: Expressed throughout all developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 11.0%; Score 85.5; DB 1; Length 1048; Best Local Similarity 25.7%; Pred. No. 9.2; Matches 36; Conservative 17; Mismatches 60; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            676 997 PIWI.
13 104 GLY-RICH.
1048 AA; 116190 MW; 3E5146343A09C541 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50821; PAZ; 1.
PROSITE; PS50822; PIWI; 1.
Developmental protein; Alternative splicing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U91995; AAC18440.1;
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Search completed: August 2, 2004, 14:49:28 Job time : 6.3 secs

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2, 2004, 14:39:17 ; Search time 29.7 Seconds (without alignments) 1604.150 Million cell updates/sec
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775
1 MKLLKVAAFAAIVVSGSALA.........HASVMVRQVGFGNNATANQY 151
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                          OM protein - protein search, using sw model
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1: Sp_archea:*
2: sp_bacteria:*
3: Sp_fungi:*
5: Sp_invertebrate:*
6: Sp_mammal:*
7: Sp_mammal:*
7: Sp_mammal:*
7: Sp_mammal:*
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	033802 salmonella Q7x243 citrobacter	Q8cw63 escherichia Q7x237 enterobacte	Q54069 salmonella Q983j5 escherichia	O33801 salmonella Q7x238 enterobacte Q8eih3 shewanella	Q7x241 citrobacter Q8cw64 escherichia	Vocali sinewalidia Q7x244 citrobacter Q7uczl shigella fl Q83ru7 shigella fl
SUMMARIES	033802 Q7X243 Q7X240	Q8CW63 Q8CW63 Q7X237	Q54069 Q9S3J5	033801 Q7X238 Q8EIH3	Q7X241 Q8CW64	Q7X244 Q7X244 Q7UCZ1 Q83RU7
DB		16	1010	1 2 2	16	16 16 16
% Query Match Length DB	152	152	29	179 151 139	152	302 151 151 160
% Query Match	88 . 47 . 6 . 6 . 6 . 6 . 6 . 6 . 6 . 6 . 6 .	65.0	15.7	14. 13.9 13.5	13.5	1 H H H E
Score	684 578.5 533	503.5 438.5	385	109 107.5 105	104.5	103.5
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OBev84 mycoplasma	093397 cyprinus ca			mycobacte	Q8efu3 shewanella	Q8y106 ralstonia s	Q8xsd6 ralstonia s	Q89jiS bradyrhizob	Q88hg0 pseudomonas	Q9p3i9 neurospora	Q8nivl neurospora	Q7v8s5 prochloroco	Q94821 tetrahymena	Q8tfa6 saccharomyc	Q89ji3 bradyrhizob	Q8ewd6 mycoplasma		Q92uu8 rhizobium m	Q9n6m8 drosophila	Q9xil0 arabidopsis	Q9ngf6 drosophila	drosophil	Q9w4f0 drosophila	Q8t819 drosophila	Q8sx56 drosophila.	4 drosoph	19 agrobacte	~	
16	348 13 093397	16	16	16	16	16	16	16	16	M	m	55 16 Q7VBS5	w	m	16	16	16	16	ហ	10	ro O	ഗ	Ŋ	ഗ	S.	'n		70	ALIGNMENTS
01 13.0	9.5 12.8	6.5 12.5	6.5 12.5	6.5 12.5	6.5 12.5 1	5 12.5 3	6,5 12,5 3	6 12.4	6 12.4	96 12.4	5:5 12.3	12.3	5 12.3 1	5 12.2	4 12.1	4 12.1	3 12.0	3 12.0 2	2 11.9	1 11.7	1 11.7	1 11.7	1 11.7 1	1 11.7 1	1 11.7 1	1 11.7 1	5 11.7	0.5 11.7	
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	8	40	41	42	43	44	45	

																						0	09	09	120	120	
	152 AA.	( <del>0</del>	sequence update)	annotation update)			Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,					Gordon J.I., Bian Z., Pfeifer J.D.,		promotes intere	mouse small intestinal epithelial					9DA7DADC2364B006 CRC64;		01	MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ	MKLLKVAAFAAIVVSGSAVAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALAQ	TQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ	SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG	ATANOY 151
	PRT;	Created	Last (	Last			mmapro	la.			3832;	, Gord		tive	with		1997)				Score	Pred 4; M	AGVVP	AGVVP(	DVGQG2	DVGQG	VGFGN
	, ,			19,			la; Gal	Salmonella			ed=939	R.G.,		grega	SR-11		5325	, T. To		15401 MW;	3.3%;	4, %	SGSAL	SGSAV	3YGNGA	SYGNGA!	SVMVRQ'
	PRELIMINARY;	(TrEMBLrel.	(TrEMBLrel	(TrEMBLrel.		.yphimurium.	oteobacteri	eae;	, ,	M N.A.	3981; PubMe	S., Lorentz	, Rhen M.;	of thin, ac	.yphimurium		ശ	14; CAAU4151.1;	4	152 AA; 154	88	Similarity 89. 5; Conservative	LKVAAFAAIV	LKVAAFAAIV	SDARKSETTITOSC	RKSETTITOSG	LVTRVVTHEMAHASVMVRQVGFGNNATANQY
1 T.1	033802	033802; 01-JAN-1998	01-JAN-1998	01-DEC-2001		Salmonella typhimurium.	Bacteria; Pr	Enterobacteriaceae;	[1]	SECUENCE FROM N.A.	MEDLINE=98053981; PubMed=9393832;	Sukupolvi S.S., Lorentz	Normark S.J., Rhen M.;	"Expression of thin, aggregative fimbriae	Salmonella t		Infect. Immun.	EMBL; AUUUUSI4;		SEQUENCE 1	Query Match	Best Local Simi Matches 135;	1 MKL	1 MKL	61 SDA	61 SDA	121 LVT
RESULT	201	D'A	DŢ	T C	3 S	SO	ပ္ပ	88	N N	유	RX	RA FA	E.A	КŢ	H T	БТ	IJ	ž E	- (	Š	ò	Ma	δ	q	δ	qq	ò

118

121

В

RESULT :

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SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 OSDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQW--GGNHHGGGSNYGPDSSLSIYQYGSNNSANALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLLKVAAIAAIVFSGSALAGVVPQYGGGGGNHGGGGNNSGPNSELNIXQYGGGNSALAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-22388234 CT0703 / ATCC 700928;
MEDLINE-22388234 CT0703 / ATCC 700928;
MEDLINE-22388234 PubMed=12471157;
Melch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. US.A. 99:17020-17024(2002).

EMBL. ACOLESS, AAN79779.1; -.
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Enterobacteriaceae, Enterobacter.
                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 16; Length 152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 AA; 15064 MW; 3BA57F34C1240E83 CRC64;
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Last annotation update)
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67.1%; Pred. No. 4.1e-33;
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NCBI_TaxID=217992;
                                                                                                                                                                                                                                                                                                                     Major curlin subunit precursor.
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Best Local Similarity 67.1%
Matches 102; Conservative
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Escherichia coli O6
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SEQUENCE FROM N.A.
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SEQUENCE 152 AA;
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"Production of Cellulose and Curli Fimbriae by Members of the Family
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 72:4151-4158 (2003).
EMBL; AJ515701; CAD566751; -
SEQUENCE 149 AA; 15260 MW; 946DD52017F648FD CRC64;
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                                                                                                                                                                                                                                 Citrobacter sp. Fec2.
Bacteria, Proteobacteria, Gammaproteobacteria; Enterobacteriales, Enterobacteriaceae, Citrobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Citrobacter freundii.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
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EMBL, AJ515700, CAD56672.1, -.
SEQUENCE 150 AA; 15016 MW; 1D7141B8D6973DC6 CRC64;
                                                                                                                                                            Last sequence update)
Last annotation update)
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Last annotation update)
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76.8%; Pred. No. 3.7e-39;
iive 13; Mismatches 21
 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
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Matches 116; Conservative
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Best Local Similarity
Matches 107; Conserv
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Q7X243;
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"Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract."; Infect. Immun. 72:4151-4156(2003).

EMBL, AJ515702; CAD56678.1; -. SEQUENCE 150 AA; 15112 MW; SD8BB2D872DF15F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
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                                                                    56.6%; Score 438.5; DB 2; Length 150; 58.9%; Pred. No. 7e-28; Live 28; Mismatches 33; Indels 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-SE30;
Cox J.M., Eglezos S., Woolcock J.B.;
Virulence of Salmonella enteritidis in chickens correla
colony morphology and expression of SE17 fimbriae.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U53207; AAA98671.1;
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 AA; 7704 MW; 2FD5411241A7BCB1 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SEF17 fimbrin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY 2000 (TrEMBLrel. 13, Created)
01-MAY 2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Curlin subunit monomer (Fragment).
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                                                                               l Similarity 58.9
89; Conservative
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les 75; Conserv
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Best Local Si
Matches 75,
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                                      MEDLINE 99314153; PubMed=10386375; La Ragione R.M., Collighan R.J., Woodward M.J.; La Ragione R.M., Collighan R.J., Woodward M.J.; Non-curliation of Escherichia coli 078:K80 isolates associated with IS1 inserti on in csgB and reduced persistence in poultry infection."; FEMS Microbiol. Lett. 175:Z47-Z53(1999).
EMBL, AJ131765, CAB42380.1; -...
NON TER 29 29 29 SEQUENCE 29 AA; 2789 MW; E290DFCO7ABBB243 CRC64;
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MEDLINE=98053981; PubMed=9393832;
Sukupolvi S.S., Lorentz R.G., Gordon J.I., Bian Z., Pfeifer J.D.,
Normark S.J., Rhen M.;
"Expression of thin, aggregative fimbriae promotes interaction of
Salmonella typhimurium SR-11 with mouse small intestinal epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Próteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBI_TaxID=602;
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Pred. No. 0.003;
1; Mismatches 2; Indels
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EMBL, AJ000514; CAA04150.1; -.
SEQUENCE 179 AA; 19318 MW; AZBCCB648B3C0B0B CRC64;
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25, Last sequence
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curlin monomers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
SEQUENCE FROM N.A.
TRANSPOSON=Insertion sequence IS1;
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163 AVVVQKQSHMAIRVTQ 178
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                                                                                                                                                                                                                                Query Match
Best Local Similarity 89.7%;
Matches 26; Conservative
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19,
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01-OCT-2003 (TrEMBLrel. 25
01-OCT-2003 (TrEMBLrel. 25
01-OCT-2003 (TrEMBLrel. 25
Nucleation component of cu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       033801;
01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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AGFB.
Salmonella typhimurium.
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  SEQUENCE
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us-09-543-407-14.rspt

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freundii
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Escherichia coli 06.
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nes 35; Conserv
                                                                                                                                                                              SEQUENCE FROM N.A.
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SEQUENCE 160 AA;
                                                                                                                                                   NCBI_TaxID=546;
                                                                                                               Citrobacter
                                                                                                                                                                                            STRAIN=Fec4
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Matches
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                                                                                                                                                                                                                                AAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETT 69
                                                                                                                                                                                                                                                                                    70 ITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQLVTRVV 126
                                                                                                                                                                                                                                                                                                 Heidelberg J.F., Paulsen I.T., Nelson K.B., Gaidos E.J., Nelson W.C., Read T.D., Elsen J.A., Seshadri R., Ward N., Methe B., Claytcon R.A., Deboy T.T. Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., Beboy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., Mitte C., Wolf A.M., Wanathevan J., Weidman J., Umpraim M., Lee K., Berry K., Lee C., Wolf A.M., Chouri H., Gill J., Utterback T.R., McDonald L.A., Feldbryum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M., Shewanella oneidensis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 SCPDSTLSIYOYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGRDNLIDLVQQGTANQGIVFQSGSDNS-AYVTQAGNDNISLVTQIGTNNEVQLLQVGAQ
                                                                                                                                                                                                         Gaps
                                                                                     Zogaj X., Bokranz W., Nimtz M., Romling U.;
"Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 72:4113-4158 (2003).
EMBL, AJS15702; CAD56677.1; -SEQUENCE 151 AA; 15985 FW; F0B82BDZAZ7882B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 NKASITQ------IGN-DNLVQ---LNQLGSGNFSIQQIADGAAISITQY 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 NNATIDOWNAKNSDITVGOYDQLVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Enterobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
                                                                                                                                                                                Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.5%; Score 105; DB 16; Length 139; 28.3%; Pred. No. 0.45;
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SEQUENCE 139 AA; 14811 MW; 41EC1CFA76957920 CRC64;
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Last annotation update)
                                                                                                                                                                                                       42;
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                                                                                                                                                                                DB 2;
                                                                                                                                                                              13.9%; Score 107.5; DB 30.8%; Pred. No. 0.31;
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01-MAR-2003 (TrEMBLrel. 23, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22297686; PubMed=12368813;
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EMBL; AE015532; AAN53942.1;
                                                                                                                                                                                Query Match
Best Local Similarity 30.89
Matches 36; Conservative
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 Enterobacter sakazakii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shewanella oneidensis.
                                                                                                                                                                                                                                                                                                             104 ITODGYGNSA---
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                                                              SEQUENCE FROM N.A.
                                     NCBI_TaxID=28141;
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                                                                           STRAIN=Fec39;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 GSKLLSVISQ-----EGSGNRAKTDQT-----GSYNFAY-----IDQTGS 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 GSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGY
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STRAIN=06.H1 / CFT073 / ATCC 700928;
MEDLINE=23388234; PubMed=12471157;
MEDLINE=22388234; PubMed=12471157;
MWEICH R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
MayNew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnanberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                 Zogaj X., Bokranz W., Nimtz M., Romling U.;
Production of Cellulose and Curli Fimbriae by Members of the Family
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 72:4151-4158 (2003).
EMBL; AJ515701; CAD566741.1. -
SEQUENCE 152 AA; 16149 MW; D063A527D45D4329 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
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Enterobacteriaceae, Escherichia.
NCBI_TaxID=217992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 GNGADVGOGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQLVTRV 125
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
EMBL; AE016759; AAN79778.1; -.
                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
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29.2%; Pred. No. 0.58;
tive 19; Mismatches
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                      Q7X241;
01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequenc
01-0CT-2003 (TrEMBLrel. 25, Last annotat
Nucleation component of curlin monomers.
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Best Local Similarity 29.1%
Matches 32; Conservative
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 DARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNS-DI-TVGQYD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 QGDDNDITIKQKGDSNGAEFQVWGDSNDVDLKQRGDANFATFGAYGTDNDFDLSSKGDNN 350
98 NLAYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQYGTQKTAIVVQRQSQMAIRV 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                         MEDLINE=1297666; PubMed=12368813; MEDLINE=2297666; PubMed=12368813; MEDLINE=2297666; PubMed=12368813; Meddelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Umayam L.A., Mhite O., Wolf A.M., Wadupu R., Peterson J.D., Umayam L.A., Mhite O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Wulf L. W., Mith H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M., "Genome sequence of the dissimilatory metal ion-reducing bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GGN----ALALQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zogaj X., Bokranz W., Nimtz M., Romling U.; Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Citrobacter sp. Fec2.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 502;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ll protein, Complete proteome.
502 AA; 52441 MW; D08CA23D6C46B62D CRC64;
                                                                                                               01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Nucleation component of curlin monomers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 104; DB 16;
Pred. No. 2.5;
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EMBL; AE015532; AAN53941.1; -.
                                                                                     PRT;
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                                                                                                                                                         Conserved hypothetical protein. SO0865.
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26.0%;
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                                                                                     PRELIMINARY;
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Best Local Similarity
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SEQUENCE 5
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Q7X244;
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Q7X244
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OBEIH4
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SEQUENCE FROM N.A.

MEDLINE=22590274; PubMed=12704152;
Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
Ban B., Perra N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
Schwartz D.C., Blattner F.R.;
"Complete genome sequence and comparative genomics of Shigella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacřeriá; Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobácteriaceae; Shigella.
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Infect. Immun. 71:2775-2786 (2003).
EMBL: AE016981; AAP16542.1; -
SEQUENCE. 151 AA; 15868 WW; 5D5D266B964014A0 CRC64;
                                                                                                   BD00AF57E1400704 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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; Pred. No. 0.65;
13; Mismatches
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Infect. Immun. 72:4151-4158(2003).
EMBL, AJ515700, CAD56671.1; -.
SEQUENCE 151 AA; 16158 MW; BD00
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28.8%;
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01-0CT-2003 (TrEMBLrel. 25,
Minor curlin subunit.
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August 2, 2004, 14:35:42; Search time 44.9 Seconds (without alignments) 950.215 Million cell updates/sec
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757
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1: geneseqp1980s:\*
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4: geneseqp2001s:\*
5: geneseqp2001s:\*
6: geneseqp2003s:\*
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Listing first 45 summaries

Database:

Post-processing: Minimum Match 0% Maximum Match 100%

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES		ם	B3634	AAR74625	AAB36341	AAW23570	34	34	34	S	AAB36352	AAB36350	35	AAB36351	S	AAR62761	356	AAB36343	ABR82651	AAR52664	AAR52663	AAB36316	AAB36321	AAB36326	AAB36338	AAB36344	AAB36325
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (BERI/TAR) nucleation depended assembly system of strains of Salmonella, Bscherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene back into the chromosome of the homologous species, replacing the native

Salmonell	Salmonell	Salmonell	Salmonell	Salmonell	Salmonell	Salmonell	Salmonell	Salmonell		E. coli c	Leishmani	Plectreur	Salmonell	Salmonell	Salmonell	E. coli c	Plectreur	Protein e	Escherich
Aab36339	Aab36320	Aab36342	Aab36322	Aab36327	Aab36337	Aab36340	Aab36324	Aab36319	Abr82649	Abr82645	Aaw32312	Aae36891	Aab36323	Aab36336	Aab36328	Abr82647	Aae36890	Abu44579	Aab36331
AAB36339	AAB36320	AAB36342	AAB36322	AAB36327	AAB36337	AAB36340	AAB36324	AAB36319	ABR82649	ABR82645	AAW32312	AAE36891	AAB36323	AAB36336	AAB36328	ABR82647	AAE36890	ABU44579	AAB36331
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22	22	151	22	22	22	23	23	23	26	26	502	2016	19		19	24	764	290	23
15.2	15.2	14.7	14.7	14.7	14.7	14.4	14.4	14.4	13.5	12.9	12.7	12.7	12.7	12.7	12.7	12.5	12.5	12.3	12.2
115	115	111.5	111	111	111	109	109	109	102	9	w	96:5	.e	o, o	96	9		0	92
26	27	28	29	30	31	32	33	34	35	36	37	38	33	40	4	42	43	44	45

ALIGNMENTS

cd; protein; 151 AA.  Instead sequence SEQ ID NO:16.  A; chromosomal gene replacement; fimbrin; epitope; response; immunogen.  Intidis.  In JL, Collison SK, Kay WW;  In JL, Collison SK, Kay WW;  Agene having a segment replaced by a foreign DNA soreign epitope or antigen, expresses recombinant Agene patotiope or antigen, expresses recombinant Agene patotiope or antigen. Agene (I) where a lighting immune response in animal.  In JS; 139pp; English.  In JS; 139pp; English.  In JS; 139pp; English.  In JS; 139pp; English.  In JS; 139pp; English.  In JS; 139pp; English.  In Secondary of a foreign DNA a segment of a foreign DNA and dependent as been replaced by a segment of a foreign DNA aggregative fimbriae (SERI)/TAF; nucleation dependent of a foreign DNA aggregative fimbriae (SERI)/TAF; nucleation dependent of a foreign of strains of Salmonella, Escherichia coll and aggregative fimbriae (Mimbriae comprising recompagination of a recombinant gene into the officence of the option of a recombinant gene into the officence of the option of a recombinant gene into the officence of the option of a recombinant gene into the officence of the option of a recombinant gene into the officence of the option of a recombinant gene into the officence of the option of a recombinant gene into the officence of the option of a recombinant gene into the officence of the option of a recombinant gene into the officence of the option of a recombinant gene into the option of a recombinant gene into the option of a recombinant gene into the option of a recombinant gene into the option of a recombinant gene into the option of a recombinant gene into the option of a recombinant gene into the option of a recombinant general pages of the option of a recombinant general pages and the option of a recombinant general pages and the option of a recombinant general pages and the option of a recombinant general pages and the option of a recombinant general pages and the option of a recombinant general pages and the option of a recombinant general pages a
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copy of that gene; and (4) eliciting an immune response in an animal, compyrising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogens(cell), the hybrid fimbrin protein ser usually strong immunogens, which may be important for directing an immune response immunogens, which may be important for directing an immune response in expensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNARNSDITVGQYGG
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100.0%; Pred. No. 2.2e-67;
iive 0; Mismatches 0;
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Matches 151; Conservative
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N-PSDB; AAQ87467.
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                                                                                                                                                                                                                                                                                      Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KING J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AgfA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
26-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR74625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      19
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                                                                                                                                                                                                                                                                                                                        Query Match
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The Salmonella AgfA protein and DNA are used in vaccine and genetic

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                                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                                                                                        SPARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQMNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
immunization compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                             SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                  1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agfA; chromosomal gene replacement; fimbrin; epitope;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella enteritidis AgfA amino acid sequence SEQ ID NO:5.
                                                                                                                      Length 151;
                                                                                                                  86.9%; Score 658; DB 2; L
llarity 90.1%; Pred. No. 1.6e-57;
Conservative 3; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                          121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                       NNAALVNQTASDSSVMVRQVGFGNNATANQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine; immune response; immunogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB36341 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-APR-2000; 2000WO-CA000356.
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                                                                                                                                       Best Local Similarity
Matches 136; Conserv
                                                                               Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAC64617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB36341;
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Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful folliciting an immune response in an animal. In a finbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/Cell), the hybrid finbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response inspected epitope, and hybrid fimbriae are easy and inspensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                           SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                              1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                             1 MKILIKVAAFAAIVVSGSALAGVVPQWGGGUNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody
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0
                                                                                                                                                                                                                                               Length 151;
                                                                                                                                                                                                                                                                            12; Indels
                                                                                                                                                                                                                                             Score 658; DB 3;
Pred. No. 1.6e-57;
3; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                            NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNAALVNQTASDSSVMVRQVGFGNNATANQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella enteritidis 27655-3b agfA.
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                                                                                                                                                                                                                                               Match 86.9%;
Local Similarity 90.1%;
hes 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAT74142.
                                                                                                                                                                                                                Sequence 151 AA;
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29-SEP-1997
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Matches
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                                                                                                                                                                                                                                                                                                                                                       SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The mucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALAQ
                                                                                                                                                                                                                                                       1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                        Length 151
                                                                                                                                                                                                                       13; Indels
                                                                                                                                                                                      Score 653; DB 2;
Pred. No. 5.1e-57;
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                                                                                                                                                                                                                                                                                                                                                                                          151
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                                                                                                                                                                                                                       3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine; immune response; immunogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB36349 standard; protein; 151 AA
                                                                                                                                                                                    86.3%;
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                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli
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                                                                                                                                                        Sequence 151 AA;
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directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the direconsome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein contraining a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a finbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid finbrin protein possesses both the immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAH--- 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --YDQLVTRVVTHEMAHASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 PDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNN
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella, agfA, chromosomal gene replacement, fimbrin, epitope, vaccine, immune response, immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 ATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 40;
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                                                                                                                                                                                                                                                                                                                                                                                              Length 151;
                                                                                                                                                                                                                                                                                                                                                                                            Score 618; DB 3; Lu
Pred. No. 1.6e-53;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AgfA::PT3#1 amino acid sequence SEQ ID NO:12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB36346 standard; protein; 151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGV---
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                                                                                                                                                                                                                                                                                                                                                                                          81.6%;
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Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella enteritidis.
Escherichia coli.
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N-PSDB; AAC64622.
                                                                                                                                                                                                                                                                                                                                                                Sequence 151 AA;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative fimbries (SEPI/TAE) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant of AffA, CSGA and AffA, homologue fimbrin subunits, respectively, (2) directing recombination of a recombinant gene into the chromosome of the homologous species, (3) directing recombinant gene into the chromosome of the homologous species, (3) directing recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene, and (4) eliciting an immune response in an animal. Comprising separating an amino acid polymer comprising a replacement segment cor segments of foreign amino acid sequence or sequences grown on a Salmonella, E coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/Cell), the hybrid finbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live immunogenicity and adhesion properties relevant for an efficient live
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protein useful for eliciting immune response in animal
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llarity 80.1%; Pred. No. 9.8e-50;
Conservative 7; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AgfA::PT3#2 amino acid sequence SEQ ID NO:14.
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                                              Page 135; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccine; immune response; immunogen.
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Best Local Similarity
Matches 121; Conserv
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative finbriae (SEPI)/TAP) mucleation depended assembly system of strains of Salmonella, Escherichia coli and Enteropacteriacae for the production of fimbriae comprising recombinant of Enteropacteriacae for the production of fimbriae comprising recombinant of AgfA, CsgA and AgfA-homologue fimbrian subunits, respectively; (2) directing recombinant gene into the chromosome of the homologue species, fill directing recombinant gene comprising separating a namino acid polymer comprising recombinant pactor of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a replacement sequent or sequents of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the antimal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant for an efficient live system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein see usually strong immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in considering the present invention present sequence is given in
                                                                                                                                                                                                                                                                                                                                 Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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Pred. No. 1.5e-49;
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                                                                                                                                                    Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 136; 139pp; English.
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                                                                                                                                                Collison SK,
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99US-0127888P.
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80.8%;
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                                                                    (UYVI-) UNIV VICTORIA
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05-APR-1999;
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                                                                                                                                                White AP,
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epicope or antigen. Also described are: (1) use'of thin aggregative finbries (SEFI/TAF) nucleation depended assembly system of strains of Salmonella. Escherichia coli and comprising recombinant of Enteropasceristicaes for the production of fimbries conjusting recombinant of a recombinant gene into the chromosome of the homologous species, (3) directing recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising separating an amino acid polymer comprising separating an amino acid polymer comprising separating an amino acid polymer comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino contention a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or constanting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000.copies/cell), the hybrid fimbrin protein possesses both the immunogens, which may be important for directing an immunogens, which may be important for directing an immunogens of the service of imminogens, which may be important for directing an immunogens of the carrier in the hybrid fimbrine seasy and in the carrier of contines and proteins are usually strong immunogens.
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80.8%; Pred. No. 1.9e-49;
iive 5; Mismatches 24; Indels
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                                                                                                                                                                                                                                                                                                                                    Kay
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                                                                                                                                                                                                                                                                                                                                  Collison SK,
                                                                                                                                                                                             05-APR-2000; 2000WO-CA000356
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                       Salmonella enteritidis.
                                                                                                                                                                                                                                                                                       (UYVI-) UNIV VICTORIA
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Matches 122; Conserv
                                        Escherichia coli.
Synthetic.
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                                                                                                          WO200060102-A2
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121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151 

В

Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;

vaccine; immune response; immunogen.

Salmonella enteritidis.

Escherichia coli.

Synthetic.

WO200060102-A2.

12-OCT-2000

AgfA::PT3#5 amino acid sequence SEQ ID NO:20.

(first entry)

26-FEB-2001

AAB36350;

AAB36350 standard; protein; 151

RESULT 10

Db

8

AAB3635(

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are:

(1) use of thin aggregative finbriae (SEPIT/TAR) nucleation depended assembly system of strains of Salmonella Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant homologue finbrin subunits, respectively; (2) directing recombination of a recombinant gene book into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and inroducing the colymer into the animal in conjunction with a carrier or dillent. (1) is useful for the animal in conjunction with a carrier or dillent. (1) is useful for the book cell, and animal. In a finbrical presentation of a representation of recombinant AghA protein which is useful for the book cells and animal. In a finbrical presentation of a representation of recombinant which is useful for the animal protein an animal. In a finbrical presentation of the contraction with a minmal or the contraction of recombinant which is useful for the contraction of recombinant and in a finbrical presentation of the contraction which is useful for the contraction and animal in a manner center or dillent.
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                                                                                                                                                                                                                               Salmonella, agfA, chromosomal gene replacement, fimbrin, epitope, vaccine, immune response, immunogen.
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                                                                                                                                                                               AgfA::PT3#7 amino acid sequence SEQ ID NO:24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Page 138; 139pp; English.
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                          AAB36352 standard; protein; 151 AA.
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                                                                                                                           26-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                        Salmonella enteritidis.
Escherichia coli.
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N-PSDB; AAC64628.
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AAB36352
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA cequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbride (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, respectively; (2) directing recombinating an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA comprising separating an amino acid polymer comprising a recombinant AgfA comprising separating an amino acid polymer comprising a recombinant AgfA comprising separating are presented and in or all meaning are protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the comprising an immune response in an animal. In a fimbrial presentation containing an immune response in an animal. In a fimbrial presentation containing the containing are usually strong immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit protein possesses both the immunogens, which may be important for directing an immune response in an immune response capainst the inserted epitope, and hybrid fimbriae are essually strong incompanist the inserted epitope, and hybrid fimbriae are essually strong capainst the inserted epitope, and hybrid fimbriae are essually strong inexpensive to purify in large amount. The presented research and when the companies and the companies and the presented and thybrid fimbriae are essually and adhesion properties research are
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 137; 139pp; English.

ME. Kay

Collison SK,

05-APR-2000; 2000WO-CA000356.

99US-0127888P

05-APR-1999;

(UYVI-) UNIV VICTORIA. White AP, Doran JL, WPI; 2000-672631/65.

N-PSDB; AAC64626

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05-APR-1999;
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                                           Length 151;
                                          Score 574; DB 3; Length 15
Pred. No. 3.9e-49;
5; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                       AgfA::PT3#9 amino acid sequence SEQ ID NO:28.
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the exemplification of the present invention
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75.8%; Soc
Best Local Similarity 80.8%; Pre
Matches 122; Conservative 6;
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                                           Query Match
Best Local Similarity
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                      Sequence 151 AA
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Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) useful for the expression of recombinant AgfA protein which is useful eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier finbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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Pred. No. 1.5e-48;
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80.1%;
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assembly system of strains of Salmonella Escherichia coli and assembly system of strains of Salmonella Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant Gaffa, CsgA and Agfa-homologue finbrin subunits, respectively (2) directing recombination of a recombination of a recombinant gene homologues species, is a recombinant gene homologue species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant Agfa protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant Agfa protein which is useful for the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid finbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit for the carrier fimbrial subunit for the carrier fimbrial subunit for the immunogenic fimbria are easy and immune response and hybrid fimbriae are easy and incompleted and hybrid fimbriae are easy and incompleted and hybrid fimbriae are easy and and the copies of the copies and hybrid fimbriae are easy and the copies of the copies and hybrid fimbriae are easy and the copies of the copies and hybrid fimbriae are easy and the copies of the copies and hybrid fimbriae are easy and the copies and the copies of the copies and hybrid fimbriae are easy and the copies and the copies and hybrid fimbriae are easy and the copies and the copies and hybrid fimbriae are easy and the copies and the copies and the copies and the copies and the copies and the copies and the copies and the copies and the copies and the copies and the copies and the copies and the copies and the copies and the copies and the copi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 567; DB 3; Length 15
Pred. No. 1.9e-48;
5; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AgfA::PT3#10 amino acid sequence SEQ ID NO:30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB36355 standard; protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 80.8%;
Matches 122; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0127888P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYVI-) UNIV VICTORIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-672631/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200060102-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
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             8
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: sequence which encodes a foreign epitope or antigen. Also described are: or sequence which are (SEPI)/TAPA nucleation depended assembly system of strains of Salmonella. Escherichia coli and Enterobacteriaceae for the production of finbriae comprising recombinant coli and investing recombination of a recombinant on the chromosome of the homologous species, replacing the native copy of that gene, and (4) eliciting an immune response in an animal. Copy of that gene, and (4) eliciting an immune response in an animal copy is separating an amino acid polymer comprising a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, B. coll or comprising separating in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgiA protein which is useful for the expression or recombinant AgiA protein which is useful for system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid finbrin protein possesses both the contains and an efficient live contains and an efficient live contains and an efficient live contains and an efficient live contains and an efficient live contains and an efficient live contains and an efficient live contains and an efficient live contains and an efficient live contains and an efficient live contains and an efficient live contains and an antimal and efficient live contains and an animal and efficient live contains and an efficient live.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                     Recombinant agfA gene having a segment replaced by a foreign DNA seq
which encodes foreign epitope or antigen, expresses recombinant AgfA
protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccine, the carrier fimbrial subunit proteins are usually strong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 566; DB 3;
Pred. No. 2.4e-48;
5; Mismatches 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Page 139; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR62761 standard; protein; 120
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80.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 80.8
Matches 122; Conservative
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N-PSDB; AAC64631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AgfA sequence.
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26-JUN-1995
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Example 2; Fig 7; 85pp; English.

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The sequence represents the Salmonella enteritis 27655-3b TnphoA mutant strain Agfa protein. The encoding DNA and isolated Agfa protein are used in genetic immunization and vaccine compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct DN field.) (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                             37 HASGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNG 96
                                                                                                                                                            Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated Salmonella gene agfA - used for diagnosis of Salmonella or enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella enteritidis 27655-3b InphoA mutant agfA fragment.
                                                                                                                                                                                                                                                                                                                                            Score 487; DB 2; Length 120;
Pred. No. 1.3e-40;
                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRNNATIDQWDAKNSDITVGQYGGNDAALVNQTASDS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                97 FRNNATIDOWNAKWSDITVGQYGGNNAALVNQTASDS 133
                                                                                               Doran JL
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                                                          UNIV VICTORIA INNOVATION & DEV CORP.
                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                               Clouthier SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW23569 standard; protein; 120 AA
                                                                                                                                                                                                    7A; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Doran JL
                                                                                                                                                                                                                                                                                                                                                                     2;
                                                                                                                                                                                                                                                                                                                                            64.3%;
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                                93US-00054452
         94WO-IB000207
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                        95; Conservative
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                                                                                               Collinson SK,
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                                                                                                                      WPI; 1994-358275/44.
N-PSDB; AAQ73066.
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAT74141
                                                                                                                                                                                                                                                                                                                    Sequence 120 AA;
                                                                                                                                                                                                    Disclosure; Fig
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          26-APR-1994;
                                  26-APR-1993;
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29-SEP-1997
                                                                                                                                                                           strains,
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                                                                                                Kay WW,
                                                          (-IAXO)
                                                                      (KING/)
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Gaps

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                             The present sequence represents an agfA fragment encoded by an agfA gene fragment derived from Salmonella enteritidis 27655-3b TnphoA mutant strain. The mucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                        37 HASGPDSTLSIXQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNG 96
                                                                                                                                                                                                                                                                                                                                                                                                                                          16 NSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIBLTQNG 75
                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                            Score 487; DB 2; Length 120;
Pred. No. 1.3e-40;
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                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
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1e : 45.9 secs
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Best Local Similarity
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Sequence 2, Appli
Sequence 32096, Appl
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Sequence 3159, Ap
Sequence 5, Appli
Sequence 6167, Ap
Sequence 2, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 1, Appli
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Sequence 199, App
Sequence 204, App
Sequence 6562, Ap
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Sequence 59, Application US/08233788A

Patent No. 5635617

GENERAL INFORMATION:
APPLICANT: Down James L.
APPLICANT: Ray, William W.
APPLICANT: Collinson, Karen S.
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Pred. No. 1.8e-60;
3; Mismatches 13; Indels
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MEDIUM TYPE: FLORY disk
COMPUTER READABLE FORM:

MEDIUM TYPE: FLORY disk
COMPUTER: IBM PC COMPATIDLE
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SUSTWARE: LAFELLO DATE:
APPLICATION NUMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASS!FICATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 920043.403C2
TELEPHONE: (206) 622-490
TELEPHONE: (206) 622-490
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US-09-072-56-199
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Best Local Similarity 89.4%;
Matches 135; Conservative
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Sequence 5434, Appl
Sequence 5434, Appl
Sequence 131, Appl
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 214, Appli
Sequence 22, Appli
Sequence 22, Appli
Sequence 12, Appli
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Sequence 2, Al
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/cgn2 6/ptcdata/2/iaa/6B_COMB.pep:*
/cgn2 6/ptcdata/2/iaa/6A_COMB.pep:*
/cgn2 6/ptcdata/2/iaa/6B_COMB.pep:*
/cgn2 6/ptcdata/2/iaa/PCTUS COMB.pep:*
/cgn2 6/ptcdata/2/iaa/PCTUS COMB.pep:*/cgn2 6/ptcdata/2/iaa/PCTUS COMB.pep:*/cgn2 6/ptcdata/2/iaa/Packfiles1.pep:*/cgn2 6/ptcdata/2/iaa/backfiles1.pep:*//prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/iaa/backfiles1.pep:*/prodata/2/ia
                                        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-134-0101-3214

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US-09-336-115C-12

US-09-336-115C-6

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Maximum Match 100% .
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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GARY BRETON
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                                                                                 61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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WESUREAL 17 Application US/08233788A

Sequence 57, Application US/08233788A

PAPLICANT: Boran, James L.

APPLICANT: Collinson, Karen S.

APPLICANT: Collinson, Karen S.

APPLICANT: Collinson, Karen S.

APPLICANT: Coluthier, Sharon C.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION

TITLE OF INVENTION: OF SALMONBILA

NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seartle

STREET: Washington

COUNTRY: U.S.A.

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: EMB PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/233,788A

FILING DATE: 26-APR-1994

FILING DATE: 26-APR-1994

FILING DATE: 26-APR-1994
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Pred. No. 2.5e-43;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 FRNNATIDOWNAKNSDITVGOYGGNNAALVNQTASDS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 FRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS 133
                                                                                                                                                      121 NNPALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                             .21 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION UMMER: 35,570
REFERENCE/DOCKET NUMBER: 920043.403C2
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 622-4900
TELEFAX: (206) 622-4900
TELEFAX: 8723836 SEEDAMBERRY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5434, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
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Best Local Similarity 97.9%;
Matches 95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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US-09-543-681A-5434
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION VUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
NUMBER OF SEQ ID NOS: 8344
SEQ ID NOS: 8344
SEQ ID NOS: 8345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1700 DVTVTITLTNDAGHASAPDYSTLAGSOH---DGKIALHGDTGK----VTYDGASTVTVVI 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83 QGADNS-----TIELTQNGFRNNATIDQWNAKNSDITVGQYGG--NNAALVNQTASDS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 ALFVSLVVSNLLGQNAPAIAATEAAYEQMMAQDVAAMFGYHAGASAAVSALTPFGQALPT 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 VAGGGALVSAAAQVTTRVFRNLGL-ANVGEGN-----VGNGNVGNFNLGSANIGNGN 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 DQLVTRVVTHEMAHASGPD-STLSIYQYGSANAALALQSDARKSETTIIQSGYGNGADVG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 AAFAAIVVSG-----SALAGVYDQLVTRVVTHEMAHASGPDSTLS-IYQYGSANAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: immunostimulatory Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.4%; Score 86.5; DB 4; Length 943; 24.8%; Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 2315;
                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 88; DB 4; Length 231; Pred. No. 6; 15; Mismatches 54; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 52888

CURRENT APPLICATION NUMBER: US/09/477,135A

CURRENT APPLICATION NUMBER: US/09/477,135A

CURRENT FILING DATE: 2000-01-03

PRIOR FILING DATE: 1997-12-15

PRIOR FILING DATE: 1996-06-14

PRIOR FILING DATE: 1996-06-14

PRIOR FILING DATE: 1995-06-15

NUMBER OF SQ ID NOS: 169

SEQ ID NO 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                          11.6%;
ilarity 28.0%;
Conservative 1
                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Proteus mirabilis
US-09-543-681A-5434
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Best Local Similarity
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Matches 39; Conserv
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TILIQSGYGNGADVGQGA-----DNSTIELTQNGFRNNATI-DQWNAKNSDITVGQYGGN 121
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                                                                                                                                                                                                                                                                                                                                           463 AAATAGATVAGRVNGAVT--ITDSAASATTAGKIATVTLGSFGAA----TIDSSAL---
                                                                                                                                                                                                                                           20;
                                                                                                                                                                                Query Match
10.8%; Score 82; DB 1; Length 1026;
Best Local Similarity 24.8%; Pred. No. 7.9;
Matches 34; Conservative 28; Mismatches 55; Indels
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MEDIUM TYPE: RADABLE FORM:
MEDIUM TYPE: RADABLE FORM:
COMPUTER: IBM PC Compartible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT: APPLICATION DATA:
APPLICATION NUMBER: US/08/614,377A
FILING DATE: 12-MAR.1996
CLASSIFICATION NUMBER: US 08/194,290
FILING DATE: 09-FEB-1994
CLASSIFICATION: 435
APPLICATION: 435
APPLICATION: 435
APPLICATION: 435
APPLICATION: 435
APPLICATION: WHERE: US 07/895,367
FILING DATE: 09-TUNE.1992
CLASSIFICATION: NUMBER: MS 07/895,367
FILING DATE: 09-TUNE.1992
CLASSIFICATION: NUMBER: 3405
REGISTRATION NUMBER: 3405
REGISTRATION NUMBER: 3405
REGISTRATION NUMBER: 3405
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APPLICANT: Smit, John
APPLICANT: Bingle, Wade H.
APPLICANT: No. 5976864ellini, John F.
TITLE OF INVENTION: EXPRESSION AND SECRETION OF
TITLE OF INVENTION: POLYPEPTIDES FROM CAULOBACTER
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08106/002001
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TELECOMMUNICATION INFORMATION
TELEPHONE: 617-542-5070
SEQUENCE CHARACTERISTICS:
LENGTH: 1026 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-194-290-7
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TOPOLOGY: li
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INFORMATION FOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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                                                                             Sequence 26438, Application US/09252991A
Patent No. 5551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEEC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: APPLICATION OF 136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | : | : : : : | | | : : : | | | 417 LAAGANGTSAVQSGANGTSVVQSQNGANIGAGASDISVVQSQNSPNIGSGVN 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 DQLVT---RVVTHEM-----AHASGPDSTLSIYQYGSANA------ALA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 LQSDARKSETTITQSGYG-----GFR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.2%; Score 85; DB 4; Length 1415; 1 Similarity 25.6%; Pred. No. 6.1; 43; Conservative 19; Minmart.
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Patent No. 5500353
GENERAL INFORMATION:
APPLICANT: Smit, John
APPLICANT: Bringle, Wade H
TITLE OF INVENTION: Bacterial surface protein expression
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Shlesinger, Arkwright & Garvey
STREET: 3000 South Eads Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,290
FILING DATE: 09-FEB-1994
CLASSIFICATION: 43.5
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 59
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Garvey, George A
REGISTRATION NUMBER: 17737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 703-836-5288
INFORMATION FOR SEQ 1D NO:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arlington
: Virginia
RY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                              RESULT 5
US-09-252-991A-26438
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 26438
LENGTH: 1415
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US-08-194-290-7
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                                                                                                                                                                                                                                                                                                                                                       511 SAFAAI----ANGGTYNNAHSIQKVVTHEGDTIEYEHTSHKAMKDYTSYMLAEILKGTF
                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22, Application US/09336115C
Sequence 22, Application US/09336115C
Sequence 22, Application US/09336115C
Sequence No. 6576244
SEGNERATION:
TERRETE INFORMATION:
TITLE OF INVENTION: And CT in Parenteral Immunization
TITLE OF INVENTION: Methods Against Helicobacter Infection
FILE REPERENCE: 66132/055002
CURRENT APPLICATION NUMBER: US/09/336,115C
CURRENT APPLICATION NUMBER: US 09/100,258
PRIOR PRIOR PILING DATE: 1999-06-18
PRIOR PRILING DATE: 1999-06-19
NUMBER: OS SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                  Length 746;
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                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                         48 YOYGSANAALALQSDARKSETTITQSGYGNGADVGQGA----
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                                                                                                                                                                                                                  DB 4;
                                                                                                                                                                                                             Query Match
10.8%; Score 81.5; DE
Best Local Similarity 26.5%; Pred. No. 5.7;
Matches 39; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.7%; Score 81; DB . 19.0%; Pred. No. 5.7; iive 27; Mismatches
                                                                                                                                                                                                                                                                                                               7 AAFAAIVVSGSALAGVYDQL--VTRVVTHE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                612 GFSPEYTMSVWMGFNK---VKQYGTNS 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 GFRNNATIDQWNAKNSDITVGQYGGNN 122
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3214
LENGTH: 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 AFAAIVVSGSALAGVYDQLVTRV----
                                                                                                                     ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3214
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; Sequence 12, Application US/09336115C
Patent No. 6576244
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 19.0%
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ...(18)
US-09-336-115C-22
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US-09-336-115C-22
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Patent No. 6210948

CENERAL INFORMATION:

CENERAL INFORMATION:

APPLICANT: Smit. John

APPLICANT: Smit. John

APPLICANT: Bingle, Wade H.

APPLICANT: No. 6210948ellini, John F.

TITLE OF INVENTION: EXPRESSION AND SECRETION OF HETEROLOGOUS POLYPEPTIDES FROM CAULC FILE REFERENCE: 08106/00202

CURRENT FILING DATE: 1999-03-30

PRIOR APPLICATION NUMBER: US/09/142,648B

PRIOR APPLICATION NUMBER: US/09/142,648B

PRIOR APPLICATION NUMBER: US/09/142,648B

PRIOR APPLICATION NUMBER: US/09/142,648B

PRIOR APPLICATION NUMBER: US/09/142,648B
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Patent No. 6380370

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                            TTITQSGYGNGADVGQGA----DNSTIELTQNGFRNNATI-DQWNAKNSDITVGQYGGN 121
                                                                                                                                                                                                                                                                         463 AAATAGATVAGRVNGAVT--IIDSAAASATTAGKIATVTLGSFGAA----TIDSSAL--- 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITIQSGYGNGADVGQGA----DNSTIELTQNGFRNNATI-DQWNAKNSDITVGQYGGN 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67
                                                                                                                                              11 AIVVSGSALAGVYDQLVTRVVTHEMAHA---SGPDSTLSIYQYGSANAALALQSDARKSE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 AIVVSGSALAGVYDQLVTRVVTHEMAHA---SGPDSTLSIYQYGSANAALALQSDARKSE
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                                                  10.8%; Score 82; DB 2; Length 1026; 24.8%; Pred. No. 7.9;
                                                                                                 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1996-03-12
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                        122 NAA--LVNQTASDSSVM 136
                                                                                                                                                                                                                                                                                                                                                                                  574 TASSTIASLVAADATTL 590
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                                                                                                    Conservative
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Matches 34; Conserv
                                                                           Local Similarity
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US-09-134-001C-3214
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US-09-142-648B-7
       US-08-614-377A-7
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                                                    Query Match
                                                                                                    Matches
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Query Match
Best Local Similarity
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US-09-206-942-69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160 GILSIDEYOKLNOÁYOI-----IQTALNÓNQGGGMPALNDITKTGVVNIQÓTNYŘITTQ 213
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Patent No. 65 Application US/09336115C

Patent No. 66 Application Sequence 6 Application Sequence 7

APPLICANT: Weltzin, Richard A.

APPLICANT: Guy, Bruno

TITLE OF INVENTION: LT and CT in Parenteral Immunization

TITLE OF INVENTION: Modera Against Helicobacter Infection

FILE REFERENCE: 06132/055002

CURRENT APPLICATION NUMBER: US/09/336,115C

CURRENT FILING DATE: 1999-06-18

PRIOR APPLICATION WHERE: US 09/100,258
                                   APPLICANT: Guy, Eruno
ITILE OF INVENTION: Hand CT in Parenteral Immunization
ITILE OF INVENTION: Hand CT in Parenteral Immunization
ITILE OF INVENTION: Hold Spainst Helicobacter Infection
FILE REPERENCE: 06132/055002
CURRENT APPLICATION NUMBER: US/09/336,115C
CURRENT APPLICATION NUMBER: US 09/100,258
PRIOR PILING DATE: 1998-06-19
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 691
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SOFTWARE: FastSEQ for Windows Version 4.0
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LOCATION: 721
OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 AFAAIVVSGSALAGVYDQLVTRV----
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ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Helicobacter pylori
APPLICANT: Weltzin, Richard A. APPLICANT: Guy, Bruno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 23.18
Matches 27; Conservative
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; LOCATION: (1)...(18)
US-09-336-115C-12
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LENGTH: 745
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| Sequence 69, Application US/09206942 | Sequence 69, Application US/09206942 | Sequence 69, Application US/09206942 | Patent No. 6432669 | Patent No. 6432669 | Patent No. 6432669 | Patent No. 6432669 | Patent No. 6432669 | Patent No. 6432669 | Patent No. 6432669 | Patent No. 6432669 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 | Patent No. 643269 |
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ELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNAT 147
                                                                       15 SGSALAGVYDQ--LVTRVVTH---EMAHASGPDSTLSIYQYGSANAALALQS-DARKSET
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US-08-038-682-2

Sequence 2, Application US/08038682

PRETENT NO. 5549804

GENERAL INFORMATION:

APPLICANT: ST. GEME III. JOSEPH W

TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS

TITLE OF INVENTION: OF NON-TYPEABLE HAEMOPHILUS

NUMBER OF SEQUENCES: 8

CORRESPONDENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSE: Shoemaker and Mattare, Ltd

STREET: 200 Jefferson Davis Hwy., 1203 Crystal Plaza

STREET: Wighina

COUNTRY: U.S.A.

ZIP: 22202-0286

COMPUTY: U.S.A.

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.6%; Score 80.5; DB 4; Length 1095; 26.4%; Pred. No. 12; ive 22; Mismatches 60; Indels 27
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/038,682
FILING DATE: 16-MAR-1993
CLASSIPICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                              27; Gaps
                                                                                                                                                                                                                                                                                                                                                 10.6%; Score 80.5; DB 1; Length 1536; 26.4%; Pred. No. 20; trive 22; Mismatches 60; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08302832

Patent No. 5603938

GENERAL INFORMATION:

APPLICANT: Barenhamp, Stephen J

TITLE OF INVENTION: High Molecular Weight Surface Proteins

TITLE OF INVENTION: of No. 5603938-Typeable Haemophilus

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Shoemaker and Mattare, Ltd.

STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza

STREET: Bidg. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/302,832
FILING DATE: 1-5-ED-1994
CLASSIFICATION: 435
PILOR APPLICATION DATA:

APPLICATION NUMBER: GB 9205704.1
FILING DATE: 16-MR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US pct/us93/02166
FILING DATE: 16-MR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Berkstresser, Jerry W
REGRERATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 1038-404
TELEPONE: (703) 415-0810
TELEPONE: (703) 415-0810
INFORMATION FOR SEQ 1D NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1281 NTVNVTANAGDLTV-----GNGAEIN 1301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 NAALVNQTASDSSVMVRQVGFGNNATAN 149
             NAME: BERNSTRESSER, JERRY W
REGISTRATION NUMBER: 22,651
REFRENCE/DOCKET NUMBER: 1038-293
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEPHONE: (703) 415-0810
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1556 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Arington STATE: Virginia COUNTRY: Urginia COUNTRY: U.S.A. ZIP: 22202-0286 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/NS-DOS.
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 26.4%
Marches 39, Conservative
                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein US-08-038-682-2
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US-08-302-832-2
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69 TITQSGYGNGADVGQGADNSTIEL-----TQNGFRNNATIDQWNAKNSDITVGQYGGN 121
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                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                            27;
                                                                                                                                                                  DB 1; Length 1536;
                                                                                                                                                                                                            Indels
                                                                                                                                                                Query Match
10.6%; Score 80.5; DB
Best Local Similarity 26.4%; Pred. No. 20;
Matches 39; Conservative 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1281 NTVNVTANAGDLTV-----GNGAEIN 1301
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Job time : 12 secs
                                                                                TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-302-832-2
                        1536 amino acids
SEQUENCE CHARACTERISTICS
LENGTH: 1536 amino ac:
                                   amino acid
EDNESS: single
                                        TYPE: amino a STRANDEDNESS:
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August 2, 2004, 14:54:48; Search time 36.8 Seconds (without alignments) 1287.123 Million cell updates/sec
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2: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUBL.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Sequence 4, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 20638, A	Seguence 72503, A	Seguence 49757, A	Sequence 1549, Ap	Sequence 146, App	Seguence 162284,	Sequence 131, App	Sequence 131, App	Sequence 131, App	Sequence 64369, A	Sequence 38, Appl
US-09-741-873B-4	US-09-741-873B-4	US-09-741-873B-2	US-09-741-873B-2	US-10-369-493-20638	US-10-282-122A-72503	US-10-282-122A-49757	US-10-238-075-1549	US-09-793-306-146	US-10-437-963-162284	US-09-996-634-131	US-09-997-182-131	US-09-997-181-131	US-10-282-122A-64369	US-10-383-930-38
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151	151	131	131	445	290	1862	182	597	154	943	943	943	3300	1554
63.5	63.5	54.7	54.7	15.0	12.3	11.8	11.8	11.7	11.4	11.4	11.4	11.4	11.4	11.2
481	481	414	414	113,5	93	89.5	89	88.5	86.5	86.5	86.5	86.5	86.5	85
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34 Sequence 107204,	4	-	(T)	Seguence 1, Appli	O	Seguence 10, Appl	П	7 Sequen	Seguence 16, Appl	Seguen	3 Sequence 13173, A	Seguen	Sequence 5343, Ap	Sequence 7, Appli	Sequence 7, Appli	Sequence 109, App	Sedner	.86 Sequence 70586, A	Seguer	Sequence 12,	equence 22,	, Appli	3 Sequence 58683,	5 Sequence 73345,	94 Sequence 54094, A	Sequence 65, App	2, Appl	63, App	
US-10-43	2 US-10-282-122A-498	0 US-09-984-33	4 US-10-004-115	4 US-10-327-1	4 US-10-156-761-	US-10-185-990-1	4 US-10-185-990	2 US-10-282-12	US-09-996-194-	2 US-10-164-966-33	4 US-10-156-761-1317	369-493-2009	5 US-10-369-493-534	US-09-379-93	4 US-10-223-597-	-787-69-769-0	US-10-282-122A-736	.282-122A-705	2 US-10-282-122A-497	US-08-834-666A-12	US-08-834-666A-2	US-08-834-666A	US-10-282-122A-586	2 US-10-282-122A-733	282-122A-540	US-10-193-764-65	US-10-092-880-	US-10-193-764-63	
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16	17	18	19	20	21	22	23	24	25	26	27	28	20	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	

## ALIGNMENTS

9

1 MKLLKVAAFPAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ

3 10:54:33 2004

Tue Aug

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39 SGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFR
                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli
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Best Local Similarity
Matches 79; Conserv
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                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09741873B

bublication No. US20040096965A9

publication No. US20040096965A9

GARDEAL INFORMATION:

APPLICANT: Olsen, Arne

TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation

FILE EFFRENCE: 012689-084

CURRENT APPLICATION NUMBER: US/09/741,873B

CURRENT APPLICATION NUMBER: US/09/741,873B

CURRENT APPLICATION NUMBER: US 08/978,878

PRIOR FILING DATE: 1998-05-06

PRIOR FILING DATE: 1999-05-04

PRIOR FILING DATE: 1999-05-04

PRIOR FILING DATE: 1991-11-06

PRIOR FILING DATE: 1991-11-06

PRIOR FILING DATE: 1991-11-06

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-10-05

NUMBER OF SEQ ID NOS: 10

SEQ ID NO 4

LENGTH: 151

TANDER: DATE: 151

TANDER: DATE: 1994-10-05

SEQ ID NO 4

LENGTH: 151
                                                                                            61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKLLKVAAIAAIVFSGSAVAGVVPQYGGGUHGGGGNNSGPNSELNIYQYGGGNSALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Normark, Staffan
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 01289-004
CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT FILING DATE: 2003-04-04
                                                                 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.5%; Score 481; DB 12; Length 151; 66.2%; Pred. No. 2.1e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                     121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                  121 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 63.5
Best Local Similarity 66.2
Matches 100; Conservative
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US-09-741-873B-2
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APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTATION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 01289-084
CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT APPLICATION NUMBER: US 8801723-1
PRIOR APPLICATION NUMBER: US 8801723-1
PRIOR FILING DATE: 1938-05-06
PRIOR FILING DATE: 1938-05-06
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR APPLICATION NUMBER: US 07/399,437
PRIOR FILING DATE: 1939-11-06
PRIOR FILING DATE: 1931-11-06
PRIOR FILING DATE: 1932-11-03
PRIOR FILING DATE: 1934-01-28
PRIOR FILING DATE: 1934-01-28
PRIOR FILING DATE: 1934-10-05
PRIOR PELING DATE: 1934-10-05
NUMBER OF SEQ ID NOS: 10
SROFTHANE: PARCETIN NUMBER: US 08/318,519
PRIOR APPLICATION NUMBER: US 08/318,519
PRIOR PLING DATE: 1934-10-05
NUMBER OF SEQ ID NOS: 10
SROFTHANE: PARCETIN VARIABIN 3.0
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S4.7%; Score 414; DB 12; Length 131;
Best Local Similarity 69.9%; Pred. No. 3.6e-37;
Matches 79; Conservative 17; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         t; Score 414; DB 12;
t; Pred. No. 3.6e-37;
17; Mismatches 17;
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1989-05-04
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR APPLICATION NUMBER: US 07/89,437
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR FILING DATE: 1992-11-03
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-01-28
PRIOR APPLICATION NUMBER: US 08/18,519
PRIOR FILING DATE: 1994-10-05
PRIOR FILING DATE: 1994-10-05
PRIOR FILING DATE: 1994-10-05
PRIOR FILING DATE: 1994-10-05
PRIOR FILING DATE: 1994-10-05
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milarity 69.9%;
Conservative 17
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60 OSDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG 119
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                               Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 72503
LENGTH: 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 12; Length 290;
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APPLICANT Xu, H.

TITLE OF INVENTION: Identification of Essentia FILE REFERENCE: ELITRA, 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: G0/191,078
PRIOR PELICATION NUMBER: G0/206,848
PRIOR PELICATION NUMBER: G0/206,848
PRIOR PELICATION NUMBER: G0/206,727
PRIOR PELICATION NUMBER: G0/207,727
PRIOR APPLICATION NUMBER: G0/207,727
PRIOR APPLICATION NUMBER: G0/230,335
PRIOR PILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR PELICATION NUMBER: G0/220,335
PRIOR APPLICATION NUMBER: G0/220,303
PRIOR APPLICATION NUMBER: G0/225,931
PRIOR APPLICATION NUMBER: G0/225,931
PRIOR APPLICATION NUMBER: G0/25,931
PRIOR APPLICATION NUMBER: G0/257,931
PRIOR APPLICATION NUMBER: G0/257,931
PRIOR APPLICATION NUMBER: G0/257,931
PRIOR APPLICATION NUMBER: G0/257,931
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PRIOR APPLICATION NUMBER: G0/257,931
PRIOR APPLICATION NUMBER: G0/257,931
PRIOR APPLICATION NUMBER: G0/257,931
PRIOR APPLICATION NUMBER: G0/257,931
PRIOR PILING DATE: 2000-10-2-22
PRIOR APPLICATION NUMBER: G0/257,931
PRIOR PILING DATE: 2000-10-2-32
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
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APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus mutans
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Wall, Daniel
Trawick, John
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Yamamoto, Rol
Forsyth, R.
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Best Local Similarity
Matches 40; Conserv
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US-10-282-122A-72503
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APPLICANT: Hinkle, Greenry J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Manden Barry S.
APPLICANT: Goldman, Manden Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Stevenry S.
APPLICANT: Wanden Warperson OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10(52052)8
FILE REPERENCE: 38-10(52052)8
FRIOR FILING DATE: 2003-02-28
FRIOR PRICK APPLICATION NUMBER: US 60/360,039
FRIOR PRICK OF SEQ ID NOS: 47374
SEQ ID NO 20538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 FNGNSGFLÓENGTLSGANLLTVKQSGNSNSVGRDIQGKQSGAGNSAAIFQEGTGSDVELQ 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 -----LQSDARKSETTI-------TQSGYGNGADVGQGADNSTIELT 93
            19 SGPNSELNTYQYGGGNSALALQTDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFG 78
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                                                                                                                                       99 NNATIDOWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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Best Local Similarity 25.0%; Pred. No. 0.0013;
Matches 46; Conservative 18; Mismatches 63; Indels 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure
LOCATION: (1)..(445)
OTHER INFORMATION: unsure at all Xaa locations
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US-10-282-122A-72503
Sequence 72503, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Mandy, Liangsu
APPLICANT: Amudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Oblsen, Kari
APPLICANT: Oblsen, Wari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                               Sequence 20638, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
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Syskind, Judith
Wall, Daniell
Trawick, John
Carr, Grant
Yamamoto, Robert
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US-10-369-493-20638
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APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21
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APPLICANT: Ovendale, Pamela
APPLICANT: Ovendale, Pamela
APPLICANT: Ovendale, Pamela
APPLICANT: Lodes, Michael
APPLICANT: Lodes, Michael
APPLICANT: Corixa Corporation
ITILE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
ITILE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
ITILE OF INVENTION: Of Tuberculosis
ITILE OF INVENTION: Of Tuberculosis
CURRENT APPLICATION NUMBER: US/09/793,306
CURRENT APPLICATION NUMBER: US 60/185,037
PRIOR FILING DATE: 2000-02-25
PRIOR FILING DATE: 2000-02-25
PRIOR FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 164
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 146
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                                                                                                                                                                                                                                                                                                                            57 LALQSDARKSETT---ITQSGYGNGADVGQGA-----DNSTIELTQNGFRNNATIDQWNA 108
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                                                                                                                                                                    : |::::| |::||::| |:|| |:| |:| | |:|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:::|| |:
                                                                                                 1 MKLLKVAAFAAIVVSGSALAGVYDQLVT---RVVTHE-MAHASGPDSTLSIYQYGSANAA 56
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11.7%; Score 88.5; DB 9; Length 597;
Best Local Similarity 35.9%; Pred. No. 1;
Matches 28; Conservative 7; Mismatches 32; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 KNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNAT 147
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Publication No. US20040123343A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 146, Application US/09793306
; Patent No. US20020098200A1
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APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yinua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Bubharov, Andrey A.
APPLICANT: Barbaruk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132 DSSVMVRQVGFGNNATAN 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Campos-Neto, Antonio APPLICANT: Skeiky, Yasir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
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US-10-437-963-162284
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/245,578
PRIOR APPLICATION NUMBER: 60/245,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269,308
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11arity 26.8%; Pred. No. 3.7;
Conservative 16; Mismatches 66;
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ORGANISM: Escherichia coli
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LENGTH: 1862
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US-09-997-182-131
, Sequence 131, Application US/09997182
; Publication No. US20030049263A1
; GENERAL INFORMATION:
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Best Local Similarity 24.84
Matches 39, Conservative
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Patent No. US20020172684A1

GENERAL INFORMATION:
APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: immunostimulatory Peptides
TITLE OF INVENTION: immunostimulatory Peptides
TILE REFERENCE: 61260
CURRENT APPLICATION NUMBER: US/09/996,634
CURRENT FILING DATE: 2001-11-28

PRIOR PLING DATE: 2000-01-03
PRIOR PLING DATE: 1997-12-15

PRIOR PLING DATE: 1996-06-14

PRIOR PLING DATE: 1996-06-14

PRIOR PLING DATE: 1996-06-14

PRIOR PLING DATE: 1996-06-14

PRIOR PLING DATE: 1996-06-15

NUMBER: OF SEQ ID NOS: 169

SOFTWARE: PATENTIN VOICE: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 DOWNAKNSDITV------GQYGGNNAALVNQTASDSSVMVRQVGFGN 144
                                                                                                                                                                                                                                               11.4%; Score 86.5; DB 16; Length 154; 23.5%; Pred. No. 0.26; ive 21; Mismatches 56; Indels 53
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                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT4530_61390C.1.pep
US-10-437-963-162284
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CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 162284
LENGTH: 154
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Best Local Similarity 23.54
Matches 40; Conservative
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                                                                                                                 TYPE: PRT
ORGANISM: Oryza sativa
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Best Local Similarity
Matches 39; Conserv
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US-09-996-634-131
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RESULT 12

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57 L----ALOSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD 112
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TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: Mymmer: US/09/997,182
CURRENT PAPPLICATION NUMBER: US/09/997,182
PRIOR FILING DATE: 2001-01-03
PRIOR PLING DATE: 1097-12-15
PRIOR PLING DATE: 1097-12-15
PRIOR PLING DATE: US/0000,254
PRIOR PLING DATE: 1996-06-14
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FILE REFERENCE: 61257

CURRENT APPLICATION NUMBER: US/09/997,181

CURRENT FILING DATE: 2000-01-11-28

PRIOR FILING DATE: 2000-01-03

PRIOR FILING DATE: 1997-12-15

PRIOR APPLICATION NUMBER: US 96/10375

PRIOR PILING DATE: 1995-06-14

PRIOR FILING DATE: 1995-06-15

NUMBER OF SEQ ID NOS: 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Mycobacterium tuberculosis US-09-997-182-131
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ORGANISM: Mycobacterium tuberculosis
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Best Local Similarity 24.8'
Matches 39; Conservative
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RESULT 15
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APPLICANT: Indiamiculo, Rouert
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA, 03.4A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PELING DATE: 2000-05-21
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PLING DATE: 2000-05-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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PRIOR FILING DATE: 2001-02-09
                                  L----ALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD 112
                                                                                                                                                                    156 VAGGGALVSAAAAQVTTRVFRNLGL-ANVGEGN-----VGNGNVGNFNLGSANIGNGN 207
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-SALAGVYDQLVTRVVTHEMAHASGPDSTLS-IYQYGSANAA 56
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 64369
LENGTH: 3300
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                                                                                                                                                                                                                           113 ITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                   IGSGNIGSSNIGFGN-VGPGLTAALNNIGFGNTGSNN 243
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 64369, Application US/10282122A Publication No. US20040029129A1
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APPLICANT: Wang, Liangsu
APPLICANT: Gardudóo, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: Oblsen, Kari
APPLICANT: Oblsen, Kari
APPLICANT: Oblsen, Kari
APPLICANT: Wall, Daniel
APPLICANT: Travick, John
APPLICANT: Travick, John
APPLICANT: Yamanoto, Robert
APPLICANT: Forsyth, R.
7 AAFAAIWVSG--
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US-10-282-122A-64369
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 38, Application US/10383930;
Sequence 38, Application US/10383930;
Publication No. US20040127400A1
| GENERAL INFORMATION:
APPLICANT: Smith, Daniel J
APPLICANT: Taubman, Martin A
ITLE OF INVENTION: Immunogenicity of Glucan Binding Protein
FILE REFERENCE: 25669-018;
CURRENT APPLICATION NUMBER: US/10/383,930
| CURRENT PILING DATE: 2003-03-07;
PRIOR FILING DATE: 2002-08-08
| PRIOR FILING DATE: 2002-08-08
| PRIOR FILING DATE: 2002-03-07;
| NUMBER OF SEQ ID NOS: 41
| SEG ID NOS: 41
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| CANCELL OF SEC ID NOS: 41
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                                                                                                                                 113 ITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                           IGSGNIGSSNIGFGN-VGPGLTAALNNIGFGNTGSNN 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 DSTLSIYQYGSANAALALQSDARKSETTITQSGY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Streptococcus sobrinus
US-10-383-930-38
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Best Local Similarity 22.74
Matches 27; Conservative
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APPLICANT White Aaron P.
APPLICANT White Aaron P.
APPLICANT White Aaron P.
APPLICANT White M.
APPLICANT Collinson, S. Karen
APPLICANT RAY, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 20043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASISEQ for Windows Version 4.0
LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION: Recombinant Salmonella enteritidis 3b afgA INFORMATION: sequence containing the replacement fragment INFORMATION: encoding PT3 from GP63 of Leishmania major.
          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1
US-09-543-407-16
Sequence 16, Application US/09543407
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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    August 2, 2004, 14:48:33 ; Search time 167.9 Seconds (without alignments) 877.809 Million cell updates/sec
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                                                                                                                                                                                                              US-09-543-407-16
757
1 MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151
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6/prodata/2/paa/US097B_COMB_pep:*
6/prodata/2/paa/US098_COMB_pep:*
6/prodata/2/paa/US098_COMB_pep:*
6/prodata/2/paa/US099B_COMB_pep:*
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2_COMB.pep:
3_COMB.pep:
4_COMB.pep:
6_COMB.pep:
7_COMB.pep:
                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                      hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                6019581 seqs, 976053577 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                 - protein search, using sw model
                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length DB
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Score

Result No.

Sequence 55, Appli Sequence 7, Appli Sequence 4, Appli Sequence 2, Appli Sequence 534, Ap Sequence 534, Ap Sequence 534, Ap Sequence 534, Ap Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli Sequence 383, Appli Sequence 383, Appli Sequence 5833, Appli Sequence 5833, Appli Sequence 5833, Appli Sequence 5833, Appli Sequence 5833, Appli

Total number of

Searched:

Minimum DB : Maximum DB :

Database

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Sequence 22, A Sequence 30, A Sequence 34, A

Sequence 2 Sequence 2 Sequence 2

Sequence 18, Sequence 12, Sequence 31,

Sequence Sequence

Sequence 57,

Sequence 35, Appl Sequence 37, Appl Sequence 39, Appl Sequence 5833, Ap Sequence 5833, Ap Sequence 6, Appl 1A Sequence 6, Appl 1A Sequence 7, Appl 1A Sequence 7, Appl 1A Sequence 7, Appl 1A Sequence 10, Appl 1A Sequence 10, Appl 1A Sequence 10, Appl 1A Sequence 10, Appl 1A Sequence 10, Appl 1A Sequence 11372, Appl 1A Sequence 11372, Sequence 29229, A

Sequence 206 Sequence 6, Sequence 10,

Sequence

Sequence

Sequence

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Washington

US-09-543-407-16

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61 SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQMNAKNSDITVGQYGG 120
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Sequence 18, Application US/09543407

APPLICANT: White, Aaron P.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

ITLE OF INVENTION: BRESENTAL FIMBRIAL SYSTEM FOR

ITLE OF INVENTION: BRESENTATION OF HETEROLOGGUS PEPTIDE SEQUENCES

FILE REFERENCE: 920043.406

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 18

LENTH: 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 653; DB 6; Length 151;
Pred. No. 1.6e-64;
3; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                           COMPUTER FELDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elem PC compatible
OPERATIOR SYSTEM: PC-005/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,642A
FILING DATE: 26-APR-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: KIDS, JOSHUA
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 920043.403C3
TELECOMMULICATION INFORMATION:
TELEPHONE: (206) 622-4900
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81.6%; Score 618; DB 19;
Best Local Similarity 76.6%; Pred. No. 1.4e-60;
Matches 131; Conservative 0; Mismatches 0;
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TELEX: 3723836 SEEDAMBERRY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 89.4%;
Matches 135; Conservative
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-233-642A-57
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RY: U.S.A.
98104-7092
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GENERAL INFORMATION:
APPLICANT: White, Aarch P.
APPLICANT: Doran, James D.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TILLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TILLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ray, William W. APPLICANT: Collinson, S. Karen APPLICANT: Collinson, S. Karen APPLICANT: Collinson, Sharon C. APPLICANT: Coluther, Sharon C. APPLICANT: Doran, James L. TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-ITLE OF INVENTION: BASED VACCINES NUMBER OF SEQUENCES: -
CORRESPONDENCE ADDRESS: -
ADDRESSES: Seed and Berry STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle
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                       Length 151;
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Best Local Similarity 90.1%; Pred. No. 4.5e-65;
Matches 136; Conservative 3; Mismatches 12; Indels
                                                                             Indels
                       Query Match 100.0%; Score 757; DB 19; Best Local Similarity 100.0%; Pred. No. 3.4e-76; Matches 151; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                 121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
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; ORGANISM: Salmonella enteritidis
US-09-543-407-5
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US-08-233-642A-57
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ORGANISM: Salmonella enteritidis
TYPE: PRT
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SOUND SEPTIDE SEQUENCES
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT APPLICATION NUMBER: US/09/543,407
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                     1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTKVVTHEMAH---
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                                                                                                                                                                                                                             101 ATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                          101 ATIDOMNAKNSDITVGOYGGNNAALVNOTASDSSVMVROVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.6%; Score 580; DB 19;
80.1%; Pred. No. 2.6e-56;
tive 7; Mismatches 23;
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| NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
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US-09-543-407-31

SEQUENCE 31, Application US/09543407

SEQUENCE 31, Application US/09543407

SEQUENCE 31, Application US/09543407

APPLICANT: White, Aaron P.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

ITILE OF INVENTION: BACTERIAL FIMBRIAL SYSTE

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTE

TITLE OF INVENTION: PRESENTATION OF HETEROL

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FASTSEQ for Windows Version 4.0

SENGTH: 131
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                             MKLLKVAAFAAIVVSGSALAGV
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ORGANISM: Artificial Sequence
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Best Local Similarity 80.13
Matches 121; Conservative
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US-09-543-407-12
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                                                                                                                                             37 HASGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNG
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                                                                                                                                                                                                                                                                          FRNNATIDOWNAKNSDITVGQYGGNNAALVNQTASDSSVWVRQVGFGNNATANQY 131
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APPLICANT White, ABRON P.
APPLICANT Collinson, S. Karen
APPLICANT Collinson, S. Karen
APPLICANT Kay, William W.
TITLE OF INVENTION: BACKERAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REPRESENT APPLICATION NUMBER: US/09/543,407
CURRENT PILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 151
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                                               Length 131;
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80.8%; Pred. No. 4.4e-56;
tive 6; Mismatches 23; Indels
                                                                                              Indels
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GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Doran, James L.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

ITILE OF INVENTION: BRACIERIAL SYSTEM FOR

ITILE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEP

FILE REFERENCE: 920043 406

CURRENT APPLICATION UNMBER: US/09/543,407

CURRENT PILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59
                                                                                           0
                                            Score 579; DB 19;
Pred. No. 2.8e-56;
2; Mismatches 0;
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                                               Query Match
Best Local Similarity 98.3%;
Matches 113; Conservative
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Best Local Similarity 80.8
Matches 122; Conservative
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US-09-543-407-26
US-09-543-407-31
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FEATURE:
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APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Callinson, S. Karen
APPLICANT: Cap. William W.
TITLE OF INVENTION: BACTERIAL FIRBRIAL SYSTEM FOR
TITLE OF INVENTION: BRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 151
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                                                                                                                     FEATURE:
COTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
COTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
US-09-543-407-26
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                                                                                                                                                                                                                                                                                  Length 151;
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Best Local Similarity 81.5%; Pred. No. 9.5e-56;
Matches 123; Conservative 5; Mismatches 23;
                                                                                                                                                                                                                                                                          tch 76.2%; Score 577; DB 19; al Similarity 80.8%; Pred. No. 5.7e-56; 122; Conservative 5; Mismatches 24;
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Best Local Similarity
                       SEQ ID NO 26
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                                                                       TYPE: PRT
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Matches
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RESULT 10 US-09-543-407-20 ; Sequence 20, Application US/09543407

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APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, & Karen
APPLICANT: Collinson, & Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.407
CURRENT PELLING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 151
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APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGCOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.8%; Score 574; DB 19; Length 151; 80.8%; Pred. No. 1.2e-55; ive 6; Mismatches 23; Indels
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Best Local Similarity 80.1%; Pred. No. 5.8e-55;
Matches 121; Conservative 4; Mismatches 26;
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Best Local Similarity 80.8<sup>3</sup>
Matches 122, Conservative
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us-09-543-407-16.rapm

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COMPUTER READABLE FORM:
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Best Local Similarity
Matches 109; Conserv
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US-08-233-642A-55
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US-09-543-407-34
     US-09-543-407-30
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61 SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQMNAKNSDITVGQYGG 120
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| Sequence 30, Application US/09543407
| GENERAL INFORMATION:
| APPLICANT: White, Aaron P. |
| APPLICANT: Collingon, S. Karen |
| APPLICANT: Collingon, S. Karen |
| APPLICANT: Collingon, S. Karen |
| APPLICANT: Kay, William W. |
| TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR |
| TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES |
| FILE REFERENCE: 920043.406 |
| CURRENT APPLICANTON NUMBER: US/09/543,407 |
| CURRENT FILING DATE: 2000-04-05 |
| NUMBER OF SEQ ID NOS: 59 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 30 |
                                                                                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
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APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Caren
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Caren
APPLICANT: Collinson, S. Caren
APPLICANT: Collinson, S. Caren
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTMARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALAQ
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ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragmen OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 151;
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74.9%; Score 567; DB 19;
Best Local Similarity 80.8%; Pred. No. 7.5e-55;
Matches 122; Conservative 5; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                              121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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APPLICANT: Ray, William W.
APPLICANT: Ray, William W.
APPLICANT: Collinson, S. Karen
APPLICANT: Clouthier, Sharon C.
APPLICANT: Doran, James L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: BASED VACCINES
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS: -
CORRESPONDENCE ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 109;
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                                                                                                   Indels
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GENERAL INFORMATION:
APPLICANT White, Aaron P.
APPLICANT Collinson, S. Karen
APPLICANT Collinson, S. Karen
APPLICANT COLLINSON, S. RATEN
APPLICANT COLLINSON, S. RATEN
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A
74.8%; Score 566; DB 19;
80.8%; Pred. No. 9.7e-55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                         5; Mismatches
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APPLICANT: Kay, William W. APPLICANT: Collinson, S. Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Salmonella enteritidis
Query Match
Best Local Similarity 80.8
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington
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STATE: Washingtor
COUNTRY: U.S.A.
ZIP: 98104-7092
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US-09-741-873C-4

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Sequence 2, Appli
Sequence 1453, Appl
Sequence 135, Appl
Sequence 109, Appl
Sequence 3231, Appl
Sequence 69, Appl
Sequence 67, Appl
Sequence 11455, A
Sequence 11455, A
Sequence 11456, A
Sequence 11456, A
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Sequence 11456, A
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                                                                                                     2, 2004, 14:49:38; Search time 17.8 Seconds (without alignments) 888.146 Million cell updates/sec
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757
1 MKLLKVAAFAAIVVSGSALA......bSSVWVRQVGFGNNATANQY
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1: /cgn2_6/ptodata/2/paa/PCT NEW COMB.pep:*

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3: /cgn2_6/ptodata/2/paa/US08 NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US08 NEW_COMB.pep:*

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3: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

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               version 5.1.6
- 2004 Compugen Ltd.
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US-09-741-873C-2
US-10-004-1153-2
US-10-004-1153-2
US-10-784-592-35
US-10-784-592-35
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US-10-784-592-35
US-10-784-592-35
US-10-70-205E-32312
US-10-170-205E-11455
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US-10-1805-394-5049
US-10-1805-394-5049
US-10-1805-394-5049
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                                                                                                                                                                                                                                                                                 601315 segs, 104695340 residues
                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                           protein search, using sw model
                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
               GenCore (c) 1993
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Maximum DB seq length: 2000000000
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Match
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Perfect score:
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| GABREAL INFORMATION:
| APPLICANT | OLSON, Are |
| APPLICANT | OLSON, Are |
| APPLICANT | OLSON, Are |
| APPLICANT | OLSON, Are |
| TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation |
| FILE FERENCE: 012869-084 |
| CURRENT APPLICATION NUMBER: US/09/741,873C |
| CURRENT FILING DATE: 1990-05-06 |
| PRIOR APPLICATION NUMBER: US 08/978,878 |
| PRIOR FILING DATE: 1990-05-06 |
| PRIOR FILING DATE: 1991-11-06 |
| PRIOR FILING DATE: 1991-11-06 |
| PRIOR FILING DATE: 1991-11-06 |
| PRIOR PRIOR APPLICATION NUMBER: US 07/970,846 |
| PRIOR FILING DATE: 1991-11-06 |
| PRIOR FILING DATE: 1994-01-28 |
| PRIOR FILING DATE: 1994-01-28 |
| PRIOR FILING DATE: 1994-01-28 |
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| PRIOR FILING DATE: 1994-01-28 |
| PRIOR FILING DATE: 1994-01-28 |
| PRIOR FILING DATE: 1994-01-65 |
| NUMBER OF SEQ ID NOS: 11 |
| SOFTWARE | PARCHIT VERSION 3.0 |
| PRIOR FILING DATE: PARCHIT VERSION 3.0 |
| PRIOR FILING DATE: PARCHIT VERSION 3.0 |
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| PRIOR FILING DATE: PARCHIT VERSION 3.0 |
| PRIO
                                                                           Sequence 7905, App Sequence 3413, App Sequence 3413, App Sequence 2, Appli Sequence 44, Appli Sequence 78, Appli Sequence 12923, A Sequence 12923, A Sequence 255, App Sequence 255, App Sequence 24, Appli Sequence 218336, Sequence 218336, Sequence 218336, Sequence 218336, Sequence 218336, Sequence 218336, Sequence 218336, Sequence 218336, Sequence 218336, Sequence 218336, Sequence 218336, Sequence 218336, Sequence 218336, Sequence 218336, Sequence 218336, Sequence 218336, Sequence 218336, Sequence 218336, Sequence 218336, Sequence 218336, Sequence 218336, Sequence 218336, Sequence 218336, Sequence 218336, Sequence 218336, Sequence 218336, Sequence 218336, Sequence 218336, Sequence 218336, Sequence 218336, Sequence 218336, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequence 310283, Sequen
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US-10-872-769-5

US-60-566-632-7905

US-60-56-632-7905

US-60-579-062-7905

US-10-170-208-3413

US-10-18-796A-19565

PCT-USO4-12070-2

PCT-USO4-12070-2

PCT-USO4-1277-78

US-10-831-070-78

US-10-831-070-78

US-60-56-841-1245

US-60-556-841-1245

US-10-748-796A-20202

US-10-748-796A-20202

US-10-748-796A-20202

US-10-748-796A-20202

US-10-748-796A-20202

US-10-748-796A-20202
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TYPE: PRT
ORGANISM: Escherichia coli
US-09-741-873C-4
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Matches 100; Conservative
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FEATURE:
NAME/KEY: mat_peptide
LOCATION: (50). (597)
OTHER INFORMATION: multi copper oxidase
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NAME/KEY: SIGNAL
LOCATION: (1)..(49)
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US-10-004-115B-34
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US-10-784-592-35
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                                              US-V9-(41-W10C-Z
OUNCE 2 Application US/09741873C
GENERAL INFORMATION:
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084
CURRENT FILING DATE: 2000-12-22
FRICH REPREDICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
FRICH REPRING DATE: 1998-08-06
FRICH REPLICATION NUMBER: US 08/978,878
FRICH RELING DATE: 1998-05-06
FRICH REPLICATION NUMBER: US 08/978,878
FRICH RELING DATE: 1999-11-26
FRICH RELING DATE: 1999-11-26
FRICH RELING DATE: 1999-11-06
FRICH RELING DATE: 1999-11-06
FRICH RELING DATE: 1991-11-06
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FRICH RELING DATE: 1991-01-28
FRICH RELING DATE: 1994-01-28
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APPLICANT: ASAKO, HIROYUKI
APPLICANT: SAKO, HIROYUKI
APPLICANT: SHIMIZU, MASATOSHI
APPLICANT: SHIMIZU, MASATOSHI
APPLICANT: SHIMIZU, MASATOSHI
APPLICANT: SHIMIZU, MASATOSHI
APPLICANT: WAKITA, KTUHEI
ITILE OF INVENTION: PROCESS FOR PRODUCING OPTICALLY ACTIVE
ITILE OF INVENTION: A-HALO-3-HYBROXYBUTANOATE
FILE REFERENCE: 7372-72249
CURRENT APPLICATION NUMBER: US/10/004,115B
FRIOR PILING DATE: 2001-12-06
PRIOR FILING DATE: 2001-01-15
PRIOR PILING DATE: 2001-01-15
PRIOR PELING DATE: 2001-05-01
PRIOR PELING DATE: 2001-05-01
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Sequence 34, Application US/10004115B
GENERAL INFORMATION:
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ORGANISM: Corynebacterium sp.
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Best Local Similarity
Matches 79; Conserv
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60 QSDARKSETTITQSGYGNGADV----GQGADNSTIBLIQNGFRNNATIDQWNAKNS--- 111
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Query Match 12.3%; Score 93; DB 6; Length 348; Best Local Similarity 24.8%; Pred. No. 0.43; Matches 40; Conservative 26; Mismatches 65; Indels
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11.1%; Score 84; DB 7; Length 385;
Best Local Similarity 25.9%; Pred. No. 3.7;
Matches 30; Conservative 21; Mismatches 53; Indels
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GENDRAL INFORMATION:
APPLICANT: Abad, Mark S.
APPLICANT: Abad, Mark S.
TITLE OF INVENTION: Genes and Uses for Plant Improvement File Reference: 38-21/53450)
CURRENT APPLICATION NUMBER: US/60/556,841
CURRENT FILING DATE: 2004-03-25
NUMBER OF SEQ ID NOS: 12463
SEQ ID NO 1453
LENGTH: 385
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TYPE: PRT
CORGANISM: Homo sapiens
US-10-170-205E-32312
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US-10-170-205E-32312
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US-10-501-035-366
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 AAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQSDAR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 -----KSETT-----ITQSGYGNG-----AD-VGQGADNST-----IELTQNGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50; Indels 53; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
10.9%; Score 82.5; DB 6; Length 597;
Best Local Similarity 26.1%; Pred. No. 9;
Matches 46; Conservative 27; Mismatches 50; Indels 5
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LOCATION: (139)..(139)
OTHER INFORMATION: putative copper binding site
FEATURE:
                                                                                                                                                                   NAME/KEY: MISC FEATURE
LOCATION: (181)..(181)
OTHER INFORMATION: putative copper binding site
                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: MISC FEATURE LOCATION: (514). (514). OTHER INFORMATION: putative copper binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: MISC_FEATURE

DCATION: (566)...(566)

/ OTHER INFORMATION: putative copper binding site

US-10-784-592-35
                                                                               NAME/KEY: MISC FEATURE
LOCATION: (141)..(141)
OTHER INFORMATION: putative copper binding site
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APPLICANT Microbial Technics Limited
APPLICANT Microbial Christophe FG
APPLICANT: Hansbro, Philip M
TILLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21129WO
CURRENT APPLICATION NUMBER: US/10/873,528
CURRENT APPLICATION NUMBER: US/09/769,787
PRIOR APPLICATION NUMBER: US/09/769,787
PRIOR PELING DATE: 2001-01-26
PRIOR PELING DATE: 1998-03-27
PRIOR PELING DATE: 1998-03-27
PRIOR PELING DATE: 1998-03-27
PRIOR PELING DATE: 1998-03-27
PRIOR PELING DATE: 1998-03-27
PRIOR PELING DATE: 1998-03-19
NUMBER OF SEQ ID NOS: 388
SOFTWARE: PALENT VET. 201-01-19
                                                                                                                                                                                                                                                                                                          copper binding
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                                                                                                                                                                                                                                                                                  LOCATION: (183)..(183)
OTHER INFORMATION: putative
                                                                                                                                                                                                                                                                 NAME/KEY: MISC_FEATURE
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US-10-873-528-109
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FOR PREDICTING TYROSINE KINAS
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TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: DEPTURE AGENTS, AND USES THEREOF
FILE REFERENCE: CL001341
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT APPLICATION NUMBER: US/206-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: Patentin version 3.2
SEQ ID NO 32312
LENGTH: 1158
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                                                                                                                295 DKNGRQVLSYNTSTMTTQGSGYTWGNGAQMNGFPAKKGYGLTSSWTVPIT--GTDTSFTF 352
                                                                   -----SETTITQ-SGY--GNGADV------GQGADNS-TIELTQNGFRNNATI 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297 RLAAMARLQENGOKDVGSY----QLPKGMSSHLNGQARTSSSKLMASKSSATVFONPMG 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    352 IIPSSPKNAGYKNSLERNNIKQAANNSLLLHLLKSQTIPKPMNGHSHSERGSIFEESSTP 411
235 GSKLIFTYTVTYVNPKTNDLGNISSMRPGYSIYNSGTSTQTMLTLGSDLGKPSGVKNYIT 294
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TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYBEPTIDE ITILE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE ITILE OF INVENTION: ACTIVITY OF COMPCUNDS THAT INVERACY WITH PROTEIN TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
FILE REPERENCE: DOISES PCT
CURRENT APPLICATION NUMBER: US/10/501,035
CURRENT APPLICATION NUMBER: US 60/350,061
PRIOR PILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 795
SOFTWARE: Batentin version 3.2
SOFTWARE: Batentin version 3.2
SEQ ID NO 3.66
LENGTH: 1158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
10.8%; Score 81.5; DB 6; Length 11
Best Local Similarity 21.1%; Pred. No. 26;
Matches 30; Conservative 28; Mismatches 67; Indels
                                                                                                                                                                                                               104 DOWNAKNSDITVGQYGGNNAALVNQTASDS 133
                                                                                                                                                                                                                                                                   353 TPYAARTDRIGINYFNGGGKVVESSTTSQS 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 32312, Application US/10170205E; GENERAL INFORMATION:
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                                                                                                352 IIPSSPKNAGYKNSLERNNIKQAANNSLLLHLLKSQTIPKPMNGHSHSERGSIFBESSTP 411
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: YANG, Yan-Ping
APPLICANT: YANG, Yan-Ping
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: PROTECTIVE RECOMBINANT HAEMOPHILUS INFLUENZAE HIGH
TITLE OF INVENTION: PROTECTIVE WEIGHT PROTEINS
FILE REFERENCE: 1038-1138 MIS
CURRENT APPLICATION NUMBER: US/09/806,709
CURRENT FILING DATE: 2001-04-09
PRIOR FILING DATE: 1999-10-07
PRIOR FILING DATE: 1999-10-07
PRIOR FILING DATE: 1999-10-07
PRIOR FILING DATE: 1999-11-08
PRIOR PLICATION NUMBER: 09/167,568
PRIOR PLICATION NUMBER: 09/206,942
PRIOR PLICATION NUMBER: 09/206,942
PRIOR PLICATION NUMBER: 09/206,942
PRIOR PLICATION NUMBER: 09/206,942
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Sequence 67, Application US/09806709

GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: WING, Wichel H.
TITLE OF INVENTION: PROTECTIVE RECOMBINANT HARMOPHILUS INFLUENZAE HIGH
TITLE OF INVENTION: MOLECULAR WEIGHT PROTEINS
FILE REFERENCE: 1038-1138 MIS
CURRENT APPLICATION NUMBER: US/09/806,709

CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 09/167,568
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 09/167,568
PRIOR FILING DATE: 1998-10-07

PRIOR APPLICATION NUMBER: 09/206,942

PRIOR APPLICATION NUMBER: 09/206,942

PRIOR APPLICATION NUMBER: 09/206,942

PRIOR APPLICATION NUMBER: 1999-11-08

WUMBER OF SEQ ID NOS: 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAALVNQTASDSSVMVRQVGFGNNATAN 149
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                                                 KSETTITQSGYGNGAD --- VGQGADNS --
                                                                                                                                                                                          TTIDEYSDNNPSFTDDSSGDES 433
                                                                                                                                                       113 ITVGQYGGNNAALVNQTASDSS 134
                                                                                                                                                                                                                                                                                                                                 Sequence 69, Application US/09806709 GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
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Best Local Similarity 26...
Best Local Sy Conservative
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US-10-170-205E-11455
Sequence 11455, Application US/10170205E
Sequence 11455, Application US/10170205E
Sequence 11455, Application US/10170205E
Sequence 11455, Application US/10170205E
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: Patentin version 3.2
SEQ ID NO 11455
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US-10-170-205E-11130
Squence 11130, Application US/10170205E
Squence 11130, Application US/10170205E
Squence 11130, Abplication US/10170205E
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OF PROTEINS
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
TITLE REFERRANCE: CL001381
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: ParentIn version 3.2
SEQ ID NO 11130
LENGTH: 503
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                                                                                                                                                                                                               27;
                                                                                                                                                                 DB 5; Length 1536;
                                                                                                                                                                                                                  Indels
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                                                                                                                                                                 10.6%; Score 80.5; DE 26.4%; Pred. No. 46; tive 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1281 NTVNVTANAGDLTV-----GNGAEIN 1301
                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 NAALVNQTASDSSVMVRQVGFGNNATAN 149
                                                                                            ; ORGANISM: Haemophilus influenzae US-09-806-709-67
                                                                                                                                                                                                                  Conservative
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PatentIn Ver.
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                                                                                                                                                              Query Match
Best Local Similarity
Matches 39; Conserv
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Best Local Similarity
Matches 35; Conserv
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                                      TYPE: PRT
  SOFTWARE: P
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Query Match
Best Local Similarity 27.2%; Pred. No. 14;
Matches 34; Conservative 14; Mismatches 43; Indels
                                                                                                      ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_94013C.1.pep
US-10-425-115-362763
                    FEATURE: NAME/KEY: unsure LOCATION: (1)..(546) OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 GFRNN 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 TFAND 205
      Zea mays
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US-60-579-902-7335
    ORGANISM:
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Job time :
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Sequence 11456, Application US/10170205E

Sequence 11456, Application US/10170205E

Sequence 11456, Application US/10170205E

REPERAL INFORMATION:
APPLICANT: ADAMS, Mark

TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF

TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF

TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF

CURRENT APPLICATION NUMBER: US/10/170,205E

CURRENT FILING DATE: 2002-06-13

NUMBER OF SEQ ID NOS: 40312

SOUTHWARE: PATCHIN VERSION 3.2

SEQ ID NO 11456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-42-

US-10-42-

Sequence 362763, Application US/10425115

Sequence 362763, Application US/10425115

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

FILE REPERBREC: 38-21(5322)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT APPLICATION NUMBER: US/10/425,115

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 362763

LENGTH: 546

TYPE: PRT
                                                                                                                                                                                                  80 DVGQGADN-----STIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTAS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294 THSIAHLVPSQTVVQTFSNPDGTVSLIQVGT-GATVATLADASELPTTVTVAQVNYSAVA 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 DVGQGADN-----STIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTAS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   353 D-GEVEONWATLOGGEMTIQTTOASEATQAVASLAEAAVAASQEMOQGATVTMALNSEAA 411
                                                                                                                                                                                                                                                                                                    353 D-GEVEQNWATLQGGEMTIQTTQASEATQAVASLAEAAVAASQEMQQGATVTMALNSEAA 411
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                                                                                                                                                                        32 THEMAHA------SGPDSTLSIYQYGSANAALALQSDARKSETTIT--QSGYGNGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 THEMAHA-----SGPDSTLSIYQYGSANAALALQSDARKSETTIT--QSGYGNGA
                                                                                                                               Gaps
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                                                                                                                               22;
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                                                                                    ; Score 80; DB 6; Length 503; ; Pred. No. 13; 14; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Mismatches
                                                                                    Query Match
Best Local Similarity 28.2%;
Matches 35; Conservative 1.
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Best Local Similarity 28.24
Matches 35; Conservative
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-205E-11130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-205E-11456
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474 HDEL----SYQRKHKFQLNLSQNLSDYGSIYVSGYLQDDWGSRSTTRSLNVGYSVNYAD 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 YGEHWRQARKLVTAHLFTVKRVHSYRRARKEEVRLVVAKVREAAVAGTATDMS---LAMN 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 VGQGADNSTIELFQNGFRNNATIDQWNAKNSDITVGQY--------GGNNAA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7335, Application US/60579902
GENERAL INFORMATION:
APPLICANT: Krasomil-Osterfeld, Karina C.
APPLICANT: W. Wei
TITLE OF INVENTION: Nucleotide and Amino Acid Sequences from Xenorhabdus;
TITLE OF INVENTION: Nucleotide and Amino Acid Sequences from Xenorhabdus;
TITLE OF INVENTION: Nucleotide and Amino Acid Sequences from Xenorhabdus;
TITLE OF INVENTION: Mad 4058 thereof
TITLE OF INVENTION: AND ACID (5344)
CURRENT FILE REPERENCE: 38-21 (53444)
CURRENT FILE OF SEQ ID NOS: 14985
SEQ ID NO 7335
1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLS-IYQYGSANAALAL
                                                                                                                                      60 QSD---------ARKSETTITQSGYGNGADVGQGADNSTIELTQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 YDQLVTRVVTHEMAHASGPDSTLSIYQYGŞANAALALQSD-ARKŞETTITQSGYG-NGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30;
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10.6%; Score 80; DB 7; Length 829;
Best Local Similarity 25.2%; Pred. No. 24;
Matches 36; Conservative 24; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               completed: August 2, 2004, 15:29:52
ne : 18.8 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       584 GLSGTALDGNVLGYSLQQRYGNN 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: Xenorhabdus bovienii
US-60-579-902-7335
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

August 2, 2004, 14:39:53 ; Search time 9.4 Seconds (without alignments) 1545.204 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-543-407-16 757 1 MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\* 2: pir1:\* 3: pir2:\* 4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score			DB	ID	Description
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0	658	86.9	rU	0	63	curlin cha
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121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151

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outer membrane pro	hypothetical prote	F3F19.21 protein -	probable PPE prote	ice nucleation pro	nucleoskeletal-īik	probable PPE prote	ice nucleation pro	hypothetical prote	hypothetical prote	paracrystalline su	S-layer protein Rs	hemolysin (importe	cell wall surface	hypothetical prote		
\$21408	C29349	C86266	D70575	A25547	S14055	E70969	SNPSO	869589	T32020	A48995	C87374	AI0452	E95206	07	E85589	
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11.5	11.5	11.5	11.4	11.3	11.1	11.1	11.0	10.8	10.8	10.8	10.8	10.8	10.8	10.8	10.8	
		87	86:5	2	84	84	83,5	82	8.2	82	82	82	82	81:5	81.5	÷
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

	idis
	C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999 C;Accession: JC6039; PC6015; A44898
	R,Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W. J. Bacteriol, 178, 662-667, 1996
	A, Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fimbriae.
	A;Keterence number: JC6039; MUID:96146512; PMID:8550497 A;Accession: JC6039
	A; Molecule type: DNA
	A,Cross-references: GB:U43280; NID:g1184712; PIDN:AAC43599.1; PID:g1184714
	A;Accession: PC6015 A:Molecula tvne: protein
-	A. Residues: 21-52 < CC2>
	A,Note: the authors translated the codon ACG for residue 44 as lle R:Collinson, S.K.; Emody, L.; Muller, K.H.; Trust, T.J.; Kay, W.W.
	J. Bacteriol: 173, 4773-4781, 1991
	A,Title: Purification and characterization of thin, aggregative fimbriae from Salmonell
	A; Scierence number: A44898; MUID:91310586; PMID:1677357
	A;COHCHILE: 7/053 Aprimarion: AddRog
	A.Status: preliminary
	A; Molecule type: protein
	A;Note: sequence extracted from NCBI backbone (NCBIP:45936)
	A. Genera agray.
	C; Function:
	A:Description: major component of thin aggregative fimbriae A:Note: fimbriae bind to fibronectin, plasminosem, risque plasminosem activator
	F;1-20/Domain: signal seguence #status predicted <sig> F;21-151/Product: fimbrin protein aqfA #status experimental <mat></mat></sig>
	Query Match  Query Match  Best Local;Similarity 90.1%; Pred No. 7.5e-52;  Matches 136; Conservative 3: Mismatches 12: Indels 0: Gaps 0:
	Oy 1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ 60
	Db 1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
	QY 61 SDARKSETTITQSGYGNGADVGQGADNSTIELIQNGFRNNATIDQWNAKNSDITVGQYGG 120
	Db 61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120

csg/

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A.Description: major component of wild-type curli, interaction between CsgA and CsgB tr3 A.Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli that and H-kininogeni, in the absence of CsgA, CsgB can self-assemble into polymers F:1-20/Domain: signal sequence #status predicted <SiG> F:21-151/Product: curlin #status experimental <MAT>
A;Title: The RpoS sigma factor relieves H-NS-mediated transcriptional repression of A;Reference number: S31202; MUD:93211294; FMID:8459772
A;Accession: S31202
A;Molecule;type: DNA
A;Residues; 1-6, 'V', 8-151 < OLS1>
A;Cross-references: EMBL:L04979
A;Accession: S34560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:BA000007; PIDN:BAB34843.1; PID:g13360880; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics: A;Gene: ECS1420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: DNA
A,Residues: 1-133, 'RQRDSGWLW' <OLG3>
A,Cross-references: EMBL:L04979; NID:g290424; PIDN:AAA23616.1; PID:g290425
A,Experimental source: strain K-12, substrain W3110
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTH-EMAHASGPDSTLSIYQYGSANAALAL
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65.8%; Pred. No. 2e-35;
cive 19; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.9%; Score 484; DB 2;
66.9%; Pred. No. 2.7e-36;
iive 18; Mismatches 32
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A;Residues: 21-42;44-50 < OLS2>
R;Olsen, A.N.; Arnqvist, A.M.
submitted to the EMBL Data Library, October 1992
A;Reference number: 834559
A;Accession: S34559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GNGAAVDQTASNSSVNVTQVGFGNNATAHQY
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Best Local Similarity 66.9
Matches 101; Conservative
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A;Status: preliminary
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Best Local Simi
Matches 100;
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A, foreserreferences EMBL: X90754, NID: g1147558, PIDN: CDA62282.1; PID: g1147564
A, Experimental source: strain K12, substrain W3110
A, Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
A, Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
B, Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cd. A, Rose, D.J.; Mau, B.; Shao, Y.
A, Title: The complete genome sequence of Escherichia coli K-12.
A, Reference number: A64720; MUID: 97426617; PMID: 9278503
A, A, Accession: G64846
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cjaces: O'S-NOV-1201 #Sequence_revision O'S-NOV-2001 #CAC_clamge_re-NOV-2001
Cjaces (C) Jaces (C) James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, R.; Powd, D.; Wain, J.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001
Ajathors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Ajathors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Ajathors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Ajathors: Parloin and Salmonella enterica seroy Ajates: preliminary
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A;Cross-references: GB:AEC00205; GB:U00096; NID:g1787265; PIDN:AAC74126.1; PID:g1787279;
A;Cross-references: GB:AEC00205; GB:U00096; NID:g1787265; PIDN:AAC74126.1; PID:g1787279;
A;Cross-references: GB:AEC01206; State Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Colored Col
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NyAlternate names: csgA protein; major curlin protein
C;Specias: Escherichia coli
C;Date: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change 01-Mar-2002
C;Accession: S70788; G64846; S31202; S34560; S34559
R;Hammar, M; Arnqvist, A; Bian, Z; Olsen, A; Normark, S.
Mol: Microbiol: 18, 661-670, 1995
A;Title: Expression of two csg operons is required for production of fibronectin- and A;Reference number: S70783; MUID:96414468; PMID:8817489
                                                                                                                                                                                                                                                                                 major curlin chain precursor [imported] - Salmonella enterica subsp. enterica serovar C;Species: Salmonella enterica subsp. enterica serovar Typhi. Almonella enterica serovar appli. Almone: this species has also been called Salmonella typhi. C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
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Pred. No. 7.5e-52;
3; Mismatches 12;
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                                                 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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ilarity 90.1%;
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A/Experimental source: strain K-12, substrain MG1655
C/Genetics:
A/Gene: csgB:
A/Gene: csgB:
A/App position: 23.15
C/Function:
A/Description: minor component of wild-type curli; interaction between CsgA and CsgB tr A/Description: minor component of wild-type curli; interaction between CsgA and CsgB tr A/Description: minor component of wild-type curli; interaction between CsgA and CsgB tr A/Description: minor component of CsgA, CsgB can self-assemble into polymers
F/1-21/Domain: signal sequence #status predicted <SIG>F/1-21/Domain: signal sequence #status predicted <MAT>
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A;Experimental source: strain 0157:H7, substrain RIMD 0509952
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A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85665
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-151 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 15.7%; Score 118.5; DB 2; Length 151
1 Similarity 31.6%; Pred. No. 0.0014;
37; Conservative 13; Mismatches 62; Indels .
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Best Local S
Matches 37
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R. Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S.
Molrobiold, 18, 661-670, 1995
A. Title: Expression of two csg operons is required for production of fibronectin- and CA; Reference number: S70783; MUID:96414468; PMID:8817489
A.; Reference number: S70783; MUID:96414468; PMID:8817489
A.; Status: nucleic acid sequence not shown; translation not shown
A.; Residues: 1-151 < Amm>
A.; Residues: 1-151 < Amm>
A.; Residues: 1-151 < Amm>
A.; Rose, b. D.; Mul. B.; Shoo, Y.
A.; Rose, D. D.; Mul. B.; Shoo, Y.
A.; Rose, D. D.; Mul. B.; Shoo, Y.
A.; Rose, D. D.; Mul. B.; Shoo, Y.
A.; Rose D. D.; Mul. B.; Shoo, Y.
A.; Rose D. D.; Mul. B.; Shoo, Y.
A.; Rose D. D.; Mul. B.; Shoo, Y.
A.; Rose D. D.; Mul. B.; Shoo, Y.
A.; Rose D. D.; Mul. B.; Shoo, Y.
A.; Reference number: A64720; MulD:97426617; PMID:9278803
A.; Accession: F64846
A.; Accession: F64846
A.; Residues: 1-151 < BLATS
A.; Residues: 1-151 < BLATS
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A.; Residues: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein csgA [imported] - Escherichia coli (strain O157:H7, substrain EDL93 C)Species: Escherichia coli (5pecies: Escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escherichia escheric
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A;Residues: 1-152 <STO>
A;Cross-references: GB;AE005174; NID:g12514574; PIDN:AAG55788.1; GSPDB:GN00145; UWGP:216
A;Experimental source: strain 0157:H7; substrain EDL933
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          curlin nucleator protein csgB precursor - Escherichia coli (strain K-12)
N;Alternate names: csgB protein; curlin nucleation component; minor curlin protein
C;Species: Escherichia coli
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 01-Mar-2002
C;Accession: S70787; F64846
119
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                                                                                                                                                                                                                                152
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                                                                                                                                120 GNNAALVNOTASDSSVMVROVGFGNNATANOY
                                                                                                                                                                                     Query Match 62.7
Best Local Similarity 65.8
Matches 100; Conservative
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Cycycraminary, releasumenty element of the status predicted (SIG) blocked carboxyl end; tetatus predicted (SIG) and activation peptide #status predicted (ATP) and activation peptide #status predicted (ATP) blocked: activation peptide #status predicted (ATP) blocked: leishmanolysin #status predicted (ATP) blocked: leishmanolysin #status predicted (ATP) blocked: leishmanolysin #status predicted (ATP) blocked: leishmanolysin propertide #status predicted (CTP) blocked: leishmanolysin #status propertide #status bredicted (CTP) blocked: leishmanolysin #status propertide #status predicted (ATP) blocked: leishmanolysin #status predicted (ATP) blocked: leishmanolysin #status predicted box predicted: leishmanolysin #status predicted box predicted box predicted site: carbohydrate (Asn) (covalent) #status predicted box predicted blocked: leishmanolysin #status predicted box predicted box predicted site: carbohydrate (Asn) (covalent) #status predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted box predicted b
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                                                                                                                                                                                                                                                                                                                                                                                              95 NGFRNNATIDOWNAKNSDIT-VGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGENNRAKVDQ--AGNYNFAYIEQTGNANDASISQSAYGNSAAIIQKGSGNKANITQY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              leishmanolysin (EC 3.4.24.36) precursor - Leishmania donovani
N;Alternate names: surfase endopeptidase glycoprotein gp63
C;Species: Leishmania donovani
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jan-2000
C;Accession: A45621
                                                                                                                                                                                                                                                                                                                       GAPGIATATNYDLARSEYNFAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-590 (WEB>
A;Experimental source: LV9
A;Note: sequence extracted from NCBI backbone (NCBIN:74958, NCBIP:74959)
                                                                                                                                                                                                                                            GSANAALALQSDARKSE-----TTITQSGYGNGADVGQ-GADNST--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Webb, J.R.; Button, L.L.; McMaster, W.R.
Mol. Biochem. Parasitol. 48, 173-184, 1991
A;Title: Heterogeneity of the genes encoding the major s
A;Reference number: A45621; MUID:92107220; PMID:1762629
                                                                                          ; Score 111.5; DB 2;
; Pred. No. 0.0057;
17; Mismatches 46;
                                                                                                  14.7%;
30.5%;
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Best Local Similarity 28.8
Matches 46; Conservative
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                                                                                                                                      Similarity
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Local Sim-
                               A, Gene: STY1180
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C,Genetics:
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A.Note: this species has also been called Salmonella typhi
A.Note: this species has also been called Salmonella typhi
C.Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C.Accession: AH0635
R.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, P.P. Connetton, P.; Cronin, A.; Davis, P.; Davis, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A.;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Atticle: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A; Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: JC6040
R;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.
Bacteriol. 178, 662-667, 1996
A;Title: Salmonella entertitidis agfBAC operon encoding thin, aggregative fimbriae.
A;Reference number: JC6039; MUID:96146512; PMID:8550497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fimbrin protein agfB precursor - Salmonella enteritidis
C,Species: Salmonella enteritidis
C,Date: 31-Dec.1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 NGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A/Accession: UG6040
A/Molecule type: DNA
A/Coss.references: GB:U43280; NID:g1184712; PIDN:AAC43598.1; PID:g1184713
A/Experimental source: strain 276755-3b
A/Gone: agf8
G/Function:
A/One: finbriae bind to fibronectin, plasminogen, tissue plasminogen active (Fx-40vords: fimbria)
F/1-21/Domain: signal sequence #status predicted <81G>F/1-21/Product: fimbrin protein agf8 #status predicted <MAT>
                                                                                                                                                                                                                                                                                           MAHASGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQ
                                                                                                                                                                                                                                                                                                                                                                  IAAAAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQ
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                                                                                                                                             Length 151;
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source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.7%; Score 111.5; DB 2;
.larity 30.5%; Pred. No. 0.0057;
Conservative 17; Mismatches 46;
                                                                                                                                      15.7%; Score 118.5; DB 2;
llarity 31.6%; Pred. No. 0.0014;
Conservative 13; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 36, Conserv
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A,Molecule type: DNA
A,Residues: 1-151 <PAR>
                                                                                                                                                                                     Similarity
                                                                                                                                                         Mac
Local Sim.
37;
   A; Experimental
                                                                                                                                             Query Match
Best Local S
Matches 37
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                                       C;Genetics:
A;Gene: csgB
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surface glycoprotein of Leishman

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stat
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••
                                                                                                                                                                                          281
                                                                                                                                                                                                                                                      -----SETTITQS--GYGNGA-----DVGQGADNSTIELTQNGFRNNATIDQWNAK 109
                                                                                                                                                                                       226 AVGVINIPAANIASRYDQLVTRVVTHEMAHALG----FSVVPFRDARILESISNVRHKDF
                                                                                                                                                                                                                                                                                                                      ---RNAQ-DELMAP
                                                                                                                           8 AFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQSDARK--
   Length 590;
                                                                  Indels
                                                                                                                                                                                                                                                                                                                  282 DVPVINSSTAVAKAREQYGCGTLEYLEMEDQGGAGSAGSHIKM---
                                                                                                                                                                                                                                                                                                                                                                                  110 NSDITVGOYGGNNAALVNQTA---SDSSVMVRQVGFGNNA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                          ASD---AGYYSALIMAIFQDLGFYQADFS-KAEEMPWGRNA 371
                                                                  59;
   DB 1;
13.4%; Score 101.5; DE
28.8%; Pred. No. 0.24;
:ive 20; Mismatches
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йOQ

for

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A;Cross-references: GB:Z82098; GB:AL123456; NID:g3261664; PIDN:CAB05045.1; PID:e280737; A;Experimental source: strain H37Rv C;Genetics: A;Gene: PPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       surface protease (gp63) of Leishmania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Daceis: Mycobacterium tuberculosis
C;Daces: 17-01-1998 #sequence_revision 17-01-1998 #text_change 15-Sep-2003
C;Dacession: F70675
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Cole, S.T.; Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Salandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-54, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Titler Deciphering the biology of Mycobacterium tuberculosis from the complete genom A;Accession: F70675
         F;122-139,188-227,311-383,390-451,403-422,412-486,463-507,512-562,532-555/Disulfide F;561,265,331/Binding site: zinc, catalytic (His) (active) #status predicted F;262/Active site: Glu #status predicted F;262/Active site: Glu #status predicted F;534/Binding site: carbohydrate (Asn) (covalent) #status predicted F;534/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature
                                                                                                                                                                                                                                                                                                                                                                       3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 GNFGSGNGRAGLPGSGNVGNGNLGNSNLGSGNTGNSNVGFGNTGNNNVGTGNAGSGNIGA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
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R.Medina-Acosta, E.; Karess, R.E.; Russell, D. submitted to the EMBL Data Library, February 1992 A.Bescription: Structurally distinct genes for the surface protAseference number: S19916
                                                                                                                                                                                                                                                                                                                                                                       34; Indels
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; Pred. No. 0.35;
19; Mismatches
                                                                                                                                                                                                                                                                               Score 101; DB 2
Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                  12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 AVGVINIPAANIASRYDQLVTRVVTHEMAHALG-
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| Similarity 23.4%;
| Gonservative 19
                                                                                                                                                                                                                                                                               13.3%;
30.2%;
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                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 32; Conserv
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A;Residues: 1-582 <COL>
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Best Local S
Matches 46
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R/Ramamoorthy, R.; Donelson, J.E.; Paetz, K.E.; Maybodi, M.; Roberts, S.C.; Wilson, M.E. Biol. Chem. 257, 1888-1895, 1992
A/Itle: Three distinct RNAS for the surface protease gp63 are differentially expressed A/Reference number: A42049; MuID:92112918; PMID:1370484
A/Accession: B42049
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A; Residues: 1-599 <MIL>
A; Residues: 1-599 <MIL>
A; Cross-references: GB:R28527; NID:g159322; PIDN:AAA29235.1; PID:g159323
A; Ramamanoorthy, K.; Donelson, J.E.; Paetz, K.E.; Maybodi, M.; Roberts, S.C.; Wilson, M.E.
J. Biol. Chem. 267, 1888-1895, 1992
A; Title: Three distinct RNAs for the surface protease gp63 are differentially expressed
A; Reference number: A42049; WUID:92112918; PMID:1370484
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C;Dates 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Jan-2000
C;Accession: A44951; A42049
R;Miller, R.A.; Reed, S.G.; Parsons, M.
Mol. Biochem. Parasitol. 39, 267-274, 1990
A;Tille: Leishmania gp63 molecule implicated in cellular adhesion lacks an Arg-Gly-Asp
A;Reference number: A44951; MulD:90205956; PMID:2320059
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F;40-97/Domain: activation peptide #status predicted <ATP>
F;98-574/Product: leishmanolygin #status predicted <AMT>
F;575-599/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;48,261,265,331/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
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A; Residues: 1-599 «RAM»
A; Cross-references: GB: M80672; NID: g159128; PIDN: AAA29238.1; PID: g159329
A; Note: sequence extracted from NCBI backbone (NCBIN: 76040, NCBIP: 76041)
A; Note: the source is designated as Leishmanla donovani chagasi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leishmanolysin (EC 3.4.24.36) precursor, log phase - Leishmania chagasiN_1Alternate names: glycoprotein gp63; surface metalloproteinase, log pl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.3%; Score 101; DB 2; Length 599; 30.2%; Pred. No. 0.27; ive 12; Mismatches 34; Indels
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Matches 32; Conservative
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A;Status: preliminary
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genome

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A; Accession: 519916
A; Accession: 519916
A; Residues: 1-646 cMED>
A; Residues: 1-646 cMED>
A; Cross-references: EMEL:X61994; NID:99559; PIDN:CMA45733.1; PID:99560
B; Modina-Accessa, E.; Karess, R.E.; Mussell, D.G.
R; Modina-Accessa, E.; Karess, R.E.; Mussell, D.G.
Mol. Bloochem. Parasitol. 57, 31-45, 1993
A; Title: structurally distinct genes for the surface protease of Leishmania mexicana are A; Reference number: A4854; MUID:93149206; PMID:93426614
A; Accession: A48564; MUID:93149206; PMID:93149206; PMID:93599
A; Modecule types: MRNA. A64394; MID:93559
A; Modecule types: MRNA. A64394; MID:93559
A; Modecule types: MRNB. A64394; MID:93559
A; Modecule extracted from NCBI backbone (NCBIP:123747)
C; Genetics:
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Best Local Similarity 30.8%; Pred. No. 0.4;
Matches 40; Conservative 15; Mismatches 66; Indels
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

August 2, 2004, 14:36:12; Search time 5.3 Seconds (without alignments) 1483.508 Million cell updates/sec US-09-543-407-16 757 1 MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151 Title: Perfect score: Run on:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

141681 segs, 52070155 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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NRF1 MOUSE 1 GP63 LEIGU 1 784C_PSESP 1 120K_RICRI 1 OMPB_RICRI 1 GLR1 MOUSE 1 GLR1_RAT 1 CAR1_RAT 1 OMPB_RICPR 1 OMPB_RICPR 1 OMPB_RICPR 1 ARGJ_CORGL 1 PANE_HALN1 1 PANE_HALN1	PRT; 151 AA. eated) st sequence update) st annotation update) cursor (Pimbrin SEF17) OR STY1181 OR T1776. ; Gammaproteobacteria;	TRAIN=SR-11; =945780; conserved between Sal spect to operon struct 1(1998). TRAIN=LT2 / SGSC1412 / =11677609; K.E. Spieth J., Clif Y. B. Spieth J., Clif Y. B. Spieth J., Clif Y. Holmes A., Grott K.,	1167608; Tames K.D., Thomson N.J. Sentley S.D., Holden Oks X., Chillingworth Asque A., Hen T.T., H Haque A., Moule S., O eather S., Moule S., O e of a multiple drug re 118."; Thy2 / ATCC 700931; Akett G. III, Mayhew G hadrett G. III, Mayhew G hadrett G. III, Mayhew G hadrett G. III, Mayhew G hadrett G. III, Mayhew G hadrett G. III, Mayhew G hadrett G. III, Mayhew G hadrett G. III, Mayhew G hadrett G. III, Mayhew G hadrett G. III, Mayhew G hadrett G. III, Mayhew G hadrett G. III, Mayhew G hadrett G. III, Mayhew G
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10. SEQUENCE OF 21-33
SEQUENCE OF 21-33
SPECIES-6.eneeritidis; STRAIN=27655-3B;
SPECIES-6.eneeritidis; Dubmed=1677357;
Collinson S.K., Emoedy L., Mueller K.-M., Trust T.J., Kay W.W.;
Purification and characterization of thin, aggregative fimbriae from Salmonella enteritidis.";
J. Bacteriol. 173:4773-4781(1991).
-: FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMBERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
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                                                                                        SEQUENCE FROM N.A. STRAIN=27655-3B;
SPECIES=8.enteritidis; STRAIN=27655-3B;
SPECIES=96146512; PubMed=8550497;
Collinson S.K., Clouther S.C., Doran J.L., Banser P.A., Kay W.W.;
"Salmonella enteritidis agfBAC operon encoding thin, aggregative
                                                                                                                                                                                                                                                                   SEQUENCE OF 21-151 FROM N.A.
SPECIES-S. enteritidis; STRAIN-27655-3B;
MEDLINE-94013373; PubMed-8104955;
Doran J.L., Collinson S.K., Buttan J., Sarlos G., Todd B.C.D.,
Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., Kay W.W.;
"DNA-based diagnostic testes for Salmonella species targeting agfa, the structural gene for thin, aggregative fimbriae.";
J. Clin. Microbiol. 31:2263-2273(1993).
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larity 90.1%; Pred. No. 4.9e-50;
Conservative 3; Mismatches 12;
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EMBL; AE008349; AAL20074.1; -.
EMBL; AL627269; CAB08268.1; -.
EMBL; AS016840; AA06939.1; -.
EMBL; U43280; AAC43599.1; -.
PIR; JC6039; JC6039.
StyGene; SG10668; csgA.
Fimbria; Signal; Complete proteome.
SIGNAL
                                                Bacteriol. 185:2330-2337(2003).
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    Bacteriol. 178:662-667(1996).

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Best Local Similarity
Matches 136; Conserv
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SEQUENCE OF 21-31.

MEDLINE=9110:586; PubMed=1677357;

Collinson S.K., Emcedy L., Trust T.J., Kay W.W.;

Collinson S.K., Emcedy L., Trust T.J., Kay W.W.;

Collinson S.K., Emcedy L., Trust T.J., Kay W.W.;

Salmontale anteritidia.

Salmontale anteritidia.",

J. Bacteriol. 173:4773-4781 (1991).

-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN.
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Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Moril H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
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STRAIN=K12 / W3110;
MEDLINE=93211294; PubMed=8459772;
Olsen A., Arnqvist A.;
"The RpoS signa factor relieves H-NS-mediated transcriptional repression of cegA, the subunit gene of fibronectin-binding curli
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SEQUENCE FROM N.A.
STRAIN=KIZ / MGJ65;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Flunkett G. III, Bloch C.A., Perna N.T., Burland V. Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Callado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Mayley M., Collado-Vides J., Glasner J.D., Goeden M.A., Rose D.J., Mau B., Shao V.S.
                                                                                                                                                                                                                                                Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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                                                               (Rel. 24, Created)
(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
   151 AA
       PRT;
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Mol. Microbiol. 7:523-536(1993)
                                                                                                                                                                                Major curlin subunit precursor
       STANDARD;
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2 / MC4100;
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                                                                           01-DEC-1992
01-OCT-1996
CSGA ECOLI
P28307;
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STRAIN=015:47/ KIND 0509952;
STRAIN=015:47/ KIND 0509952;
HAYDSHIA=1156231; PubMed=11258796;
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HATCOTI M., Shinagawa H.;
Complete genome sequence of enterohemorrhagic Escherichia coli
015:777 and genomic comparison with a laboratory strain K-12.";
NNA Res. 8:11-22(2011).
--- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI ARE
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STRAIN=XI2 / MC4100;
MDDLINE=S6414468; PubMed=8817489;
Hammar M., Arnqvist A., Bian Z., Olsen A., Normark S.;
Hammar M., Arnqvist A., Bian Z., Olsen A., Normark S.;
"Expression of two csg operons is required for production of "Expression of two csg operons is required for production of "Expression of two csg operons is required for production of "Expression of two csg operons is required.""
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                                                                                                                                                                                                                                                                                                                                                                                                     COLÍED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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01-FBB-1995 (Rel. 31, Created)
01-FBB-2003 (Rel. 34, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Minor curlin subunit precursor.
CSGB OR B1041 OR Z1675 OR ECS1419.
Escherichia coli ol57:H7.
Bacherichia coli ol57:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.7%; Score 474.5; DB 1; Length 152; 65.8%; Pred. No. 3.2e-34; ive 19; Mismatches 32; Indels 1;
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R EMBL; AF275733; AAK5312.1; -.

R EMBL; AP0025315, AAC55780.1; -.

DR EMBL; AP002554; BAB34843.1; -.

DR PIR; D90806; D90806.

DR PIR; H88665; H85665.

KW Finbria; Signal; Complete protecome.

TONAL 20 BY SIMILARITY.

1 152 MAJOR CURLIN SUBUNIT.

1 152 MAJOR CURLIN LEGGA;
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Best Local Similarity 65.8
Matches 100; Conservative
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MEDLINE=21218556; PubMed=11319125;
Uhlich G.A., Keen J.E., Blder R.O.;
"Mutations in the csgD promoter associated with variations in curli expression in certain strains of Escherichia coli 0157:H7.";
Appl. Environ. Microbiol. 67:2367-2370(2001).
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BOBLINE=21074935;
Perna N.T., Plunkett G. III, Buzland V. Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Anahhew G.F., Lim A., Gregor J., Miller L.,
Grocheck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
"Melch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
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A -> E (IN REF. 1).
C003470D208D395F CRC64;
   SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
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Last annotation update)
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EcoGene; EG11489; csgA.
Fimbria; Signal; Complete proteome.
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EMBL; X90754; CAA62282.1; -.
EMBL; AE0002026; AAC74126.1; -.
EMBL; D90741; BAA35832.1; -.
EMBL; D90742; BAA35840.1; -.
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CSGA OR Z1676 OR ECS1420.
Escherichia coli O157:H7.
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28-FEB-2003 (Rel. 41, Last seqn
28-FEB-2003 (Rel. 41, Last anno
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Q93U24;
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MEDLINE=2115621; PubMed=11258796;

Hayashi T., Makino K., Chnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino E., Nakayama R., Murata T., Tanaka M., Tobe T., Lida T., Takami H., Honda T., Sasakawa C., Ogasawara M., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=K12;
MEDLINE=97051202; PubMed=8905222;
MEDLINE=97051202; PubMed=8905222;
Ikemoto K., Aiba H., Baba T., Fujita K., Hayashi K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Kinura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Mocomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     **RIGHTAND AND STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET S
                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
STRAIN=S7426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=015:H7 (BDL933 / ATCC 700927;

MEDLINE=21074935; PubMed=11205551;

MEDLINE=21074935; PubMed=11205551;

MEDLINE=21074935; PubMed=111. Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;

"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yano M., Horiuchi T.; "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mau B., Shao Y.; "The complete genome sequence of Escherichia coli K-12."; Science 27:1453-1474(1997).
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STRAIN=K12;
MEDLINE=95157246; PubMed=7854117;
                                            Mol. Microbiol. 18:661-670(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Gregor J., Dave.
Shao Y.;
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EMBL; X90754; CAA62281.1; -.

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                       73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davies R.M., Mowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Mitchead S., Barrell B.G., "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi (T18.")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIR-TY2 / ATCC 700931;
STRAIR-TY2 / ATCC 700931;
BULLINE-22531367; PubMed-12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Bacteriol. 185:2330-2337 (2003).
-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI, CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 IAAAAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQ
                                                                                                                                                                                                                                                                                                       5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             95 NGFRNNATIDOWNAKNSDITVGOYGGNNAALVNQTASDSSVMVROVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
                                                                                                                                                                                                                                                                15.7%; Score 118.5; DB 1; Length 151; 31.6%; Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                      151 MINOR CURLIN SUBUNIT.
15882 MW, B18D266B964014B8 CRC64;
                                                                                                                                                                                                                                                                                                         62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Minor curlin subunit precursor.
CSGB OR SIY1180 OR 11777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.
                                                                                                                                                                                                                                                                                                       13; Mismatches
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                                                                                                                                                                                       POTENTIAL.
                                                                                                                                       Ecocene, Edi2621; csgB.
Fimbria, Signal, Complete protecme.
SIGNAL 1
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EMBL; AE000205; AAC74125.1; --
EMBL; AB0741; BAA55831.1; --
EMBL; AE005515; A8655787.1;
EMBL; AP002554; BAB34842.1; --
EMBL; AP0806; C90806.
PIR, G9806; C90806.
PIR; S70787; S70787.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterobacteriaceae; Salmonella
                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 413:848-852(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Thes 37; Conserva
                                                                                                                                                                                                        22 1
151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=601;
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                                                                                                                                                                                                                                SEQUENCE
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                          GSANAALALQSDARKSE----TITITQSGYGNGADVGQ-GADNST-----IELTQ 94
                                                                                                                                                                                                                                                                                                                             14 GAPGIĄTATNYDLARSEYNFAVNELSKSSFNQAĄIIGQVGTDNSARVRQEGSKLLSVISQ 73
                                                                                                                                                                                                                                                                                                                                                                  NGFRNNATIDQWNAKNSDIT-VGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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J. Bacteriol. 178:662-667(1996).
J. Bacteriol. 178:662-667(1996).
-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES Typhimurium, STRAIN=LTZ / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MCC1611and M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan B., Sun H., Florae L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SPECIES=S.typhinurisum; STRAIN=SR-11;
MEDLINE=99117058; PubMed=9457880;
Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;
"Curli fibers are highly conserved between Salmonella typhinurium and
"Curli fibers are highly conserved between Salmonella typhinurium and
Escherichia coli with respect to operon structure and regulation.";
J. Bacteriol. 180:722-731(1998).
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                     EGENNRAKVDQ--AGNYNFAYIEQTGNANDASISQSAYGNSAAIIQKGSGNKANITQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBL_TaxID=602, 592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96146512; PubMed=8550497;
Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W.W
"Salmonella enteritidis agfBAC operon encoding thin, aggregative
                                                                                                                                                                                                                                                       19;
                                                                                                                                                                                                                    DB 1; Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        minor subunit)
                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                151 AA; 16254 MW; 161C54326E573495 CRC64;
                                                                                                                                                              MINOR CURLIN SUBUNIT.
                                                                                                                                                                                                                                                       46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ...... 34, Last sequence update)
...sb-2003 (Rel. 41, Last annotation update)
Minor curlin subunit precursor (Fimbrin SEF17 1:
SSIMonella typhimurium, and
Salmonella enteritidis.
Bacteria, Protecht
                                                                                                                                                                                                                  Score 111.5; DB Pred. No. 0.0058;
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                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                             POTENTIAL
                                                                                     EMBL, AL627269, CAD08267.1; -.
BENEL, AB016840; AAG69400.1; -.
Fimbria; Signal; Complete proteome.
SIGNAL
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30.5%;
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                                                                                                                                                                                                                                                       36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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SIMILARITY: BELONGS
                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSGB_SALTY
                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 NGFRNNATIDQWNAKNSDIT-VGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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Mol. Biochem. Parasitol. 48:173-184(1991).

-! FUNCTION: Has an integral role during the infection of macrophages
-! CATALYTIC ACTIVITY: Preference for hydrophobic residues at Pl and
Pl'sand basic residues at P2 and P3'. A model nonapeptide is
-!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
-!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
-!- SIMILARITY: Belongs to peptidase family M8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                --IELTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 GAPGIATATNYDLARSEYNFAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISQ
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leishmania donovani.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=LV9;
MEDINE=2107220; PubMed=1762629;
WEDD J.R., Button L.L., McMaster R.W.;
"Heterogeneity of the genes encoding the major surface glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
110-OCT-2003 (Rel. 42, Last annocation update)
Leishmanolysin precursor (EC 3 4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface endopeptidase)
                                                                                                                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                                                                                                                                                                                                                                                    ; DB 1; Length 151; .0058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                GSANAALALQSDARKSE----TTITQSGYGNGADVGQ-GADNST---
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                             COFC5430E6DD361D CRC64;
                                                                                                                                                                                                                                                                                                            MINOR CURLIN SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                       46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                590 AA
                                                                                                                                                                                                                                                                                                                                                                                     30.5%; Pred. No. 0.00
ive 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                    14.7%; Score 111.5;
30.5%; Pred. No. 0.0
                                                                                                                                                                EMBL, AJ002301; CAA05316.1; -.
EMBL, AE008749; AAL20073.1; -.
EMBL, U43280; AAC43598.1; -.
EMBL, UG640; JG6040.
StyGene; SG10609; CG9B.
Fimbria; Signal; Complete proteome.
SIGNAL
                                                                                                                                                                                                                                                                                                                               151 AA; 16182 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M60048; AAA29244.1; -. HSSP; P08148; 1LML.
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                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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PIR; A44951; A44951.
HSSP; P08148; 1LML.
MEROPS; M08.001; -.
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GP63_LEIME
ID GP63_LEIME
AC P43150;
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REMOUTED IN MATURE FORM (BY SIMILARITY).
ZINC (CATLATIC) (BY SIMILARITY).
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MEDLINE=92112918; PubMed=1370484;
Ramanorthy R., Donelson J.E., Paetz K.E., Maybodi M., Roberts S.C.,
Wilson M.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leishmania chagasi.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=90205976; PubMed=2320059;
Miller R.A., Reed S.G., Parsons M.;
"Leishmania gp63 molecule implicated in cellular adhesion lacks an
Arg-Cly-Asp sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell surface protesse)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface endopeptidase).
MEROPS; M08.001; -., Pept M_Zn_BS.
InterPro; IPR006025; Pept M_Zn_BS.
InterPro; IPR00157; Peptidase_M8.
Pfan; PP01457; Peptidase_M8.
PRINTS; PR00782; LSHMANDLYSIN.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc; Zymogen; Signal; Cell adhesion; GPI-anchor; Lipoprotein.
Zymogen; Signal; Cell adhesion; GPI-anchor; Lipoprotein.
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GPI-anchor amidated asparagine (By
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | | | : : : | | | 335 ASD--AGYYSALTMAIFQDLGFYQADFS-KAEEMPWGRNA 371
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251
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Matches 46; Conserv
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NCBI_TaxID=44271;
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GP63_LEICH
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expressed during development of Leishmania donovani chagasi promastigotes to an infectious form.";

J. Biol. Chem. 267:1888-1895(1992).

-!- FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.

-!- CAPARAVET Asserver...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY).
                                                                                                                                                                                     -!- CATALYTIC ACTIVITY: Preference for hydrophobic residues at Pl a Pl' and basic residues at P2 and P3'. A model nonapeptide is cleaved at -Ala-Tyra-|-Leu-Lyg-Lys-. -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity). -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.-!- SIMILARITY: Belongs to peptidase family M8.
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LEISHMANOLYSIN.
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InterPro; IPR01577; Peptidase_M8.
Pfam; PF01457; Peptidase_M8: 1.
PRINTS; PR00142; LSHMANOLYSIN.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprofease; Glycoprotein; Metal-binding; Zinc; Zymogen; Signal; Cell_adhesion; GPI-anchor; Lipoprotein.
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EMBL; M28527; AAA29235.1; -.
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1656 AA;
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                                                                                                                                                                                                                                                                                                                                                                                  MEDINE=93149206, PubMed=8426614, Medina-Acosta E., Karess R.B., Russell D.G., Structurally distinct genes for the surface protease of Leishmania mexicana are developmentally regulated.", Mol. Biochem. Parasitol. 57:31-46(1993).
-! FUNCTION Has an integral role during the infection of macrophages in the mammalian host.
-! CATALYTIC ACTIVITY: Preference for hydrophobic residues at Pl and Pl' and basic residues at P2 and P3'. A model nonapeptide is cleaved at Ala-Tyr-|-Leu-Lys-Lys-.|
-!-COFACTOR: Binds 1 zinc ion per subunit (By similarity).
-!-DEVELOPMENTAL STAGE: Expressed in both the promastigote and the
                                                                                                                                                                                                                                        Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
LeishmanoLysin CI precursor (ECC 3.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
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(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MERODE; Mos.vo.,

GlycoSuiteDB; P43150; -.

GlycoSuiteDB; P43150; -.

InterPro; IPR006025; Pept M Zn BS.

InterPro; IPR001577; Peptidase_M8.

Pfan; PF01457; Peptidase_M8.

PRINTS; PR001782; ZINN_DROTEASE; 1.

PROSITE; P800142; ZINN_DROTEASE; 1.

Pydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc; Zymogen; Signal; Cell adhesion; Multigene family.

Zymogen; Signal; Cell adhesion; Multigene family.

Proceeding Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company Company 
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ZINC (CATALYTIC) (BY SIMILARITY)
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SIMILARITY: Belongs to peptidase family M8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X64394; CAA45733.1; -. PIR; S19916; S19916.
                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
STRAIN=MNYC/BZ/62/M379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P08148; ILML.
MEROPS; M08.001; -.
                                                                                                                                                                                                                  Leishmania mexicana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Eugler
NCBI_TaxID=5665;
                                                                                                                                                   endopeptidase)
GP63-C1.
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                                                                                                                                                                                                                                                       66 SETTITQSGYGNGADVGQGADN-STIELTQNGFRNNA--TIDQWNAKNSDITVGQYGGNN 122
                                                                                                                                                                                                                                                                                                           297 NVSVITSSTVVAKAREQYGCNSLEYLEIEDQGGAGSAGSHIKMRNAKDELMAPPAASAGYY 356
                                                                                                                                                                         241 AVGVINIPAANIASRYDQLVTRVVTHEMAHAVGFSGTF----FGAVGIVQEVPHLRRKDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Outer membrane protein B precursor (168 KDa surface-layer protein)

(Surface protein antigen) (Cell surface antigen 5) (Sca5) (NompB)

(romp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (surface protein antigen) (antigen) (Surface)
                                                                                                                                 AFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQSDARK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR (By similarity)
-!- SUBCELLIAR LOCATION: Cell wall. This bacterium is covered by a SIMILARETY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Uchiyamä T., "Sequencing of the gene encoding the protein rOmp B of Rickettsia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        japonica.";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE 120 kDs SURPACE-EXPOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rickettsia japonica.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsiaae; Rickettsia.
NCBI_TaxID=35790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 kDa SURFACE-EXPOSED PROTEIN.
32 kDa BETA PEPTIDE.
                        Length 646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.1%; Score 99; DB 1; Length 1656; 24.4%; Pred. No. 1.1; ive 23; Mismatches 51; Indels E
                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168097 MW; 3132A69C9DD5999F CRC64;
                        ;
                     Score 99.5; DB
Pred. No. 0.33;
13.1%; Scor.
30.8%; Pred. No. o...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1656 AA
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InterPro; IPR006315; Autotransport.
InterPro; IPR005546; Autotransporter.
Pfam; PF03797; Autotransporter; I.
IIGRFAMs; TIGR01414; autotrans_barl; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-GLY
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                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                         123 AALVNQTASD 132
                                                                                                                                                                                                                                                                                                                                                                                                                                357 TALTMAVFOD 366
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                                                                                                               ---TLTLGGANIISANGGTINFQANGGTIKLTST--QNNIVVDCDLAIATDQTGVVDASS 602
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VAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQSDARK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    uredovora.";
Biosci. Biotechnol. Biochem. 58:762-764(1994).
-!- FWNGTION: Ice nucleation proteins enable bacteria to nucleate
-!- SUNCTION: Ice nucleation proteins enable bacteria to nucleate
-:- Crystallization in supercooled water.
-!- SUBCELIGIAR LOCATION: Outer membrane.
-!- DOMAIN: CONTAINS IMPERFECT REPEATS OF A CONSENSUS OCTAPEPTIDE
A-G-Y-G-S-T-X-T; PURTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE
                                  VLAAGAITLDGSA------TITGDIGNGGG------GAALQSITLANDATK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 IVVSGSALAGVY-DQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQSDARKSETTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=KUIN-3;

PRDLINE-24564407; PubMed=7764866;

Michigami Y., Watabe S., Abe K., Obata H., Arai S.;

"Cloning and sequencing of an ice nucleation active gene of Erwinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PERIODICITY IS SUPERIMPOSED.
MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Pantoea.
                                                                                                                                                      QWNAKNSDI -- TVGQYGGNNAAL-----VNQTASDSSVMVRQVGFGNNAT 147
                                                                                                                                                                            SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.9%; Score 97.5; DB 1; Length 1034; 28.7%; Pred. No. 0.85; ive 24; Mismatches 46; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OCTAPEPTIDE PERIODICITY. W; FA222523D333EADD CRC64;
                                                                          SETTITOSG----YGNGADVGQGADNSTIELTQNGFRNNATID-
                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                         PRT; 1034 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ice nucleation; Repeat; Outer membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00327; IČENUCLEATN.
PROSITE; PS00314; ICE_NUCLEATION; 34
                                                                                                                                                                                                                                                                                                                                                                                                                             Pantoea ananas (Erwinia uredovora).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; JC2143; JC2143.
HSSP; P0620; 11NA.
InterPro; IPR00258; Ice_nucleatn.
Pfam; PF00818; Ice_nucleation; 51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103378 MW;
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Best Local Similarity 28.7%;
Matches 43; Conservative
                                                                                                                                                                                                                                                                                         STANDARD;
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TQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG-----GNNAAL 125
                                         209 V-AGYGSTQTAGEESSQMA----GYGSTQT----GWKGSDLTAG-YGSTGTAGDDSSL 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LetsmanolyShin.";
Structure 6:1035-1046(1998).
-!- FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.
-!- CATALYTIC ACTIVITY: Preference for hydrophobic residues at Pl and Pl' and basic residues at P2 and P3'. A model nonapeptide is cleaved at - Ala-Tyr-|-Leu-Lys-Lys-.
-!- COFACTOR: Binds 1 zinc ion per subunit.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
-!- FULLY SATURATED, UNBRANCHED 1-0-ALKYL CHAIN (MAINLY C24:0) AND A MIXTURE OF FULLY SATURATED UNBRANCHED 2-0-ACYL CHAINS (C12:0).
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leishmanolysin, the major surface metalloproteinase from Leishmania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schnoider P., Ferguson M.A.J., McConville M.J., Mehlert A., Homans S.W., Bordier C., Thomans S.W., Bordier C., Structure of the glycosyl-phosphatidylinositol membrane anchor of the Leishmania major promastigote surface protease."; J. Biol. Chem. 265:16955-16964(1990).
                                                                                                                                                                                                                                                                  01-AUG-1986 (Rel. 08, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (1.86 ANGSTROMS).
MEDLINE=98416698, PubMed=9739094;
Schlagenhauf E., Etges R., Metcalf P.;
"The crystal structure of the Leishmania major surface proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Button L.L., McMaster W.R.; "Molecular cloning of the major surface antigen of leishmania."; J. Exp. Med. 167:724-729(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
MEDLINE=59406217; PubMed=7675788;
Schlagenhauf E., Etges R., Metcalf P.;
"Crystallization and preliminary X-ray diffraction studies of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Belongs to peptidase family M8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 101-123.
MEDLINE=89154764; PubMed=3346625;
                                                                                                                                                                                                                               602 AA
                                                                                                                        257 IAGYGSTÓTÁGEDSSLT--AGYGSTOTÁOK 284
                                                                                   126 V----NQTASDSSVMVRQVGFGNNATANQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91009116; PubMed=2145267;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Button L.L., McMaster W.R.; J. Exp. Med. 171:589-589(19
                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Leishmania major.
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                                                                                                                                                                                                                               GP63 LEIMA
P08148; P15906;
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                                                                                                                                                                                                         GP63_LEIMA
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Gaps
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae; Pantoea.
NCBI_TaxID=549;
                                                                                                                                                                                                                                                                                               Length 602;
                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                    63953 MW; 982EF3245D87C43E CRC64;
                                                                                                                                                                                                                                                                                                                             AVGVINIPAANIASRYDQLVTRVVTHEMAHALGFSGP 275
                                                                                                                                                                                                                                                                                                                      8 AFAAIVVSGSALAGVYDQLVTRVVTHEMAHA---SGP 41
                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                               Score 96.5; DB
Pred. No. 0.56;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                           DECENT ENTRY STANDARD; PRT; 1258 AA. 106239; O1-APR-1990 (Rel. 14, Created) 10-APR-1990 (Rel. 14, Last sequence update) 10-CCT-2001 (Rel. 40, Last annotation update) 10-CCT-2001 (Rel. 40, Last annotation update) 10-CCT-2001 (Rel. 40).
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Best Local Similarity 59.5%;
Matches 22; Conservative
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                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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      entities requires a license agreement (S or send an email to license@isb-sib.ch).
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those of Pseudomonas species and regions required for ice
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Best Local Similarity
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                                                                                                                                                                                  family.
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ID _ICEN_XANCT
AC P18127;
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                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 V-AGYGSTQTAGEESSQMA----GYGSTQT----GMKGSDLTAG-YGSTGTAGDDSSL 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70
                                                                                                                                             -!- FUNCTION: Ice nucleation proteins enable bacteria to nucleate crystallization in supercooled water.
-!- SUBCELLULIAR LOCATION: Outer membrane.
-!- DOMAIN: CONTAINS 126 INFERENCY REPEATS OF A CONSENSUS OCTAPERTIDE A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
-!- MISCELLANEOUS: A STRUCTURAL OF SYMMETRY RELATED TO THAT OF ICE.
NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
-!- SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 IVVSGSALAGVY-DQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQSDARKSETTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pantoea ananas (Erwinia uredovora).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
                                                                           Warren G.J., Corotto L.V.; "The consensus sequence of ice nucleation proteins from Erwinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37;
                                                                                                          herbicola, Pseudomonas fluorescens and Pseudomonas syringae.";
Gene 85:239-242(1989).
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01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V-----NQTASDSSVMVRQVGFGNNATANQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1322 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000258; Ice_nucleatn.
Pfam; PF00818; Ice_nucleation; 65.
PRINTS; PR00327; ICENUCLEANN.
PROSITE; PS00314; ICE_NUCLEANI.
Ice_nucleation; Repeat; Outer membrane.
DOMAIN 162 1217 OCTAPEPTID
                                                        MEDLINE=90152370; PubMed=2515997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1258 AA; 125084 MW;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 209 V-AGYGSTQTAGEESSQMA-----GYGSTQT----GMKGSDLTAG-YGSTGTA----G 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Xanthomonas campestris pv. translucens.";
Mol. Gen. Genet. 223:163-166(1990).
-!- FUNCTION: Ice nucleation proteins enable bacteria to nucleate
crystallization in supercooled water.
-!- SUBCELLULAR LOCATION: Outer membrane (By similarity).
-!- DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhao J., Orser C.S.; "Conserved repetition in the ice nucleation gene inaX from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PSO0314, ICE NUCLEATION; 49.
Ice nucleation; Repeat; Outer membrane
DOMAIN
SEQUENCE 1322 AA; 131094 MW; 89B0EE24AA837039 CRC64;
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01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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29.3%; Pred. No. 2.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S07053; S07053.
HSSP; P06620; IINA.
InterPro; IPR000258; Ice_nucleatn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00818; Ice nucleation; 69.
PRINTS; PR00327; ICENUCLEATN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 SDSSVMVRQVGFGNNATANQ 150
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions along as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85 ADNSTIE---LTON-GFRNNATI----DOWNAKNSDITVGOYG-----GNNAALV---- 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 SGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGN-----GADV-----GQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
MISCELLANBOUG: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE. SIMILARITY: Belongs to the bacterial ice nucleation protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.4%; Score 93.5; DB 1; Length 1567; 29.9%; Pred. No. 3; Live 26; Mismatches 30; Indels 45;
                                                                                                                                                                                                                                                                                                          EMBL, X52970, CAA37140.1; -.
HSSP, P06620, INA.
HSSP, P06620, INA.
HTA-EVO. IFROU0258, ICe_nucleatn.
Pfam; PF0918; ICe nucleation; 81.
PRINTS; PR00327; ICENUCLEATIN.
PROSITE; PS00314; ICE NUCLEATION, 57.
ICE nucleation; Repeat; Outer membrane.
SEQUENCE 1567 AA; 152548 MW; C8B451D959ECAD63 CRC64;
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Search completed: August 2, 2004, 14:49:29 Job time : 6.3 secs

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1 MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	033802 salmonella	Q7x243 citrobacter	Q7x240 citrobacter	Q8cw63 escherichia	Q7x237 enterobacte	Q54069 salmonella	Q8eih4 shewanella	Q8cw64 escherichia	Q83ru7 shigella fl	Q7uczl shigella fl	Q89ji6 bradyrhizob	Q89ji3 bradyrhizob	Q8eih3 shewanella	Q89ji4 bradyrhizob	Q7x244 citrobacter	Q89ji5 bradyrhizob
SUMMARIES	А	033802	Q7X243	Q7X240	S Q8CW63	Q7X237	Q54069	5 QBEIH4	5 Q8CW64	5 Q83RU7	5 Q7UCZ1	5 Q89JI6	S Q89JI3	5 Q8EIH3	5 Q89J14	Q7X244	5 Q89JI5
	ngth DB	152 2	150 2	149 2	152 16	150 2	76 2	502 16	160 16	160 16	151 16	153 16	171 16	139 16	130 16	151 2	154 16
	* Query Match Length DB	85.7	74.4	69.2	62.3	0.09	44.9	17.6	15.9	15.9	15.7	15.7	15.3	15.2	14.5	14.3	14.2
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## ALIGNMENTS

; 152 AA. ed) sequence update) annotation update)	Gammaproteobacteria; Enterobacteriales; hella.	Bian promot all in	Score 649; DB 2; Length 152; Pred: No. 1.1e-44; Mismatches 13; Indels 0; Gaps	MKLIKVAAFAAIVVSGSALAGVYDQIVTRVVTHEMAHASGPDSTLSTYQYGSANAALALQ 	SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 
PRT; Created' Last sec Last an	ammapro 11a.	93832; ., Gord ative f   with (1997).	8 H.	LAGVYDQ       VAGVVPQ	ADVGQGA         ADVGQGA
INARY; Lrel. 05, Lrel. 05, Lrel. 19, ment).	a; mor	2 R R G G G C C C C C C C C C C C C C C C	85.7%; 88.7%; 9	AAIVVSGSAI           AAIVVSGSAV	ITQSGYGNG?          ITQSGYGNG?
PRELIMINARY; (TYEMBLYEL: (TYEMBLYEL: (TYEMBLYEL: (TYEMBLYEL).	typhimur roteobac riaceae; 602;	OM N.A. 53981; N.S., Los, Rhen cyphimum, 65:E	isz AA; istu 85. ilarity 88. Conservative	LLKVAAF?        LLKVAAF?	ARKSETT:        ARKSETT:
1 1 2 033802 033802; 01-JAN-1998 01-JAN-1998 01-DEC-2001 AgfA protein	AGFA. Salmoneila typhimurium. Bacteria; Proteobacteria; Enterobacteriaceae; Salmor	SECUENCE FROM N.A. MEDLINE-98053881; PubM Sukupolvi S.S., Lorent Normark S.J., Rhen M.; Warpression of thin, a Salmonella typhimurium cells."; Infect. Immun. 65:5320 Infect. Immun. 65:5320 Infect. Immun. 65:5320 Infect. Immun. 65:5320 Infect. Immun. 65:5320 Infect. Immun. 65:5320 Infect. Immun. 65:5320 Infect. Immun. 65:5320 Infect. Immun. 65:5320	SEQUENCE 152 AA; Query Match Best Local Similarity Matches 134; Conser	ж—ж Ж—ж	61 SD 61 SD
SUL 380	•		SQ SEQUENCE Query Match Best Local Matches 13	<i>k</i> 5 93	Sy Dp

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121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151

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(TrEMBLrel. 25, C (TrEMBLrel. 25, I (TremBLrel. 25, I

01-OCT-2003 01-OCT-2003 01-OCT-2003

Citrobacter sp. Fec2

Curlin-csgA protein.

PRELIMINARY;

Q7X243

RESULT 2

Q7X243

121

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SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                            59 SDARKSDVTITQHGRGNGAVVGQGADDSTISLKQTGFQNSAIIDQWNAKNADISVTQFGG 118
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Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,

Wasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,

Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

Mobley H.L.T., Donnenberg M.S. Blattner F.R.;

"Extensive mosaic structure revealed by the complete genome sequence

of uropathogenic Escherichia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli 06.
Bacteria; Protecbacteria; Gammaprotecbacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae, Enterobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 AA; 15064 MW; 3BA57F34C1240E83 CRC64;
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Last annotation update)
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STRAIN=Fec39;
Zogaj X., Bokranz W., Nimtz M., Romling U.;
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01-WAR-2003 (TrEMBLrel. 23, Last
01-WAR-2003 (TrEMBLrel. 23, Last
Major curlin subunit precursor:
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SEQUENCE FROM N.A.
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SEQUENCE 152 AA;
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01-OCT-2003
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STRAIN=FEG2;
STRAIN=FEG2;
Sodaj X., Bokranz W., Nimtz M., Romling U.;
Production of Cellulose and Curli Finbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.", Infect. Immun. 72:4151-4158 (2003).
EMBL; AJS15700; ASD56672.1; -.
SEQUENCE 150 AA; 15016 MW; 1D7141B8D6973DC6 CRC64;
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"Production of Cellulose and Curli Fimbriae by Members of the Family
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 72:4151-4158(2003).
EMBL; AJ515701; CAD566751; -.
SEQUENCE 149 AA; 15260 MW; 946DD52017F648FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Citrobacter.
NCBI_TaxID=213763;
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Enterobacteriaceae; Citrobacter.
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Last annotation update)
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                                   NNAALVNOTASDSSVMVROVGFGNNAPANOY 151
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01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25,

Curlin-csgA protein.

freundii

CSGA. Citrobacter

[1] -SEQUENCE FROM N.A. STRAIN=Fec4; NCBI\_TaxID=546;

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A Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Redalberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherry S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., A Madugu K., Person J.D., Umayan L.A., White O., Wolf A.M., A Wanathevan J., Weidman J., Indrain M., Lee K., Berry K., Lee C., A Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., A Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; Genome: sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis."; 123(2002).

IL Mat. Biotechnol. 20:1118-1123(2002).
REBL; SO0865; -
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Enterobacteriaceae, Escherichia.
NCBI_TaxID=217992;
                                                                                                                                                                                                                                                                                                                                                                                                      17.6%; Score 133; DB 16; Length 502; 29.6%; Pred. No. 0.013; ive 21; Mismatches 59; Indels
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llarity 28.7%; Pred. No. 0.036;
Conservative 17; Mismatches 67; Indels 1
                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; Complete proteome.
SEQUENCE 502 AA; 52441 MW; D08CA23D6C46B62D CRC64;
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Last annotation update)
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nes 37; Conserv
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                                     SEQUENCE FROM N.A.
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NCBI_TaxID=70863;
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"Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract."; Infect. Immun. 7:4151-4158(2003).
EMBL, AJ515702; CAD56678.1; -. SEQUENCE ISO AA, 15112 MW; SD8B82D872DF15F3 CRC64;
                                                                                                                                                         Gaps
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Enterobacteriaceae, Salmonella.
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Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
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                                                                                                                    DB 2; Length 150;
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STRAIN=SE30;
Cox J.M., Eglezos S., Woolcock J.B.;
wirulnorce of Salmonella enteritidis in chickens correls
colony morphology and expression of SEF17 finbriae.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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QBEIH4;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Conserved hypothetical protein.
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Pred. No. 3.1e-20;
2; Mismatches 0;
                                                                                                                  60.0%; Score 454.5; DB 2
62.1%; Pred. No. 4.6e-29;
live 24; Mismatches 29
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hes 67; Conservative
                                                                                                                                     Local Similarity 62.1
nes 95; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=592;
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01-NOV-1996
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                                                                                                                    Query Match
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RESULT 6 Q54069

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          69 TITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQ 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 IIGQAGTNNSAQLRQGGSKLLAVVAQEGSSNRAKIDQTGDYNL-AYIDQAGSANDASISQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MYDQVQGDNMKNKLLFMMLTILGAPGIAAAAGYDLANSEYNF----AVNELSKSSFNQAA 56
                                 IIGQAĞTINNSAQLRQGGSKLLITVVAQEGSSNRAKIDQTGDYNL-AYIDQAGSANDASISQ
                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441 (2002).
EMBL; AE015131; AAN42658.1; -.
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                                                                                                                                                                                                                                                                                                    STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin O., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Jin O., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.9%; Score 120; DB 16; Length 160; 28.7%; Pred. No. 0.036; cive 17; Mismatches 67; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 AA; 16919 MW; 50269F5268D2A32F CRC64;
                                                                                                                                                                  01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Minor curlin subunit precursor, similar ro CsgA.
CSGB OR SF1035.
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Last annotation update)
                                                                                                                                              160 AA
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STRAIN=2457T / ATCC 700930 / Serotype 2a;
MEDLINE=22590274; PubMed=12704152;
                                                                               116 GAYGNTAMIIQKGSGNKANITQY 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 GAYGNTAMIIQKGSGNKANITQY 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 TASDSSVMVRQVGFGNNATANQY 151
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Enterobacteriaceae; Shigella.
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01-0CT-2003 (TYENBLYE1. 2
01-0CT-2003 (TYENBLYE1. 2
01-0CT-2003 (TYENBLYE1. 2
Minor curlin subunit.
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SEQUENCE 160 AA;
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Q7UCZ1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 EENSKVNIARVIQIG-----GSGTVDATI--IQNGTRNYANVIQMGG-TTNAAVGQSG 108
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    IAAAAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQ
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MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashina K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 NGFRNNATIDOWNAKNSDITVGOYGGNNAALVNOTASDSSVMVRQVGFGNNATANQY
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DNA Res. 9:189-197(2002).
BMBL; APO059554; BAC50562.1; -.
Complete proteome.
SEQUENCE 153 AA; 15991 MW; 4CE71DBAC375145B CRC64;
                                A.
Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Fournier G., Maybew G.F., Plunkett G. III, Rose D.J., Darling A Mau B., Perna N.T., Paynes S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R., "Complete genome sequence and comparative genomics of Shigella flexneri serotype 2a strain 2457T."; Infect. Immun. 71:2775-2786 (2003).
EMBL, AE016981; Aphl6542.1; -. SEQUENCE 151 AA, 15868 MW; 5D5D266B96401AA0 CRC64;
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                  DB 16; Length
                                                                                                                                                                                                                                                                                                                                          Indels
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Last annotation update)
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27.0%; Pred. No. 0.046;
... M'ematches 56;
                                                                                                                                                                                                                                                                               15.7%; Score 118.5; DB 16; larity 31.6%; Pred. No. 0.045; Conservative 13; Mismatches 62;
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NCBI_TaxID=375;
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Matches 41; Conservative
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91 VQLLQVGAQNKASIT-----QIGNDNLVQLNQLAGS-GNFSIQQIADGAAISIT 137
                                                                                                                IELTONGFRNNATIDOWNAKNSDITVGOYGGNNAALVNQTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 RKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNA 123
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DNA Res: 9:189-197(2002).
BNB1, ABOOS9554, BACS0564.1; -.
Complete proteone SEQUENCE 130 AA, 12699 MW, ACFB2D66A48D260F CRC64;
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Enterobacteriaceae, Citrobacter.
NCBI_TaxID=213763;
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22484998; PubMed=12597275;
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MEDLINE=22484998; PubMed=12597275;
Rancko T., Nakamurra Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DAA Res 9.189-197(2002).
EMBL; AP005954; BAC50565.1; -.
Complete proteome.
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Alteromonadaceae, Shewanella.
NCBI_TaxID=70863,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 171;
                                                                                                       Bradyrhizobium japonicum.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Bradyrhizobiaceae, Bradyrhizobium.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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EMBL; AE015532; AAN53942.1; -.
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CSGA OR BLL5300.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

August 2, 2004, 14:35:42 ; Search time 44.9 Seconds (without alignments) 950.215 Million cell updates/sec Run on:

US-09-543-407-18 Title: Perfect score:

780 1 MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151 Sednence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

1586107

length: 0 length: 2000000000 sed Minimum DB Maximum DB

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* A Geneseq 29Jan04:\* geneseqp1980s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp1990s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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w	675	86.5	151	m	AAB36353	Aab36353
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7	618	79.2	151	ო	AAB36348	Aab36348
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- 4.0	115	115	111	111	111	109	107:5	106:5	102	101	96	96	96	96	95	93.5	93	92		91.5
	26	27	28	20			32	33	3.4	3	36	3.7	38	9	40	41	4	43	44	45

## ALIGNMENTS

RESULT 1

Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; AgfA::PT3#4 amino acid sequence SEQ ID NO:18. vaccine; immune response; immunogen. AAB36349 standard; protein; 151 AA (first entry) Salmonella enteritidis. Escherichia coli 26-FEB-2001 Synthetic. AAB36349; AAB36349 

WO200060102-A2. 12-0CT-2000.

05-APR-2000; 2000WO-CA000356. 99US-0127888P. 05-APR-1999; Kay WW; Collison SK, White AP, Doran JL,

(UYVI-) UNIV VICTORIA.

WPI; 2000-672631/65. N-PSDB; AAC64625.

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 136; 139pp; English.

The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antiqen. Also described are: (1) use of thin aggregative fimbriae (SEFI7/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene back into the chromosome of the homologous species, replacing the native

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copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign animo acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogensicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                                                                                                                                                                                                                                                                                                                                                                                            MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                                                                                                                                                                                                                                                                                                                                 Gaps
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0
                                                                                                                                                                                                                                                                                                                   Length 151;
                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                               100.0%; Score 780; DB 3; ilarity 100.0%; Pred. No. 1.7e-67; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Doran JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VICTORIA INNOVATION & DEV CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clouthier SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Fig 7B, 95pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR74625 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94WO-IB000207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella; AgfA; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collinson SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1994-358275/44.
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 151; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ87467.
                                                                                                                                                                                                                                                                                Sequence 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AgfA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UNIV
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26-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eliciting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR74625;
                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
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(KING/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
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The Salmonella AgfA protein and DNA are used in vaccine and genetic

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                                                                                                                                                                                                                                                                            120
                                                                                                                                                                                                                                                                                                        SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                    9
immunization compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                 9
                                                                                                                                                                                                                                  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                              SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                 1 MKLLKVAAFPAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella, agfA, chromosomal gene replacement, fimbrin, epitope,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella enteritidis AgfA amino acid sequence SEQ ID NO:5.
                                                                                                                       Length 151;
                                                                                                                   88.6%; Score 691; DB 2;
90.7%; Pred. No. 6.8e-59;
live 3; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                        121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W.W.
                                                                                                                                                                                                                                                                                                                                                                                     121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 135; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine; immune response; immunogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB36341 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-APR-2000; 2000WO-CA000356.
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                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella enteritidis.
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                                                                                                                                        Similarity
                                                                                Sequence 151 AA;
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                                                                                                                   Query Match
Best Local Simi
Matches 137;
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W.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Page 138; 139pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB36353 standard; protein; 151
                                                                                                                                                                                                                                   87.9%;
90.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0127888P
                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.1
Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        enteritidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-672631/65.
N-PSDB; AAC64629.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli.
                                                                                                                                                                                            Sequence 151 AA;
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for
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Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant Agfa protein which is useful foeliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to $500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inserted epitope, and hybrid fimbriae are easy and the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALO
                                                                                                                                                                                                                                                                                                                                                                                                                                       MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 27655-3b. The nucleic acid can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody
                                                                                                                                                                                                                                                                                                                                                          .;
                                                                                                                                                                                                                                                                                                                     Length 151;
                                                                                                                                                                                                                                                                                                                                                          11; Indels
                                                                                                                                                                                                                                                                                                              Score 691; DB 3;
Pred. No. 6.8e-59;
i; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "Encoded by GCC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   enteritidis 27655-3b agfA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW23570 standard; protein; 151 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Fig 7; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                       'n
                                                                                                                                                                                                                                                                                                                88.6%;
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(first entry)
                                                                                                                                                                                                                                                                                                                                  Local Similarity 90.7 es 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella enteritidis
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Misc-difference
                                                                                                                                                                                                                                                                          Sequence 151 AA,
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                                                                                                                                                                                                                                                                                                                   Query Match
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used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDARKSETTITOSGYGNGADVGQGADNSTIELTONGFRNNATIDOWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 686; DB 2;
Pred. No. 2.1e-58;
3; Mismatches 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segment or sequence or sequences grown on a Salmonella, B. coli or acid sequence or sequences grown on a Salmonella, B. coli or Enterobacteriaceae host cell, from the host cell and introducing the copymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful coliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein for an efficient live vaccine, the carrier fimbrial subunit protein are usually strong immunogens, which may be important for directing an immune response of inpercent seconds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 LVTRVVTHEMAHALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQ 105
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                                                                                                                                                                                                                                                                                                                                   inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                Score 675; DB 3; Lt
Pred. No. 2.4e-57;
0; Mismatches 0;
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Best Local Similarity 81.9%;
Matches 136; Conservative
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N-PSDB; AAC64626.
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Synthetic.
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA complement encoded and assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and directing recombination of a recombinant gene into the chromosome of the homologue imperiating recombinant gene back into the chromosome of the homologue species; (3) directing recombination of a recombinant gene back into the chromosome of the homologue species, replacement of a recombinant gene back into the chromosome of the homologue species, replacement of a recombinant gene back into the chromosome of the homologue species, replacement of protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the protein in an immune response in an animal. In a finbrial presentation containing a recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a finbrial presentation warening immunes response in an animal in conjunction with a carrier finbrial subunit proteins are usually strong immunogenicity and adhesion properties relevant for an efficient live considering the inserted epitope, and hybrid fimbring are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and the animal invention of the present sequence is given in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKLLKVAAFAALVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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protein useful for eliciting immune response in animal
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Pred. No. 3.3e-52;
0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the exemplification of the present invention
                                          Disclosure; Page 137; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine; immune response; immunogen.
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Best Local Similarity 73.6
Matches 128; Conservative
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Kay ww;

Collison SK,

Doran JL,

White AP,

WPI; 2000-672631/65.

N-PSDB; AAC64622

99US-0127888P.

05-APR-1999;

(UYVI-) UNIV VICTORIA

05-APR-2000; 2000WO-CA000356

Salmonella enteritidis.

Escherichia coli.

Synthetic.

WO200060102-A2

12-OCT-2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        directing recombination of a recombinant gene into the chromosome of the homologue finbrin submits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologue species, replacing the native back into the chromosome of the homologue species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, In a finbrial presentation colliciting an immune response in an animal. In a finbrial presentation solved in manue response in a sequence or solved in this numbers (but the hybrid fimbriae are usually strong immunogens, which may be important for directing an immune response in an hybrid fimbriae are usually strong incontaint the inserted epitope, and hybrid fimbriae are usually strong incontaint the inserted epitope, and hybrid fimbriae are usually strong incontaint the inserted epitope, and hybrid fimbriae are usually strong incontaint the inserted epitope.
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                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative fimbriae (SETI//TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVIHEMAH---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 PDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                Recombinant agfA gene having a segment replaced by a foreign DNA sequentic encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 ATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 ATIDOWNAKNSDITVGOYGGNNAALVNOTASDSSVMVROVGFGNNATANOY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.2%; Score 618; DB 3; Length 151; 76.6%; Pred. No. 8e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inexpensive to purify in large amount. The pr
the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                      Kay WW;
                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 136; 139pp; English.
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                                                                                                      Collison SK,
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99US-0127888P.
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                                                 (UYVI-) UNIV VICTORIA.
                                                                                                      Doran JL,
                                                                                                                                                  WPI; 2000-672631/65
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                                                                                                                                                                                 N-PSDB; AAC64624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 151 AA;
05-APR-1999;
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                                                                                                      White AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA control of the mondes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbried (SPEDI/TAP) mucleation depended assembly system of strains of Salmonella, Escherichia coli and control of the comprising recombination of fimbriae comprising recombinant of a recombination of fimbriae comprising recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a r
Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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Pred. No. 2.4e-51;
7; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNAALVNYDQLVTRVVTHEMAHANNATANQY
                                                                                                                                                                                                                  Disclosure; Page 135; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.6%;
80.8%;
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Best Local Similarity 80.8
Matches 122; Conservative
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SDARKSETTITOSGYGNGADVGQGADNSTIELTONGFRNNATIDOWNAKNSDITVGQYGG 120

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The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEP1/TAR) nucleation depended assembly system of strains of Salmonella Escherichia coli and Enterobacteriaceae for the production of fimbriae comprision are combinant of directing recombination of a recombinant gene homologous species; (3) directing recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; (3) directing recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal comprising separating an amino acid polymer response in an animal cold polymer comprising are animal acid polymer comprising are combinant Agrapha cold polymer animal are placement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or colymer into the animal in conjunction with a carrier or diluent. (1) is useful for the azimal in conjunction with a carrier or diluent. (1) is useful for the animal in conjunction with a carrier or diluent. (2) system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine; the carrier fimbrial subunit protein sare usually strong immunogens, which may be important for directing an immune response in an hybrid fimbriae are easy and incompant the inserted epitope, and hybrid fimbriae are usually strong immunogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                             chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                 AgfA::PT3#2 amino acid sequence SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Page 136; 139pp; English
                                                                                                                                                                                                                      vaccine; immune response; immunogen.
                    AAB36347 standard; protein; 151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                    05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0127888P
                                                                                                          (first entry)
                                                                                                                                                                                                                                                           Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-672631/65.
N-PSDB; AAC64623.
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Best Local Similarity
Matches 123; Conserv
                                                                                                                                                                                               agfA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                 WO200060102-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-1999;
                                                                                                          26-FEB-2001
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                                                                                                                                                                                               Salmonella;
                                                                                                                                                                                                                                                                                                                                                                                             12-OCT-2000
                                                                                                                                                                                                                                                                                                          Synthetic
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                                                              AAB36347;
AAB36347
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N-PSDB; AAC64628.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               78.3%; Score 611; DB 3;
81.5%; Pred. No. 3.8e-51;
iive 6; Mismatches 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ilarity 81.5%;
Conservative
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative finbriae (SEP17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprision grecombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene homologous species; (3) directing recombination of a recombinant gene box into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a replacement segment or segment of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for every consist of the bushing are presented in high numbers (1) the consist of the bushing are presented in high numbers (1) the consist of the bushing an election or presented in high numbers (1) the consist of the bushing an election or the public and presented in high numbers (1) the consist of the bushing an election of the profession of the consist of the bushing an election of the consist of the bushing an election of the bushing an election of the bushing an election of the bushing an election of the bushing an election of the bushing an election of the bushing an election of the bushing and election of the bushing an election of the bushing and election of the bushing an election of the bushing and election of the bushing an election of the bushing and election of the bushing and election of the bushing and election of the bushing and ele
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SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
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                                                                                                                                                                           121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
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                                                                                                121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine; immune response; immunogen.
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                                                                                                                                                                                                                                                                                                                                                                                          AAB36352 standard; protein; 151
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                               SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                     61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
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                                                                                                 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
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                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                  Salmonella, agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                           ..
                                                 Length 151;
                                                                        Indels
                                                                           22;
                                                 Score 608; DB 3;
Pred. No. 7.4e-51;
                                                                                                                                                                                                                                                                                                                                                         AgfA::PT3#9 amino acid sequence SEQ ID NO:28.
 of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kay WW;
                                                                        5; Mismatches
                                                                                                                                                                                               NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                     HEMAHANOTASDSSVMVROVGFGNNATANOY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 138; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               vaccine; immune response; immunogen.
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                                                 77.9%;
82.1%;
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                                                           Best Local Similarity 82.1
Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella enteritidis
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 the exemplification
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                         Sequence 151 AA;
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Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000.copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                             Score 601; DB 3;
Pred. No. 3.5e-50;
4; Mismatches 25;
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Best Local Similarity 80.8%;
Matches 122; Conservative
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cc (1) use of thin aggregative fimbriae (SEP17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterbaceriacae for the production of fimbriae comprising recombinant of AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively, (2) directing recombination of a recombination of a recombinant gene into the chromosome of the homologue species, respectively, (2) directing recombination of a recombinant gene comprising separating an enhologue species, replacing the native comprising separating an amino acid polymer comprising a recombinant AgfA comprising separating an amino acid polymer comprising separating an enhologum of a protein containing a replacement segment or segments of foreign amino compressing separating and animo acid polymer conditions the Enterbacteriaceae host cell, from the host cell and introducing the coli or confidence or sequences grown on a Salmonella, E coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli or coli o
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative finbriae (SEPI)/TMFP) mucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively, (2) directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene, and (4) eliciting an immune response in an animal, or comprising separating are placement segment comprising a recombinant of protein containing a replacement segment or segments of foreign amino acid polymer comprising separating are all aciding an immune response in an immune acid polymer comprising separating are all aciding an immune capture or segments of sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or anterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or dilutent. (I) is useful for the expension of recombinant AgfA protein which is useful for liciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogens, which may be important for directing an immune response in manimal sequence is given in the exemplification of the present invention requence is given in the exemplification of the present invention
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 599; DB 3;
Pred. No. 5.5e-50;
5; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                    Disclosure; Page 139; 139pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΑĀ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.8%;
81.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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Best Local Similarity 81.5
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 151 AA;
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The invention relates to an isolated peptide capable of binding a mammalian plasma protein or of generating an immune response in a mammal selected from sequences shown in ABRE2642, ABRE2646-49. The peptide or antibody is useful for treating a bacterial infection in a human or animal or in the manufacture of a medicament for the prophylactic treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infection. The peptide that is immobilized on a solid support is also useful as a reagent for determining the ability of a plasma protein to bind to bacteria. The present sequence represents an E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated peptide capable of binding a mammalian plasma protein, useful in the manifacture of a medicament for the prevention and/or treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKLLKVBAIAAIVFSGSALAGVVPQYGGGGNHGGGGGNNSGPNSELNIYQYGGGNSALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALO
Plasma protein; immune response; antibacterial; vaccine; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.4%; Score 518; DB 7; Length 151;
68.2%; Pred. No. 3.8e-42;
Live 20; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                              Herwald H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNGAAVDQTASNSSVNVTQVGFGNNATAHQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 41-42; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                              Wikstroem M,
                                                                                                                                                                                                                    30-JAN-2003; 2003WO-EP000943.
                                                                                                                                                                                                                                                                    31-JAN-2002; 2002GB-00002275
                                                                                                                                                                                                                                                                                                                        (HANS-) HANSA MEDICAL RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                              Olsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   completed: August
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-646136/61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                         Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ACF36153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 151 AA;
                                                                                                            WO200306446-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103;
                                                                                                                                                                                                                                                                                                                                                                              Bjoerck L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Matches 10
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  d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequent of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative finbries (SERTI/TAR) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant of Enterobacteriaceae for the production of fimbriae comprising recombinant of directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene comprising separating an amino acid polymer comprising a recombinant pact comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino soid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is clearly for the expression of recombinant AgfA protein which is useful considering an immune response in an animal. In a fimbrial presentation system the hererologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein sare usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are usually strong inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention research and epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                                                                                 Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
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68.9%; Pred. No. 1.2e-42;
iive 20; Mismatches 27;
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                                                                                                                                                                Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY
                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 135; 139pp; English.
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                                                                                                                                                                Collison SK,
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  05-APR-2000; 2000WO-CA000356.
                                                      99US-0127888P.
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                                                                                                            (UYVI-) UNIV VICTORIA
                                                                                                                                                                Doran JL,
                                                                                                                                                                                                              WPI; 2000-672631/65.
N-PSDB; AAC64619.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coli CsgA
                                                         05-APR-1999;
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                                                                                                                                                                White AP,
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Matches 10
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Query Match
Best Local Similarity 90.1
Matches 136; Conservative
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Sequence 57, Appl
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Sequence 2, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2,
Sequence 2,
Sequence 4,
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                                                                                                                             1 MKLLKVAAFAAIVVSGSALA.......bssvmvrqvgFGNNATANQY
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/cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
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US-08-8173-2

US-08-8173-2

US-08-172-372-1

US-08-172-372-1

US-08-172-372-1

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US-09-336-447A-5

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US-09-336-199

US-09-072-596-199

US-09-072-596-199

US-09-072-596-138

US-09-072-595-4

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US-09-072-967-24

US-09-08-133-12-2

US-09-38-467-4

US-09-38-467-4

US-08-38-467-4

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                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                 389414 segs, 51625971 residues
                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                         using sw model
                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                       Issued Patents AA:*
                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                       US-09-543-407-18
780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein search,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
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Perfect score:
                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                          protein
                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                 Searched:
                                                                                                                               Sequence:
                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Result
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Sequence 16, Sequence 14, Sequence 42, Sequence 26, Sequence 4, P Sequence Sequence Sequence Sequence Sequence Sequence RESULT 1
US-08-233-7884-59
i Sequence 59, Application US/08233788A
i Betent No.;5635617
i GENERAL INFORMATION:
APPLICANT: Doran, James L.
APPLICANT: Collinson, Karen S.
APPLICANT: Collinson, Karen C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
ITILE OF INVENTION: OF SALMONELLA
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSE: Seed and Berry
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US-09-268-347-36
US-08-318-33401
US-08-312-711-16
US-08-312-711-16
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US-08-312-711-16
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US-08-312-71-16
US-08-312-71-16
US-08-312-71-16
US-08-312-71-16
US-08-313-71-16 ALIGNMENTS : 151 amino acids amino acid 

9 1 MKLLKVAAFPAIVVSGSALAGVVPQWGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ . 0 87.9%; Score 686; DB 1; Length 151; 90.1%; Pred. No. 2.2e-62; ive 3; Mismatches 12; Indels

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JS-08-254-573-2
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                                                SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 VVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGADV 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS 133
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Doran, James L.
APPLICANT: Kay, William W.
APPLICANT: Collinson, Karen S.
APPLICANT: Collinson, Karen S.
APPLICANT: Clouthier, Sharon C.
ATITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION TITLE OF INVENTION: OF SALMONELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 120; Score 506; DB 1; Length 120; I Similarity 87.5%; Pred. No. 3.4e-44; 98; Conservative 3; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPRESSED Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
STATE: Washington
COUNTRY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORDY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,788A
FILING DATE: JC-APR.1994
ATTONEY/AGENT INFORMATION:
REGISTRATION NUMBER: 35,570
RESTRENCE/POCKET UNMBER: 35,570
REGISTRATION NUMBER: 35,570
REGISTRATION NUMBER: 35,570
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: CLOR SEQ ID NO: 57:
SEQUENCE CHARATICNISTICS:
                                                                                                                                           121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                      121 NNPALVNÓTASDSSVMVRQVGFGNNATANQY 151
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; Sequence 57, Application US/08233788A
Patent No. 5635617
; GENERAL INFORMATION:
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 6. CORRESPONDENCE ADDRESS:
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Best Local Similarity
Matches 98; Conserva
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APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: GTC99-03PB CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 RKSETTITQS-----GYGNGADVGQGADNSTIELTQNGF-----RNNATIDQWNAKNS 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 AGNGIA-----SGNGEHNYGIGNGADDVD--ITAPITGVLNISGNSFTLIGNSSSSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----AHALQSDA
                                                                                                                                                                                                                                                                                                                                                                                                                           36; Gaps
                                                                                                                                                                                                                                                                                                                                                                11.8%; Score 92; DB 4; Length 975; ilarity 23.8%; Pred. No. 0.75; Conservative 24; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: KANBOJ, Rajender
APPLICANT: KANBOJ, Rajender
APPLICANT: BLIOTT, Candace
APPLICANT: NUTT, Stephen
TITLE OF INVENTION: AMPA-BINDING HUMAN Glurl RECEPTORS
UNDMER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 SGSALAGVVPQWGGGGNHNGG-GNSSGPDYDQLVTRVVTHEM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USB

CONFUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: Floppy disk

COMPUTER: ELEM PC compatible

COMPUTER: THE PC compatible

COMPUTER: PATENT PC-DOS/MS-DOS

SOFTWARE: PATENT PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US 07/896,611

FILING DATE: 10-JUM-1992

ATTORNEY/AGENT INFORMATION:

NAME: BENTY: STEPHEN A.

REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16777/179 ALLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 DIT-----VGQYGGNNAALVNQTASDS 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08254573
Patent No. 5610032
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TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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TELEFAX: (703)683-4109
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Virginia COUNTRY: USA
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250 VTGFQLVNYTDIIPAKIMQQM------KNSDARDHTRVDWKRPKYTSALTYDGVKVM 300 358 KGRRINYTLHVIEMKHDSIRKIGYWNEDDKFVPAATDAQAGGDNSSVQNRIYIVTILED 417 301 AEAFQSLRRQ----RIDISRRGNAGDCLANPAVPWGQGIDIQRALQQVRFEGLTGNVQFNE 357 ----IDQWNAKNSDI---IVGQYGGNNAALVNQT----ASD 132 358 KGRRTNYTLHVIEMKHDSIRKIGYMNEDDKFVPAATDAQAGGDNSSVQNRTYIVTILED 417 56 AHALQSDARKSETTITQSGYGNGADV------GQGAD-----NSTIELTQ 94

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: Diskette, 3.50 inch, 1.44 MB storage
IBM Compatible
NYSTEM: Microsoft Windows 95
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11.5%; Score 90; DB 4
Best Local Similarity 22.6%; Pred. No. 1.1;
Matches 45; Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 16777/229/ALLE
TELECOMMUNICATION INFORMATION:
TELEPRONE: (202) 672-5300
TELEFAX: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08864038A Patent No. 6001592 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            418 PYVMLKK-----NANOF 429
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: CONT
TITLE OF INVENTION: SAII
TITLE OF INVENTION: SAII
TITLE OF INVENTION: TO SAII
TITLE OF INVENTION: TO SAII
WHERE OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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               ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopby o
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MOLECULE TYPE: protein
US-08-216-326-2
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514-01
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CITY: Tsu-city
STATE: Mie-pref
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    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     358 KGRRINYTLHVIEMKHDGIRKIGYWNEDDKFVPAATDAQAGGDNSSVQNRTYIVTILED 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 AEAPQSLRRQ----RIDISRRGNAGDCLANPAVPWGQGIDIQRALQQVRFEGLTGNVQFNE 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---IDQWNAKNSDI----TVGQYGGNNAALVNQT----ASD 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 VAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQL-----VTRVVTHE----M
APPLICANT: Snyder, Yvonne M
APPLICANT: Sharp, Robert L
TITLE OF INVENTION: HUMAN GLUTAMATE RECEPTOR AND RELATED DNA
TITLE OF INVENTION: COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.5%; Score 90; DB 4; Length 906; llarity 22.6%; Pred. No. 1.1; Conservative 26; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ELIOTT, Candace
APPLICANT: ELIOTT, Candace
APPLICANT: NUTT, Stephen
TITLE OF INVENTION: APPA-BINDING HUMAN GLURI RECEPTORS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 8000 K Street N.W., Suite 500
CITT: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/172,332
FILING DATE: 22-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/879,688
FILING DATE: MAY 1, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 AHALQSDARKSETTITQSGYGNGADV------GOGAD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEE: Foley & Lardner
: 3000 K Street N.W., Suite 500
Washington, D.C.
                                                                                    STREET: Lilly Patent Division/JPL STREET: Lilly Corporate Center CITY: Indianapolis
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-216-326-2
; Sequence 2, Application US/08216326
; Patent No. 6406868
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     418 PYVMLKK-----NANOF 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Leeds, James P.
REGISTRATION NUMBER: 35241
REFERENCE/DOCKET NUMBER: X-
TELECOMUNICATION INFORMATION:
TELEPHONE: 317-276-1667
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 NGFRNNAT-
                                                                                                                                                                                                              USA
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                                                                                                                                                                                                            COUNTRY:
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Kunio NAKASHIWA et al.
VENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
VENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
VENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
VENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
VENTION: TO SAID POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250 VIGFQLVNYIDIIPAKIMQQW------KNSDARDHIRVDWKRPKYISALIYDGVKVM 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 AEAFQSLRRQ---RIDISRRGNAGDCLANPAVPWGQGIDIQRALQQVRFEGLTGNVQFNE 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 VAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGFDYDQL-----VTRVVTHE----M 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --IDQWNAKNSDI----TVGQYGGNNAALVNQT----ASD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 AHALQSDARKSETTITQSGYGNGADV-----GQGAD----
COMPUTER: IEMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,326
FILING DATE: 23 MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/896,611
FILING DATE: 10-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
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28 GGGNHNGGGNSS---GPDYDQLVTRVVTHEMAHALQSDARKSETTI----TQSGYGNGAD 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark STREET: 444 So. Flower St., Suite 2000 CITY: Los Angeles STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version #1.25
                                                                                                                                                             NNAALV----NQTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                 189 NNSTVAGGSHNQATGEGSF---AAGVENKANAN 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: Cailled States
ZIP: $90071-2921
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OBERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
RILING DATE: 19910813
CLASSIFICATION: 4355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Reiter Ph.D., Stephen E.
REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: P31 8962
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 907 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 22.68
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 9103330318
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                  VGQG-----ADNSTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MOLECULE TYPE: protein US-07-718-575-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --- GG 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 LLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQSD 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.2%; Score 87.5; DB 3; Length 738; 25.6%; Pred. No. 1.5; tive 11; Mismatches 59; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.8%; Score 84; DB 4; Length 892; illarity 26.8%; Pred. No. 4.3; Conservative 17; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGALAAALAAAGAGGGLGGGGGGALAAALAAAGAGGGGFGGLGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 YGGNNAALVNQTASDSS-----WWRQVGFGNNATA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        504 LGGGSAAAAAAAAAAGGGGRALRRALRRQMRGGGSAAA 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | NAME/KEY: peptide | Lo 738 | LOCATION: from 1 to 738 | LOCATION: from 1 to 738 | LOCATION METHOD: E (by experiment) US-08-864-0388-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFWARE: Patentin Ver. 2.1
SEQ ID NO 5
                                                     FILING DATE: MAY 28, 1997
PHIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: JP 8-184459
FILING DATE: JS-July-1996
ATTORNEY/AGBWT INFORMATION:
NAME: C. BULCE Hamburg
REGISTRATION NUMBER: Z2,389
REGISTRATION NUMBER: P-5610
TELEPROMUNICATION INFORMATION:
TELEPROMUNICATION INFORMATION:
TELEPROMU (212)986-2340
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: J38
                                        US/08/864,038A
                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pinctada fucata
CELL TYPE: mantle epithelial cell
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41; Conservative
                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPDLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Pinctada fuc
                     CURRENT APPLICATION DATA APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 41; Conserv
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310 Q---RIDISRRGNAGDCLANPAVFWGGGIDIQRALQQVRFEGLTGNVQFNEKGRRTNYTL 366 367 HVIEMKHDGIRKIGYWNEDDKFVPAATDAQAGGDNSSVQNRTYIVTILEDPYVMLKK-- 424 75 GGKDNBAKGNYSTVGGGDYNBAKGNYST--VGGGSSNTAKGEKSTIGGGDTNDANGTYST 132 -ELTQNGFRNNATIDQWNAKNSDITVGQYG---G 120 -----IDQWNAKNSDI----TVGQYGGNNAALVNQT-----ASDSSVMVRQVG 141 250 VIGFQLVNYIDIIPARIMQQMRISDSRDHIRVDWKRPKYTSALIYDGVKVMAEAFQSLRR 6 VAAFAAIVVSGSALAGVVPQWGGGGNHNGGG-NSSGPDYDQLVTRVVTHEMAHALQSDAR 65 KSETTITQSGYGNGADV-----GQGAD------NSTIELTQNGFRNNAT-Gaps 54; US-07-718-575-2; Sequence 2; Application US/07718575; Patent No.:S20257; Patent No.:S2025 10.8%; Score 84; DB 1; Length 907; 22.6%; Pred. No. 4.4; tive 24; Mismatches 69; Indels

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65 KSETTITQSGYGNGADV------GQGAD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/013,767
FILING DATE: 04-FBB-1993
APPLICATION NUMBER: 07/718,575
FILING DATE: 21-UN-1991
APPLICATION NUMBER: PCT/US90/06153
FILING DATE: 25-OCT-1990
APPLICATION NUMBER: 07/428,116
FILING DATE: 27-OCT-1987
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9866
                                                         ; Sequence 2, Application US/08486269A; Patent No. 5945509; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Reiter, Stephen E
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Is Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 907 amino acids amino acid
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TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
es 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER:
                                      JS-08-486-269A-2
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 KSETTITQSGYGNGADV------GQGAD------NSTIELTQNGFRNNAT- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     310 Q---RIDISRRĞNAĞDCLANPAVPWĞQĞIDIQRALQQVRFEGLIGNVQFNEKĞRRINYTL 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --IDOWNAKNSDI---TVGQYGGNNAALVNOT-----ASDSSVMVRQVG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          367 HVIEMTCHDGIRKIGYMNEDDKFVPAATDAQAGGDNSSVQNRTYIVTILEDPYVMLKK-- 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 VAAFAAIVVSGSALAGVVPQWGGGGNHNGGG-NSSGPDYDQLVTRVVTHEMAHALQSDAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54;
                                                                                                                                                                                                       APPLICANT: Helmeann Ph.D., Stephen F.
APPLICANT: Helmeann Ph.D., James R.
APPLICANT: Holleann Ph.D., James R.
APPLICANT: Holleann Ph.D., James R.
APPLICANT: Heller Ph.D., Bernhard NWN
APPLICANT: Bettler Ph.D., Jam E.
TITLE OF INVENTION: GLUTAMATE RECEPTOR COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 So. Flower St., Suite 2000
CITY: Los Angeles
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
10.8%; Score 84; DB 1; Length 907;
Best Local Similarity 22.6%; Pred. No. 4.4;
Matches 43; Conservative 24; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: P31 8962
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
PRICR APPLICATION DATA:
APPLICATION NUMBER: US/08/013,767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Reiter Ph.D., Stephen E.
REGISTRATION NUMBER: 31192
                                                                                                                                             Sequence 2, Application US/08481206
Patent No. 5739291
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (619) 535-9001
(619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          907 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 9103330318
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / MOLECULE TYPE: protein US-08-481-206-2
                                         ----NANOF 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 90071-2921
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
142 FGNNATANOY 151
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      310 Q----RIDISRRGNAGDCLANPAVPWGQGIDIQRALQQVRFEGLTGNVQFNEKGRRTNYTL
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APPLICANT: Heinemann, Stephen F.
APPLICANT: Boulter, James R.
APPLICANT: Boulter, Michael
APPLICANT: Heilmann, Michael
APPLICANT: Bettler, Bernhard
APPLICANT: Gensen, Jan E.
TITLE OF INVENTION: GLUTAMATE RECEPTOR COMPOSITIONS
TITLE OF INVENTION: AND METHODS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Gray Cary Ware & Freidenrich LLP STREET: 4365 Executive Drive, Suite 1600 CITY: San Diego
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TUBERCULOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42;
              APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: STED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 84; DB 4; Length 943; Pred. No. 4.7; 9; Mismatches 41; Indels
                                                                                                                                                                             STREET: 0.0.0. - CITY: Seattle
STATE; Washington
COUNTRY: USA
ZIP: 198104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
PTI.ING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 SGTGNVGI----GNSGTGNWGIGNSGNSYN-----
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Job time : 13 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVIG J. 392
REGISTRATION NUMBER: 31,392
REFRENCE/DOCKET NUMBER: 21012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
INFORMATION FOR SEQ ID NO: 199: SEQUENCE CHARACTERISTICS:
LENGTH: 943 amino acids
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Best Local Similarity 25.2%;
Matches 31; Conservative
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TYPE: amino acid
STRANDEDNESS:
Vedvick,
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                                                                                                                                           Sequence 204 Application US/09056556

Patent No. 6350456

GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Ollion, Davin C.
ITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STREET: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Pure Floppy disk
COMPUTER: Parent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.8%; Score 84; DB 4; Length 943; 25.2%; Pred. No. 4.7; tive 9; Mismatches 41; Indels
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US-09-072-596-199
Sequence 199, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
(206) 622-4900
TELEFAX: (206) 682-6931
INFORMATION FOR SEQ ID NO: 204:
SEQUENCE CHARACTERISTICS:
LENGTH: 943 amino acids
TYPE: amino acid
STRANDENNESS:
TOPOLACY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION UNMER: 31,392
REPERENCE/DOCKET NUMBER: 21C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 25.2'
Matches 31; Conservative
                                            ----NANOF 429
  142 FGNNATANOY 151
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US-09-056-556-204
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2, 2004, 14:54:48 ; Search time 36.8 Seconds (without alignments) 1287.123 Million cell updates/sec
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780
1 MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                               1291235 segs, 313682936 residues
                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                 OM protein - protein search, using sw model
                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                          August
                                                                                                                         Title:
Perfect score:
                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                   Sequence:
                                                                                                                                                                                                               Searched:
                                                                          Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

			Description	Sequence 4, Appli	Seguence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 20638, A	Seguence 44999, A	Sequence 4, Appli	Sequence 146, App	Sequence 7, Appli	Sequence 2, Appli	Seguence 998, App	Sequence 203972,	Seguence 37715, A	Seguence 114193,	Sequence 232271,
00.17.7.7.00		;	4D	US-09-741-873B-4	US-09-741-873B-4	US-09-741-873B-2	US-09-741-873B-2	US-10-369-493-20638	US-10-282-122A-44999	US-10-647-057-4	US-09-793-306-146	US-10-233-449-7	US-10-251-661-2	US-10-408-765A-998	US-10-424-599-203972	US-10-425-114-37715	US-10-437-963-114193	US-10-424-599-232271
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			Match Length DB	151	151	131	131	445	974	580	597	906	906	1448	204	244	253	283
	9/0	Query	Match	66.7	66.7	56.9	56.9	13.9	11.9	11.7	11.7	11.5	11.5	11.4	11.3	11.3	11.3	11.3
		,	Score	520	520	444	444	108.5	66	91.5	91	90	06	89	88.5	88.5	88.5	88.5
		Result	NO.	н	2	m	4	Ω.	9	7	œ	σ	10	11	12	13	14	15

16	89		61	12	-282-122A-6776	equence 67768,
17	89	-		12	-282-122A-677	eguence 67793,
18	~	4	17	12	-425-114-46013	se 46013
19	Θ	ä	0	16	-475-970-1	7
20	TU:	i.	-	Φ	810-264-2	28
21	85.5	ij	Θ	7	-282-122A-648	9
22	4,	ö	0	15	-369-493-1283	7
23	4,		4	16	-437-963-	7
24	84	ö	α	12	-424-599-16889	Sequence 168890,
25	84	0	9	70	-952-267-	Sequence 5, Appli
26	84	10.8	943	6		Sequence 131, App
27	84	ö	4	10	-997-182-13	Sequence 131, App
28	84	0	4	10	-997-181-	Sequence 131, App
29	.80 44	Ö	4	14	-193-002-19	Sequence 199, App
30	84	Ö	4	14	1-084-843-204	Sequence 204, App
31	84	o.	24	12	-282-122A-4	Sequence 49773, A
32	84	0	0	12	1-282-122A-6436	Sequence 64369, A
33	m	0	65	σ	996-194-16	Sequence 16, Appl
34	83.5	0	9	12	1-164-966-3	Sequence 33, Appl
35	ന	0	N	12	-282-122A-	Sequence 53269, A
36	ന	o.	873	10	1-952-267-	Sequence 13, Appl
37	83	ö	α	14	1-238-075-1	154
38	83	ö	S	10	1-820-843A-2	21,
6 6	83	0	•	σı	976-29	quence 2, A
40	83	Ö	~	σ	801-368-	equence 176,
41	83	Ö	Θ	12	1-282-122A-7	763
42	83	o.	30		1-282-122A-6440	equence 64405
43	83	o.	ß	თ	797-862-3	, Ap
44	LA	ö	3	15	-	e 594,
45	82.5	ö	7		1-282-122A-5	equence 55429
	114				ALIGNMENTS	
	7-11					
RESULT 1	F <sub>1</sub> per					
US-09-741	1-873B-4			0	[	

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GENERAL INFOGRATION:
APPLICANT Normark, Staffan
APPLICANT Olsen, Arne
APPLICANT Olsen, Arne
APPLICANT Olsen, Arne
APPLICANT Olsen, Arne
APPLICANT Olsen, Arne
TITLE OF INVANTON: Pibronectin Binding Protein As Well As Its Preparation
FILE REPERBNCE: 012889-084
CURRENT FILING DATE: 2003-04-04-04-04
CURRENT PELING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR FILING DATE: 1997-11-06
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR APPLICATION NUMBER: US 08/318,519
PRIOR FILING DATE: 1994-10-06
PRIOR APPLICATION NUMBER: US 08/318,519
PRIOR APPLICATION NUMBER: US 08/318,519
PRIOR PILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 10
SOGTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 151
TYPE: RAT
ORGANISM: Escherichia coli
US-09-741-873B-4
QUETY MATCh
Best Local Similarity 68.2%: Pred: No. 2.2e-45;
MATCHS: 103; CONSERVATIVE 21; Mismatches 27; Indels 0; Gaps
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Sequence 4; Application US/09741873B Publication No. US20020081722A1 GENERAL INFORMATION:

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US-09-741-873B-2
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TTTLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
TTTLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 0.1289-084
CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT FILING DATE: 2003-04-04
FRIOR PELLING DATE: 1998-05-04
FRIOR PELLING DATE: 1998-05-04
FRIOR APPLICATION NUMBER: US 07/347,189
FRIOR APPLICATION NUMBER: US 07/789,437
FRIOR APPLICATION NUMBER: US 07/789,437
FRIOR APPLICATION NUMBER: US 07/789,865
FRIOR APPLICATION NUMBER: US 07/970,846
FRIOR APPLICATION NUMBER: US 08/187,865
FRIOR PILING DATE: 1994-01-28
FRIOR FILING DATE: 1994-10-05
FRIOR FILING DATE: 1994-10-05
FRIOR FILING DATE: 1994-10-05
FRIOR FILING DATE: 1994-10-05
FRIOR FILING DATE: 1994-10-05
FRIOR FILING DATE: 1994-10-05
FRIOR PILING DATE: 1994-10-05
                                                                                                        61 IDARNSDLIITQHGGGNGADVGQSSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG 120
                                                                              61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 01288-0408
CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT FILING DATE: 2003-04-04
1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 66.7%; Score 520; DB 12; Length 151; Best Local Similarity 68.2%; Pred. No. 2.2e-45; Matches 103; Conservative 21; Mismatches 27; Indels
                                                                                                                                                                         121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                           121 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09741873B Publication No. US20020081722A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 10 SOFTWARE: Patentin version.3.0 SEQ ID NO 4 LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Normark, Staffan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Escherichia coli
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US-09-741-873B-2
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US-US-741-873B-2

US-US-741-873B-2

Sequence 2, Application US/09741873B

Publication No. US200400969659

GENERAL INFORMATION:
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TILE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REPERBORG: 012899-084

CURRENT APPLICATION NUMBER: US/09/741,873B

CURRENT APPLICATION NUMBER: US 8801723-1

PRIOR APPLICATION NUMBER: US 08/978,878

PRIOR APPLICATION NUMBER: US 07/347,189

PRIOR PILING DATE: 1990-05-04

PRIOR APPLICATION NUMBER: US 07/347,189

PRIOR APPLICATION NUMBER: US 07/389,437

PRIOR APPLICATION NUMBER: US 07/789,437

PRIOR APPLICATION NUMBER: US 08/187,865

PRIOR PLING DATE: 1992-11-06

PRIOR APPLICATION NUMBER: US 08/187,865

PRIOR FILING DATE: 1994-01-28

PRIOR APPLICATION NUMBER: US 08/187,865

PRIOR FILING DATE: 1994-01-28

PRIOR PLING DATE: 1994-01-28

PRIOR PRIOR APPLICATION NUMBER: US 08/187,865

PRIOR PRIOR APPLICATION NUMBER: US 08/187,865

PRIOR PRIOR APPLICATION NUMBER: US 08/187,865

PRIOR PRIOR PRIOR DATE: 1994-01-28

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PARCENT NOS: 10

SOFTWARE: PARCENT NOS: 10

SOFTWARE: PARCENT NOS: 10

SOFTWARE: PARCENT NOS: 10
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                  PRIOR AFELLAGION.

PRIOR APPLICATION NUMBER: US 08/978,878

PRIOR FILING DATE: 1998-05-06

PRIOR FILING DATE: 1997-11-26

PRIOR PELING DATE: 1989-05-04

PRIOR APPLICATION NUMBER: US 07/347,189

PRIOR PAPLICATION NUMBER: US 07/769,437

PRIOR FILING DATE: 1999-11-06

PRIOR FILING DATE: 1992-11-03

PRIOR FILING DATE: 1994-01-08

PRIOR FILING DATE: 1992-11-03

PRIOR PILING DATE: 1994-01-28

PRIOR APPLICATION NUMBER: US 08/18/519

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-10-05

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PATCHIN VERSION 3.0
SE 8801723-1
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US-09-741-873B-2
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Length 131;

DB 12;

Score 444;

56.98;

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APPLICANT: KANSAS STATE UNIVERSITY RESEARCH FOUNDATION
APPLICANT: NAGARAJA, T.
APPLICANT: STEWART, GEORGE
APPLICANT: STEWART, GEORGE
APPLICANT: NARAYANAN, SANDERV
APPLICANT: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/10/647,057
CURRENT FILING DATE: 2003-08-22
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
APPLICANT Carr, Grant
APPLICANT Summeror, Robert
APPLICANT Summeror, Robert
APPLICANT Summeror, Robert
APPLICANT Forestth, R.
APPLICANT Forestth, R.
APPLICANT TY, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TILE REPERENCE: ELITAA.034A
CURRENT APPLICATION NUMBER: 60/10/282,122A
CURRENT APPLICATION NUMBER: 60/20.20
FRIOR APPLICATION NUMBER: 60/200,438
FRIOR PILING DATE: 2000-05-26
FRIOR PILING DATE: 2000-05-26
FRIOR APPLICATION NUMBER: 60/200,335
FRIOR PILING DATE: 2000-09-06
FRIOR FILING DATE: 2000-09-06
FRIOR FILING DATE: 2000-10-23
FRIOR APPLICATION NUMBER: 60/230,347
FRIOR FILING DATE: 2000-10-23
FRIOR APPLICATION NUMBER: 60/242,578
FRIOR APPLICATION NUMBER: 60/253,625
FRIOR APPLICATION NUMBER: 60/253,625
FRIOR APPLICATION NUMBER: 60/267,931
FRIOR FILING DATE: 2000-10-23
FRIOR FILING DATE: 2000-10-23
FRIOR APPLICATION NUMBER: 60/267,931
FRIOR FILING DATE: 2000-10-23
FRIOR APPLICATION NUMBER: 60/267,936
FRIOR APPLICATION NUMBER: 60/269,308
FRIOR FILING DATE: 2001-02-06
FRIOR APPLICATION NUMBER: 60/269,308
FRIOR FILING DATE: 2001-02-06
FRIOR FILING DATE: 2001-02-06
FRIOR FILING DATE: 2001-02-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
11.9%; Score 93; DB 12; Length 974;
Best Local Similarity 24.5%; Pred. No. 1.5;
Matches 36; Conservative 23; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 SGSALAGVVPQWGGGGNHNGG-GNSSGPDYDQLVTRVVTHEM-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acinetobacter baumannii
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SEQ ID NO 44999
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Publication No. US2003023675A1

GENERAL INFORMATION:

APPLICANT: Good, Yongwei

APPLICANT: Good, Yongwei

APPLICANT: Good, Willer Steven C.

APPLICANT: Good, Willer Steven C.

APPLICANT: Good, Willer Steven C.

APPLICANT: Good, Willer Steven C.

APPLICANT: Good, Willer Steven C.

APPLICANT: Good, WILL BATT S.

APPLICANT: Good, WILL BATT S.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF FILE REFERENCE: 38-10 (5.05.2) B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER: OF SEQ ID NOS: 47374
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                                                                                                                                                                                                                                                 81 VGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQV 140
                                                                                                                                                                                                                                                                                           61 VGQGSDDSSIDLIQRGFGNSATILDQWNGKNSEMTVKQFGGGNGAAVDQTASNSSVNVTQV 120
                                                                                                                                                                               1 GVVPQYGGGGNHGGGGNNSGPNSELNTYQYGGGNSALALQTDARNSDLTITQHGGGNGAD 60
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                                                                                                                       GVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGAD 80
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                                                    26; Indels
                 Pred. No. 1.2e-37;
9; Mismatches 26
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COTHER INFORMATION: unsure at all Xaa locations US-10-369-493-20638
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Sequence 44999, Application US/10282122A
Publication No. US20040029129A1
GENERAL INPORMATTON:
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haeelbeck, Robert
APPLICANT: Ohlsen, Rari
APPLICANT: Ohlsen, Rari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Rhodopseudomonas palustris
                 Best Local Similarity 65.6%; Pr
Matches 86; Conservative 19;
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Best Local Similarity
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LENGTH: 445
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| GENERAL INFORMATION:
| APPLICANT: Campos-Neto, Antonio
| APPLICANT: Campos-Neto, Antonio
| APPLICANT: Campos-Neto, Pamela
| APPLICANT: Ovendale, Pamela
| APPLICANT: Lodes, Michael
| APPLICANT: Lodes, Michael
| APPLICANT: Corixa Corporation
| TITLE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
| TITLE OF INVENTION: Of Tuberculosis
| FILE REFERENCE: 014058-008740US
| FILE OF INVENTION: Of Tuberculosis
| FILE PAPLICATION NUMBER: US/09/793,306
| CURRENT FILING DATE: 2001-02-26
| PRIOR APPLICATION NUMBER: US 60/185,037
| PRIOR FILING DATE: 2000-08-08
| NUMBER: OF SEQ ID NOS: 164
| SOFTWARE: Patentin Ver: 2.1
| SEQ ID NO 146
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                                                                                                                                                                                                                                                                                                                   -----DVGQGADNSTIELTQNGFRN 99
                                                                                                                                                                                                                      -----GGGNSSGPDYDQLVTRVVTHEMAH
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                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence:mTTC#3-His US-09-793-306-146
                                                                                                                 Query Match 11.7%; Score 91.5; DB 12; Length 580; Best Local Similarity 23.1%; Pred. No. 1.1; Matches 40; Conservative 18; Mismatches 56; Indels 59
                                                                                                                                                                                                                                                                                                                                                                  303 AKHVNVAKSSTVVVNAASGASKDASGMGSGAWDSNDTAKVDKGRSADSNV---
                                                                                                                                                                                                                                                                     257 KKAKKKGAVVNAASVAGTDKSAGGVAAVNTVKNKKASGSNKAGD-----
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                                                                                                                                                                                                                                                                                                                   ALOSDARKSETTITO-----SGYGNGA---
                                                                                                                                                                                                                    5 KVAAFAAIVVSGSALAGVVPQWGGGGNHN-
                       TYPE: PRT ORGANISM: Fuscbacterium necrophorum
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LENGTH: 580
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RESULT 9 US-10-233-449-7 Sequence 7, Application US/10233449 ; Publication No. US20030211040A1

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              APPLICANT: Repaske, David
APPLICANT: Repaske, David
APPLICANT: SNyder, Gretchen
TITLE OF INVENTION: PHOSPHODIESTERASE ACTIVITY AND REGULATION OF
TITLE OF INVENTION: PHOSPHODIESTERASE
TITLE OF INVENTION: B-MEDIATED SIGNALING IN BRAIN
FILE REFERENCE: 11181-010-999
CURRENT APPLICATION NUMBER: 05/10/233,449
CURRENT PILING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: 60/316,320
PRIOR FILING DATE: 2001-08-30
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.0
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Publication No. US20301665581

GENERAL INFORMATION:

APPLICANT: Alberini, Cristina M.

APPLICANT: Alberini, Cristina M.

TITLE OF INVENTION: Methods and Compositions for Regulating

TITLE OF INVENTION: Memory Consolidation

FILE REFERENCE: 3499.1001-003

CURRENT APPLICATION NUMBER: US/10/251,661

CURRENT PILING DATE: 2002-09-20

PRIOR FILING DATE: 2000-03-31

PRIOR FILING DATE: 2001-04-02

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FRACE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PRICE PR
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11.5%; Score 90; DB 14; Length 90
Best Local Similarity 22.6%; Pred. No. 2.8;
Matches 45; Conservative 26; Mismatches 56; Indels
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APPLICANT: Greengard, Paul
APPLICANT: Repaske, David
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US-10-251-661-2
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Best Local Similarity
Thes 45; Conserva
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Sequence 37715, Application US/10425114

Sequence 37715, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:
APPLICANT: Inu, Jingdong
APPLICANT: Thou, Yihua

APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313) B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                  135 QGRGSDG------NGQGRGRWGGNWSNBERNKDBESRGNGSWGFGNAGSGNBNS- 182
                                                                                                                                                                                                                                                                                                 81 VGQGADNSTIELTQNGFRNNATIDQMNAKNSDIT------VGQYGGNNAALVNQTAS 131
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                                                                                                                                                                                                                                                     106 GRVP-W-GGNSHERGGYSDG-------NSD------SGWGQGQD 134
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                                                                                                               12; Length 204;
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                                                                                                                                                         30; Indels
                   FEATURE:
, OTHER INFORMATION: Clone ID: PAT_MRT3847_26213C.1.pep
US-10-424-599-203972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: LIB3170-053-G12_FLI.pep
US-10-425-114-37715
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                                                                                                          Query Match
11.3%; Score 88.5; DB
Best Local Similarity 25.7%; Pred. No. 0.61;
Matches 35; Conservative 10; Mismatches
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Sequence 114493, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                               132 DSSVMVRQVGFGNNAT 147
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ORGANISM: Glycine max
ORGANISM: Glycine max
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Best Local Similarity
Matches 32; Conserva
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Publication No. US20040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: A Royalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21(5223)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 203972
TYPE: PRT
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                                                                                                                           301 AEÁFÓSLRRO---RÍDISRRGNAGÞCLANPAVÞWGQGIÐIQRALQQVAFEGLTGNVQFNE 357
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  --NSTIELTO 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                         Sequence 998, Application US/10408765A

Publication No. US20040101874A1

GENERAL INFORMATION:
APPLICANT: Glosh, Sounitra S.
APPLICANT: Zhang, Bing
APPLICANT: Zhang, Bing
APPLICANT: Glosh, Steven W.
APPLICANT: Glosh, Steven W.
APPLICANT: Glosh, Bradford W.
APPLICANT: Glosh, Bradford W.
APPLICANT: Glosh, Bradford W.
APPLICANT: Glosh, Bradford W.
APPLICANT: Glosh, Bradford W.
APPLICANT: Glosh, Bradford W.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
FILE REFERENCE: 660088.465
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077

SOFTWARE: FASTSEQ for Windows Version 4.0
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    AHALQSDARKSETTITQSGYGNGADV------GQGAD-
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Pred. No. (
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                                                                                                                                                                                                                                      418 PYVMLKK-----NANOF 429
                                                                                                                                                                                       133 SSVMVRQVGFGNNATANQY 151
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24.4%;
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Best Local Similarity 24.45
Matches 39; Conservative
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ORGANISM: Homo sapiens
US-10-408-765A-998
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LENGTH: 1448
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APPLICANT: Wu, Wei
APPLICANT: Boucharov, Andrey A.
APPLICANT: Boucharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)8
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 204966
SEQ ID NOS: 204966
SEQ ID NO 114193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 232271, Application US/10424599
Sequence 232271, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: LA ROSE Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cao Youwa
APPLICANT: Cao Youwa
APPLICANT: Cao Youwa
APPLICANT: David Woleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILLE DEPENDER: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILLING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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11.3%; Score 88.5; DB 16; Length 253;
Best Local Similarity 26.6%; Pred. No. 0.8;
Matches 38; Conservative 14; Mismatches 48; Indels 43.
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US-10-424-599-232271
                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_17908C.1.pep
US-10-437-963-114193
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US-10-424-599-232271
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Search completed: August 2, 2004, 15:36:11 Job time : 37.8 secs

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Run on:

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Result

Sequence:

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Sequence 22, Appliance 20, Appliance 30, Appliance 4, Appliance 4, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 2, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 2, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 2, Appliance 3, Appliance 3, Appliance 2, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 3, Appliance 4, Appliance 4, Appliance 4, Appliance 4, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, Appliance 5, App
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25818, A
25818, A
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358, App
357, App
358, App
                                                   Sequence 26,
                                                                   Sequence 20,
Sequence 16,
                                                                                                           Sequence 12,
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APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
TITLE APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 151
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           19 US-09-543-407-5
6 US-08-233-642h-57
19 US-09-543-407-26
19 US-09-543-407-16
19 US-09-543-407-16
19 US-09-543-407-16
19 US-09-543-407-14
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US-09-614-1508-25818
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US-60-191-637-25957
US-01-191-637-25957
US-10-191-637-25957
US-10-191-637-25957
US-10-455-719-358
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US-60-446-775-358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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1308
1249
1249
RESULT 1
US-09-543-407-18
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108:5
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106:5
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276
250.5
175
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                                                         2, 2004, 14:48:33 ; Search time 167.9 Seconds (without alignments) 877.809 Million cell updates/sec
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780
1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY
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(ggn2_6/ptodata/2/paa/US06_COMB.pep:*
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(ggn2_6/ptodata/2/paa/US082_COMB.pep:*
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(ggn2_6/ptodata/2/paa/US091_COMB.pep:*
(ggn2_6/ptodata/2/paa/US094_COMB.pep:*
(ggn2_6/ptodata/2/paa/US004_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                6019581
                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                           6019581 segs, 976053577 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                             protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length DB
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Maximum DB seq
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                                                                                                                                                                                                                                 Perfect score:
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Sequence 26, Application US/09543407 GENERAL INFORMATION:
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TELEFAX: (206) 682-631
TELEX: 3723836 SEBDANBERY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87.9%;
90.1%;
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-08-233-642A-57
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Matches 136; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 136; Conserv
                      COUNTRY: U.S.A.
ZIP: 98104-7092
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APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
TITLE OF LYNENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
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                                           Length 151;
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Sequence 57, Application US/08233642A
Sequence 57, Application US/08233642A
GENERAL INFORMATION:
APPLICANT: Collinson, S. Karen
APPLICANT: Clouthier, Sharon C.
APPLICANT: Dozen, James L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: BASED VACCINES
NUMBER OF SEQUENCES: 5
NUMBER OF SEQUENCES: -
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 151;
                                                                                    Indels
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STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                      100.0%; Score 780; DB 19;
100.0%; Pred. No. 3.7e-75;
1ive 0; Mismatches 0;
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Pred. No. 1.4e-65;
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; TYPE: PRT
; ORGANISM: Salmonella enteritidis
US-09-543-407-5
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Best Local Similarity 90.7%;
Matches 137; Conservative
                                      Ouery Match
Best Local Similarity 100.0
Matches 151; Conservative
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US-09-543-407-18
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 92043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTRARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 151
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ORGANISM: Artificial Sequence
PRATURISM: Artificial Sequence
ORGANISM: Artificial Sequence
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.5%; Score 675; DB 19; Length 151; larity 81.9%; Pred. No. 7.3e-64; Conservative 0; Mismatches 0; Indels 3:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elem PC compatible
OPERATIONS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,642A
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REFERENCE/DOCKET NUMBER: 920043.403C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 686; DB 6;
Pred. No. 4.8e-65;
3; Mismatches 12.
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Gaps

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RESULT 8
US-09-543-407-14
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US-09-543-407-12
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                                                LVTRVVTHEMAHALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQ 105
                                                                            1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGFDSTLSIYQYGSANAALALQ 60
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Calinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGGUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT FILING DATE: 2000-04-05
SUPPREST FILING DATE: 2000-04-05
SUPPREST FILE RESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                              APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT APPLICATION NUMBER: US/09/543,407
SUFTRANE: FASICEO for Windows Version 4.0
SEQ ID NOS: 59
CSTARRE: FASICEO for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 622; DB 19; Length 151;
Pred. No. 3.6e-58;
0; Mismatches 0; Indels 46
                                                                                                                                                                     106 WNAKNSDITVGOYGGNNAALVNOTASDSSVMVRQVGFGNNATANOY 151
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GENERAL INFORMATION:
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Best Local Similarity 73.6'
Matches 128; Conservative
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US-09-543-407-16
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LENGTH: 151
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                                                                                                                                                                                                                                                                                                                                                                                  -------YDQLVTRVVTHEMAHASG 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATIDOWNAKNSDITVGOYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                   40;
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                               FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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                                                                                                                                                                                                       Length 151;
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                                                                                                                                                                                                                                                                   0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT White, Aaron P.
APPLICANT White, Aaron P.
APPLICANT Collinson, S. Karen
APPLICANT COLLINSON, S. Karen
APPLICANT COLLINSON, S. Karen
APPLICANT SAY, William W.
ITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
ITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
ITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
ITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
CURRENT FILING DATE: 2000-04-05
SOFTWARE: FastSEQ for Windows Version 4.0
SSEQ ID NO 1.
LENGTH: 151
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78.6%; Score 613; DB 19;
Best Local Similarity 80.8%; Pred. No. 3.4e-57;
Matches 122; Conservative 7; Mismatches 22;
                                                                                                                                                                                                       79.2%; Score 618; DB 19;
.larity 76.6%; Pred. No. 9.8e-58;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNAALVNYDQLVTRVVTHEMAHANNATANQY
                                                                                                                                                                                                                                                                                                                                                                                     MKLLKVAAFAAIVVSGSALAGV-----
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
ORGANISM; Artificial Sequence
                                                                                                                                                                                                                                      Best Local Similarity
Matches 131; Conserv
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ 60
                                                                                                                         121 NNAALVNOTASDSSVMVROVGFGNNATANOY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 28, Application US/09543407; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Salmonella enteritidis
US-09-543-407-31
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                                                                                                                                                                                                                                                        RESULT 10
US-09-543-407-31
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APPLICANT: Collinson, S. Karen.

APPLICANT: Ray, William W.

TITLE OF INVENTION: BRACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

FILE REPERENCE: 220043, 406

CURRENT APPLICATION NUMBER: 406

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 14

LENGTH: 151

TYPE: PRT
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GENERAL INPORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043, 406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEO ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 78.3%; Score 611; DB 19; Length 151; Best Local Similarity 81.5%; Pred. No. 5.5e-57; Matches 123; Conservative 6; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 77.9%; Score 608; DB 19; Length 151; Best Local Similarity 82.1%; Pred. No. 1.2e-56; Matches 124; Conservative 5; Mismatches 22; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NNAALVNQTASDSSVMVRQVGFGNNATANOY 151
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US-09-543-407-24
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LENGTH: 151
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61 VGQGADNSTIELTQNGFRNNATIDQWNAKUSDITVGQYGGNNAALVNQTASDSSVMVRQV 120
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                                                                                                                                                                      Sequence 31, Application US/09543407

GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: APPLICANT: BACTERIAL FIMBRIAL SYSTEM FOR
ITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
ITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
ITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
CURRENT APPLICATION UNMERR: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE PRESENCE
SOFTWARE FRANCE: Raindows Version 4.0
SEQ ID NO 31
LENGTH: 131
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: CAy, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT APPLICATION NUMBER: US/09/543,407
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH. 151
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                                                                                     SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQMNAKNSDITVGQYGG 120
                                                            SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
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                                                                                                                                                                                                                                                                                                                      APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PASISEQ for Windows Version 4.0
LENGTH: 151
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APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PASLSEQ for Windows Version 4.0
LENGTH: 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 151;
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76.9%; Score 600; DB 19;
Best Local Similarity 81.5%; Pred. No. 8.4e-56;
Matches 123; Conservative 5; Mismatches 23;
                                                                                                                                           121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                               121 NNAALVNOTASDSSVMVROVGFGNNATANOY 151
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                                                                                                                                                                                                                                                                                    Sequence 22, Application US/09543407 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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GENERAL INCRMATION:
APPLICANT: NORMARK, Staffan
APPLICANT: OLSEN, Arne
TITLE OF INVENTION:
FILE REFERENCE: 012889-001
CURRENT APPLICATION NUMBER: US/08/978,878
CURRENT APPLICATION NUMBER: US/08/978,878
EARLIER APPLICATION NUMBER: SE 8801723-1
EARLIER APPLICATION NUMBER: SE 8801723-1
                                                                                                                                                                                                                                                                    1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
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APPLICANT White, Aaron P.
APPLICANT Doran, James L.
APPLICANT Collinson, S. Karen
APPLICANT (Collinson), S. Karen
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REPERENCE: 920043.407
CURRENT PELICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
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Recombinant Salmonella enteritidis 3b afgh sequence containing the replacement fragment encoding PT3 from GP63 of Leishmania major.
                                                                                                                              Length 151;
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                                                                                                                           Score 599; DB 19;
Pred. No. 1.1e-55;
5; Mismatches 23;
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GENERAL INFORMATION:
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Best Local Similarity 68.99
Matches 104; Conservative
                                                                                                                                                    Best Local Similarity 81.5
Matches 123; Conservative
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 66.7%; Score 520; DB 13; Length 151; Best Local Similarity 68.2%; Pred. No. 3.4e-47; Matches 103; Conservative 21; Mismatches 27; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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EARLIER APPLICATION NUMBER: US 07/347,189
EARLIER FILING DATE: 1989-05-04
EARLIER APPLICATION NUMBER: US 07/789,437
EARLIER APPLICATION NUMBER: US 07/789,637
EARLIER FILING DATE: 1991-11-06
EARLIER FILING DATE: 1992-11-03
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-01-65
EARLIER FILING DATE: 1995-06-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PALENTH Ver: 2.0
SEQ ID NO 4
LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
; ORGANISM: Escherichia coli
US-08-978-878-4
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Search completed: August 2, 2004, 15:26:43 Job time : 167.9 secs

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US-09-741-873C-4
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Sequence 2, Appli
Sequence 1659, A
Sequence 1659, A
Sequence 9, Appli
Sequence 7906, Ap
Sequence 7906, Ap
Sequence 312468,
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
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280, App
13, Appl
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22578, A
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Sequence 13,
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Sequence
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1 MKLLKVAAFAAIVVSGSALA.......bSSVMVRQVGFGNNATANQY
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(cgn2 6/ptodata/2/paa/VCT NEW COMB.pep:*

(cgn2 6/ptodata/2/paa/US06_NEW COMB.pep:*

(cgn2 6/ptodata/2/paa/US08 NEW COMB.pep:*

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(cgn2 6/ptodata/2/paa/US08 NEW COMB.pep:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-741-873C-2
US-10-170-205E-16659
US-10-170-205E-16659
PCT-US04-09988-9
US-60-556-841-11622
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US-60-579-062-7906
US-10-952-2678-5
US-10-972-2678-5
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US-10-490-953-14
US-10-737-290-171
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US-10-490-953-14
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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GENERAL INFORMATION:
APPLICANT Normark, Staffan
APPLICANT Normark, Staffan
APPLICANT Olsen, Ane
TITLE OF INVENTION: Fibrenectin Binding Protein As Well As Its Preparation
FILIS REFERENCE: 01289-084.
CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 1090-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-04
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-01-05
NUMBER OF SEQ ID NOS: 11
SCOTTWARE: PALEATION NUMBER: US 08/318,519
PRIOR FILING DATE: 1994-10-05
SEQ ID NOS: 11
SEQ ID NO 4
                                    Sequence 591, App
Sequence 22, App
Sequence 22, App
Sequence 30662,
Sequence 7905, Ap
Sequence 30330,
Sequence 317, App
Sequence 317, App
Sequence 31875,
Sequence 282, App
Sequence 26, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 26, Appl
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US-10-723-981-14
US-10-045-674A-521
US-10-045-674A-521
US-10-045-674A-527
US-10-491-001-22
US-10-491-001-22
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US-10-565-632-7905
US-10-565-632-7905
US-10-425-115-304391
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US-10-0931-070-36
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ORGANISM: Escherichia coli
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Matches 103; Conservative
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APPLICANT: TRAN, UPON K.; YANG, YONGHONG G.;
APPLICANT: TRAN, UPON K.; YANG, YONGHONG G.;
APPLICANT: TANN, UPON K.; YANG, YONGHONG G.;
APPLICANT: TANG, TOM, CHANLA, Narinden T.;
APPLICANT: ELLIOTT, VICKE S.; CHEN, David;
APPLICANT: ISON, Craig H., KHARE, Reena;
APPLICANT: ISON, Craig H., KHARE, Reena;
APPLICANT: TOW. FOISTIND D., RICHARDSON, Thomas W.,
APPLICANT: FAVERO, Kristin D., RICHARDSON, Thomas W.,
APPLICANT: HAFALIA, APRIL J.A.; BAUGHN, Mariah R.,
APPLICANT: BECHA, Shanya D., WILSON, AMY D.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH
TITLE PEPERBOUG: PF-1531 PCT
CURRENT APPLICATION NUMBER: PCT/USO4/09388
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16659, Application US/10170205E
GENERAL INFORMATION:
APPLICANT: ADAMS, Mark
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
FILLE REPERENCE: CLOO1301
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT PILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: Patentin version 3.2
SEQ ID NO 16659
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                                                                                                                                                                                                 - KNSDARDHIRVDWKRPKYISALIYDGVKVM 313
                                                                                                        314 AEAFQSLRRQ----RIDISRRGNAGDCLANPAVPWGGGIDIQRALQQVRFEGLTGNVQFNE 370
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11.4%; Score 89; DB 6; Length 1627;
Best Local Similarity 24.4%; Pred. No. 19;
Matches 39; Conservative 18; Mismatches 47; Indels
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PRIOR FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: US 60/465,568
PRIOR FILING DATE: 2003-04-24
                                                      56 AHALQSDARKSETTITQSGYGNGADV-
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  263 VTGFQLVNYTDTIPAKIMQQW--
                                                                                                                                                                                                                                                                          133 SSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                        431 PYVMLKK------NANQF 442
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US-10-170-205E-16659
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                                                                                                                                                               95 NGFRNNAT---
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TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE REFERENCE: CLOO1381
CURRENT ADALICATION NUMBER: US/10/170,205E
CURRENT ADALICATION DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: Patentin version 3.2
SEQ ID NO 3413
LENGTH: 852
                                                                                                                      APPLICANT: Olsen, Arne
APPLICANT: Olsen, Arne
FILE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 1999-05-06
FRIOR APPLICATION NUMBER: US 08/978,878
FRIOR APPLICATION NUMBER: US 08/978,878
FRIOR APPLICATION NUMBER: US 07/347,189
FRIOR APPLICATION NUMBER: US 07/347,189
FRIOR FILING DATE: 1999-11-06
FRIOR FILING DATE: 1991-11-06
FRIOR FILING DATE: 1991-11-06
FRIOR FILING DATE: 1994-01-08
FRIOR FILING DATE: 1994-01-08
FRIOR FILING DATE: 1994-01-08
FRIOR APPLICATION NUMBER: US 08/187,865
FRIOR APPLICATION NUMBER: US 08/318,519
FRIOR APPLICATION NUMBER: US 08/318,519
FRIOR APPLICATION NUMBER: US 08/318,519
FRIOR APPLICATION NUMBER: US 08/318,519
FRIOR APPLICATION NUMBER: US 08/318,519
FRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 11
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65.6%; Pred. No. 1.5e-32;
iive 19; Mismatches 26,
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                                                    Sequence 2, Application US/09741873C GENERAL INFORMATION:
                                                                                                             APPLICANT: Normark, Staffan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT; ORGANISM: Escherichia coli
US-09-741-873C-2
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Matches 86; Conservative
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US-10-170-205E-3413
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US-60-579-062-7906
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 11.2%; Score 87; DB 7; Length 461; Similarity 24.2%; Pred. No. 6.7; 40; Conservative 22; Mismatches 69; Indels
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GENERAL INFORMATION:
APPLICANT: Abad, Mark S.
ATILE OF INVENTION: Genes and Uses for Plant Improvement FILE REFERENCE: 38-21(53450)
CURRENT APPLICATION NUMBER: US/60/556,841
CURRENT FILING DATE: 2004-03-25
NUMBER OF SEQ ID NOS: 12463
SEQ ID NO 11622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            868 TLKPGPQQN-----WASKPQDNNVSNWGG--AASVKQTGT 900
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                                                                                                                                                                                                                                           ) NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7525307CD1
PCT-US04-09388-9
PRIOR APPLICATION NUMBER: US 60/476,135 PRIOR FILING DATE: 2003-06-04 PRIOR APPLICATION NUMBER: US 60/476,583 PRIOR FILING DATE: 2003-06-06 NUMBER OF SEQ ID NOS: 40 SOFTWARE: PERL Program SEQ ID NO 9
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US-60-565-632-7906
Sequence 7906, Application US/6056532
GENERAL INFORMATION:
APPLICANT: Monsanto Technology, LLC
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US-60-556-841-11622
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Kovalic, David K.
Larosa, Thomas J.
                                                                                                                                                                                                ORGANISM: Homo sapiens
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Best Local Similarity
Matches 40; Conserv
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US-60-556-841-11622
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APPLICANT:
APPLICANT:
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ORGANISM:
                                                                                                                                                                             TYPE: PRT
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APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Zhang, Bei
TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
TITLE OF INVENTION: Compositions Thereof
FILE REFERENCE: 38-21(53403)B
CURRENT APPLICATION NUMBER: US/60/565,632
CURRENT APPLICATION NUMBER: 2004-04-27
NUMBER OF SEQ ID NOS: 15449
SOFTWARE: Patentin version 3.2
SEQ ID NO 7906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wu, Wei APPLICANT: Wu, Wei APPLICANT: Wu, Wei APPLICANT: Wu, Wei APPLICANT: Tabnacy, Hei APPLICANT: Tabnacy, Hei Compositions thereof TITLE OF INVENTION: Compositions thereof TITLE OF INVENTION: Compositions thereof TITLE OF INVENTION: Compositions thereof CURRENT APPLICATION NUMBER: US/60/579,062 CURRENT APPLICATION NUMBER: US/60/579,062 CURRENT FILING DATE: 2004-06-11 NUMBER OF SEQ ID NOS: 41445 SOFFWARE: Patentin version 3.2 SEQ ID NO 7906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----FRNNATIDQWN------AKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360 GNENGTAAGNNANPD-------VONDAAOVNDNGTAAENNGNADAAGSNDN 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature; LOCATION: (810); LOCATION: (810)...(810); OTHER INFORMATION: Xaa can be any naturally occurring amino acid US-60-565-632-7906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature; LOCATION: (810); COCATION: (810); CTHER INFORMATION: Xaa can be any naturally occurring amino acid US-60-579-062-7906
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Best Local Similarity 24.7%; Pred. No. 17;
Matches 40; Conservative 17; Mismatches 47; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNGAAAENTGNADPAQGNDNGAAAENSGNENGIAAENNANAD 505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 7906, Application US/60579062; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Baum, James A
APPLICANT: Kovalic, David K
APPLICANT: Larosa, Thomas J
APPLICANT: Lu, Maolong
APPLICANT: Lu, Maolong
APPLICANT: Roberts, James K
Lu, Maolong
Munyikwa, Tichifa R.
Roberts, James K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Diabrotica virgifera
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Best Local Similarity
Matches 41; Conserv
JS-09-952-267B-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 312468, Application US/10425115
GENERAL INFORMATION: A Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: AND STORMAN Can A REPLICANT: A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA A ROSA 
----AKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNSTIELTQNGFRN------NATIDQWNAKN-----SDITVGQYGGNNAAL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/09952267B
GENERAL INFORMATION:
APPLICANT: HANSEN, ER.C.J.
APPLICANT: ARBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
APPLICANT: COPE, LESLIE D.
APPLICANT: PREDBNBURG, ROSS A.
TITLE OF INVENTION: USPAI AND USPAZ ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/09/952,267B
CURRENT PILING DATE: 2001-09-12
PRIOR PLILING DATE: 2001-09-12
PRIOR PRILING DATE: 1999-06-21
PRIOR PLILING DATE: 1999-06-21
                                                                                                                                               26 WGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGADVGQGA
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                                                                                                                                                                                                                                     ASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                               464 DNGAAAENTGNADPAQGNDNGAAAENSGNENGIAAENNANAD 505
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                                                                                                    ---FRNNATIDOWN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: MRT4577_48027C.1.pep
US-10-425-115-312468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.9%; Score 85; 27.1%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Moraxella catarrhalis
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Matches 38, Conservative
360 GNENGTAAGNNANPD-
                                                                                                82 GQGADNSTIELTQNG-
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SOFTWARE: Patentin Ver. 2
SEQ ID NO 5
LENGTH: 892
                                                                                                                                                                                                                                  121 NNAALVNQT
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US-10-425-115-312468
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US-09-952-267B-5
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                                                                                                                                                                                                                                                      ---ELTQNGFRNNATIDQWNAKNSDITVGQYG---G 120
                                                                                                                                                                                                                                                                                                           133 IGGGYYSRAIGDSSTIGGGYYNQATGEKSTVAGGRNN----QATGNNSTVAGGSYNQATG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 VGQG-----ADNSTI------ELTQNGFRNNATIDQWNAKNSDITVGQYG---G 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 IGGGYYSRAIGDSSTIGGGYYNQATGEKSTVAGGRNN----QATGNNSTVAGGSYNQATG 188
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                                                                                                                                 80
                                                                                                                                 28 GGGNHNGGGNSS---GPDYDQLVTRVVTHEMAHALQSDARKSETTI----TQSGYGNGAD
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                                                                           40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: OCE, MESLIE D.
APPLICANT: MACIVER, MESTIVE D.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
TITLE OF INVENTION: USPAI AND USPAZ ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMOY:024
CURRENT APPLICATION NUMBER: US/10/872,768
CURRENT FILING DATE: 1999-06-21
PRIOR FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PATENTIN VET: 2.1
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GRNERAL INFORMATION:
APPLICANT: HANSEN, ERIC 7.
APPLICANT: ACIDE, LEGLIE D.
APPLICANT: COPE, LEGLIE D.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: PREDENBURG, ROSS A.
TITLE OF INVENTION: USPAI AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REPERRACE: AMCY:024
CURRENT APPLICATION NUMBER: US/10/872,769
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                                                                           Indels
                                                                           55;
            ; Score 84; DB 5;
; Pred. No. 27;
17; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                   189 NNSTVAGGSHNQATGEGSF---AAGVENKANAN 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.8%; Score 84; DB 6;
llarity 26.8%; Pred. No. 27;
Conservative 17; Mismatches 55
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Sequence 5 Application US/10872768

GENERAL INFORMATION

APPLICANT: HANGEN, ERIC J.

APPLICANT: AEBI, CHRISTOPH

APPLICANT: COPE_LEGIED D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Moraxella catarrhalis US-10-872-768-5
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Query Match
Best Local Similarity 26.8%
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Plueckthun, Andreas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 415 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 280:
SEQUENCE CHARACTERISTICS:
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29.2%;
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Best Local Similarity
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US-09-952-267B-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1016 MGGFNTTISALSNNGRVLVGGDNQTVGRM-----LTVAGDYSGNNGTVSLSTALAADNS 1069
                                                                                                                                                                                                                                                                                                                                                                         81 VGQG-----ADDNSTI------ELTQNGFRNNATIDQWNAKNSDITVGQYG---G 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 QGADNSTIELTQNGFR----NNATIDQWNAKNSDITV-GQYGGNN--AALVNQTASDSS 134
                                                                                                                                                                                                                                                                                                              75 GGKDNEAKGNYSTVGGGDYNEAKGNYST -- VGGGSSNTAKGEKSTIGGGDTNDANGTYST 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 GGGN---HNGGGN----SSGPDYDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGADVG 82
                                                                                                                                                                                                                                                                             ---TQSGYGNGAD 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6263, Application US/60579902

Sequence 6263, Application US/60579902

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Krasomil-Osterfeld, Karina C.
APPLICANT: Wu, Wulcotide and Amino Acid Sequences from Xenorhabdus TITLE OF INVENTION: and Uses thereof FILE REPERDER: 38-21 (53444) A

CURRENT APPLICATION NUMBER: US/60/579,902

CURRENT FILING DATE: 2004-06-15

NUMBER OF SEQ ID NOS: 14985
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                          40;
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                                                                                                                                                                                          DB 6; Length 892;
27;
                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                           28 GGGNHNGGGNSS---GPDYDQLVTRVVTHEMAHALQSDARKSETTI-
                                                                                                                                                                                                                                        55;
                                                                                                                                                                                                                                                                                                                                                                                                                         121 NNAALV----NQTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 84; DB ; Fred. No. 27; 17; Mismatches
CURRENT FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US/09/336,447
PRIOR FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SSGTWARE: Patentin Ver: 2.1
SEQ ID NO 5
LENGTH: 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 280, Application US/09490324
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
                                                                                                                              ; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-10-872-769-5
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ORGANISM: Xenorhabdus bovienii
                                                                                                                                                                                                    ch
1 Similarity 26.8%;
41; Conservative 1
                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 41, Conserv
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US-60-579-902-6263
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250 GGGSEGGGSGGSGGSGDFDYEKMANAKGAMTENADENALÓSDAKGKLDSVATDYGAAID 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 GGG--GNHNGGGNSSGP-DYDQLVT----RVVTHEMAHALQSDAR-KSETTITQSGYGNG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13. Application US/09952267B

GENERAL INFORMATION:
APPLICANT: HANSEN, ERIC J.
APPLICANT: ABEL: CRRISTOPH
APPLICANT: COPE, LESLIE D.
APPLICANT: COPE, LESLIE D.
APPLICANT: PISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMC: 024
CURRENT APPLICATION NUMBER: US/09/952,267B
CURRENT FILING DATE: 1001-09-12
FRICH APPLICATION NUMBER: US/09/336,447
FRICH APPLICATION NUMBER: 1999-06-21
NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
                                                                                c/o Fish & Neave
                                                                                                                                                                                                           COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

COMPUTER ISM PC COMPATIBLE
COMPUTER PLODY disk
COMPUTER PC SYSTEM: PC-DOS/MS-DOS
COFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION DATA:
RELING PATE: 24-Jan-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
TITLE OF INVENTION: Profession (Poly) peptide libraries NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
FILING DATE: 18-RB-1995
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DΒ
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Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQUENCE DESCRIPTION: SEQ ID NO: 280:
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5.1.6	Compugen
version	- 2004
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	Copyright (c) 1993 - 2004 Compugen Ltd.
OM protein – pr	OM protein - protein search, using sw model
Run on:	August 2, 2004, 14:39:53; Search time 9.4 Seconds (without alignments) 1545.204 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-543-407-18 780 1 MKLLKVAAPAAIVVSGSALADSSVMVRQVGFGNNATANQY 151
Scoring table: BLOSUM62 Gapop 10	BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seg length: 0 Maximum DB seg length: 2000000000

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	fimbrin protein ag	major curlin chain	curlin protein csg	curlin major subun	н	cnjB protein - Tet	n nuclea	npn	curlin minor chain	fimbrin protein ag	nucleation compone	conserved hypothet		probable PPE prote	hypothetical prote	cal	05B5	£	hypothetical glyci	ద	H	glutamate receptor	glutamate receptor	recep	ņ	cal pr	leishmanolysin (EC	te recep	PPE
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0 8	32	e e	ი გ. დ	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

RESULT 1	
JC6039	
fimbrin pro	limbrin protein agità precursor - Salmonella enteritidis n'eneries calmonalla entevitidis
C;Date: 3	C;Date: 31-Dec-1996 #sequence revision 31-Dec-1996 #text_change 08-Oct-1999
C;Accessi	
R;Colline	R;COllinson, S.K.; Clouthler, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.
A;Title:	.cor. 176, 962-967, 1559 Salmonella enteritidis agfBAC operon encoding thin, aggregative fimbriae.
A;Referer	JC6039; MUID:96146512; PMID:8550497
A; Access:	AlAccession: JCSG39 - MAJecule type, DNA
A;Residue	
A; Cross-1	A;Cross-references: GB:U43280; NID:g1184712; PIDN:AAC43599.1; PID:g1184714 a.acession: Poffits
A, Molecul	A, Molecule type: protein
A;Residue	A;Residues: 21-52 <cc2></cc2>
A; Experim	A;Experimental source: strain 27655-3b A:Nore: the authors translated the codon ACG for residue 44 as Ile
R, Collins	T.J.; Kay, W
J. Bacter	riol: 173, 4773-4781, 1991
A;Ticie: Pur A:Reference	inication and characterization of thin, aggregative timbilae from himber: A44898: MHD:91310586: PMID:1677357
A; Contents:	
A;Access1	A;Accession::A44898
A; Status	preliminary
A; Molecui	e type: protein
A; Note: 8	A;Note: sequence extracted from NCBI backbone (NCBIP:45936)
C;Genetic	
A;Gene: agfA	agfA
C; Function	nn: . . major component of thin addredative fimbriae
A; Note: 1	Ajloce: finbriae bind to fibronectin, plasminogen, tissue plasminogen activator
C; Keyword	
F;1-20/Dc F;21-151/	F;1-20/Domain: signal sequence #status predicted <sig> F;21-151/Product: fimbrin protein agfA #status experimental <mat></mat></sig>
70 to 10	90
Query m Best Lo Matches	cal.: cal.:Similarity 00.7%; Pred. No. 9.7e-53; 137; Conservative 3; Mismatches 11; Indel
ઠે	1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ 60
: 셤	1 MKLLKVAAPAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
δλ	61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
QQ	61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
Qy	121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151

csgł

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A;Description: major component of wild-type curli; interaction between CsgA and CsgB tri
A;Noce: curli are thin, coiled fibers expressed on the surface of Escherichia coli that
and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers
F;1-20/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    curlin major subunit CsgA [imported] - Escherichia coli (strain O157:H7, substrain RIMD C,Species: Escherichia coli C,Species: Escherichia coli C,Date: 18-Uul-2001 #sequence_revision 18-Uul-2001 #text_change 18-Uul-2001 C,Accession: D90806 R. Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res: 8, 11-22, 2001 R. Han, C.G. A;Reference number: A99629; MUD:21156231; PMID:11258796
                  transcriptional repression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: GB:BA000007; PIDN:BAB34843.1; PID:g13360880; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A,Gene: EC81420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: S34559
A;Molecule type: DNA
A;Residues: 1-13, 'RQRDSGWLW' <OLS3>
A;Experimental source: EMBL:L04979; NID:g290424; PIDN:AAA23616.1; PID:g290425
A;Experimental source: strain K-12, substrain W3110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKLIKVAAIAAIVFSGSALAGVVPQYGGGGHGGGGGNNSGPNSELNIYQYGGGNSALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 OSDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLLKVAAFRAIVVSGSALAGVVPQW-GGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
A;Title: The RpoS sigma factor relieves H-NS-mediated t:
A;Reference number: S31202; MUID:93211294; PMID:8459772
A;Accession: S31202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.1%; Score 523; DB 2;
68.9%; Pred. No. 3.1e-38;
iive 20; Mismatches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.3%; Score 501.5; DB 2
67.1%; Pred. No. 2.3e-36;
iive 21; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;21-151/Product: curlin #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151
                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 21-42;44-50 <CLS2>
R;Olsen, A.N.; Armqvist, A.M.
submitted to the EMBL Data Library, October 1992
A;Reference number: S34559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY
                                                                                       A;Molecule type: DNA
A;Residues: 1-6, V', 8-151 <0L61>
A;Cross-references: EMBL:L04979
A;Accession: 534560
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ses 104; Conserv
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A;Molecule type: DNA
A;Residues: 1-152 <HAY>
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A;Note: this species has also been called Salmonella typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: A16635
R;Parkhill, J; Dougan, G; James, K.D; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gacra, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Retaus: preliminary
A;Molecule type: DNA
A;Residues: 1-151 <PAR>A;Cross-references: GB:AL513382; PIDN:CAD08268.1; PID:g16502315; GSPDB:GN00176
C;Genetics:
A;Genetics:
A;Genetics:
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Pred. No. 9.7e-53;
3; Mismatches 11;
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                  NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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Best Local Similarity 90.7%;
Matches 137; Conservative
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Subjects to the nucleator protein csgB precursor - Escherichia coli (strain K-12)

NyAlternate hames: csgB protein; curlin nucleation component; minor curlin protein C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Accession: S70787; F64846
R;Hammar, M; Armquist, A.; Bian, Z.; Olsen, A.; Normark, S.
Mol. Microbiol. 18, 661-670, 1995
A;Title: Expression of two csg operons is required for production of fibronectin- and C.
A;Reference number: S70783; MUID:96414468; PMID:8817489
A;Reference number: S70783; MUID:96414468; PMID:8817489
A;Reference number: S70787
A;Reference number: S70783
A;Reference subject: S70783; MUID:9147558; PIDN:CAA62281.1; PID:91147563
A;Rosalues: 1-151 cHMA
A;Residues: 1-151 cHMA
A;Residues: 1-151 cHMA
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A;Residues:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A)Description: minor component of wild-type curli, interaction between CsgA and CsgB tr A,Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli that and H-kinhingen, in the absence of CsgA, CsgB can self-assemble into polymers F;1-21/Domain: signal sequence #status predicted <&IG>
F;22-151/Product: minor curlin chain #status predicted <MAT>
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A;Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74125.1; PID:g1787278
A;Experimental source: strain K-12, substrain MG1655
A,Cross-references: EMBL:X06462
C,Genetics:
A,Genetic code: SGC5
A,Genetic code: SGC5
A,Introns: 85/3; 136/1; 157/3; 201/2; 290/2; 327/3; 499/1; 573/2; 607/3; 708/3; 777/3; 2,1164-1450/Region: glyothe-rich
E,1451-1464/Region: zinc finger CCHC motif
E,1451-1464/Region: zinc finger CCHC motif
E,1501-1514/Region: zinc finger CCHC motif
E,1530-1543/Region: zinc finger CCHC motif
E,1551-1568/Region: zinc finger CCHC motif
E,1551-1568/Region: zinc finger CCHC motif
E,1602-1615/Region: zinc finger CCHC motif
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14.6%; Score 114; DB 2; Length 1748;
Best Local Similarity 30.5%; Pred. No. 0.11;
Matches 39; Conservative 22; Mismatches 27; Indels 4
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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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A;Residues: 1164-1174;1179-1198;1233-1252;1285-1293;1297-1309;1316-1326;1331-1341;1343-
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R,Martindale, D.W.; Taylor, F.M.
Nucleid, Acids Res. 16, 2189-2201, 1988
A;Title: Multiple introns in a conjugation-specific gene from Tetrahymena thermophila.
A,Reference number: 803650; MUID:88189811; PMID:3357771
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A,Molecule type: DNA
A,Residues: 1-1748 <TAX-A
A,Fassidues: 1-1748 <TAX-A
A,Cross-references: EMBL:L03710; NID:g161751; PID:g161752
R,Taylor, F.M.; Martindale, D.W.
Nucleic Acids Res. 21, 4610-4614, 1993
A,Fitle: Retroviral-type zinc fingers and glycine-rich repeats in a protein encoded )
A,Reference number: S42135; MUID:94051569; PMID:8233798
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C;Species: Tetrahymena thermophila
C;Date: 19-Mar-1997 #sequence revision 18-Jul-1997 #text_change 07-Dec-1999
C;Accession: S42136; S42135; S03650
R;Taylor, F;M.; Martindale, D.W.
submitted to the EMBL Data Library, October 1992
A;Reference number: S42136
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Pred. No. 2.3e-36;
1; Mismatches 28;
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A;Molecule type: DNA
A;Residues: 236-250,'I',252-255,'N',257-773 <WAR>
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67.1%;
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Best Local
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C,Accession: AH0635
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, L.; T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 846-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AH0635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleation component of curlin monomers [imported] - Salmonella enterica subsp. enterica C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
                                                                                                                                                                                         fimbrin protein agfB precursor - Salmonella enteritidis
C;Species: Salmonella enteritidis
C;Species: Salmonella enteritidis
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999
C;Accession: JC6040
R;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.
A;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.
A;Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fimbriae.
A;Reference number: JC6039; MUID:96146512; PMID:8550497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Description: minor component of thin aggregative fimbriae A;Note: fimbriae bind to fibronectin, plasminogen, tissue plasminogen activator
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A;Molecule type: DNA
A;Residues: 1-151 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD08267.1; PID:g16502314; GSPDB:GN00176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:U43280; NID:g1184712; PIDN:AAC43598.1; PID:g1184713 A;Experimental source: strain 276755-3b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IATATNYDLARSEYNFAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISQEGGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C: Reywords: fimbria
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-151/Product: fimbrin protein agfB #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 MAHALQSDARKSE----TTITQSGYGNGADVGQ-GADNST-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.7%; Score 106.5; DB 2; 30.7%; Pred. No. 0.029; iive 17; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.7%; Score 106.5; DB 2; 30.7%; Pred. No. 0.029; ive 17; Mismatches 43;
     151
  130 ASDSSVMVRQVGFGNNATANQY
                                   Conservative
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Best Local Similarity 30.7
Matches 35, Conservative
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Best Local Similarity
Matches 35; Conserv
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A; Residues: 1-151 <COL>
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RiPerna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A; Title: Genome sequence of enterchemorrhagic Escherichia coli 0157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Accession: G8566
A; Status: preliminary
A; Relember: DNA
A; Residues: DNA
A; Residues: 1-151 < 8TO>
A; Cross-references: GB:AE005174; NID; g12514573; PIDN:AAG55787.1; GSPDB:GN00145; UWGP:216
C; Genetics:
A; Gene: CsgB
                                                                                                                                                                                                                                                                                                                                                                                      minor curlin subunit precursor CsgB [imported] - Escherichia coli (strain O157:H7, subst C,Species: Bscherichia coli
C,Species: Bscherichia coli
C,Accesion: C90806
F,Haysabi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. Basawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A,Feference number: A99629; MUID:21156231; PMID:11258796
A,Accession: C90806
A,Accession: C90806
A,Accession: C90806
A,Accession: C90806
A,Accession: C90806
A,Accession: C90806
A,Residues: 1-151 chay.
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                                                                                   ITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQT 129
                                                                                                                       70 ITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:BA000007; PIDN:BAB34842.1; PID:g13360879; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics: CGB1419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 ITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQT 129
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Pred. No. 0.024;
9; Mismatches 43; Indels
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Pred. No. 0.024;
9; Mismatches 43;
Pred. No. 0.024;
9; Mismatches 43;
                                                                                                                                                                                                                                                        129
                                                                                                                                                                                                  ASDSSVMVROVGFGNNATANOY 151
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llarity 35.4%;
Conservative
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Best Local Similarity 35.4%;
Matches 29; Conservative
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Best Local Similarity 35.4%;
Matches 29; Conservative
Similarity
29; Conserv
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Best Local
Matches 2
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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
CiSpecies: Mycobacterium tuberculosis
CiSpecies: Mycobacterium tuberculosis
CiSpecies: Mycobacterium tuberculosis
CiAccession: 17-011-1998 #sequence_revision 17-011-1998 #text_change 15-Sep-2003
CiAccession: F70675
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlini, K.; Feltwell, T.; Gentles, S.; Amilin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Anthors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Anthors: Squares, R.; Sulston, J.E.; Taylor, R.; Whitehead, S.; Barrell, B.G.
A;Anthors: Deciphering the biology of Mycobactrium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70675
A;Accession: DAA,
A;Anthors: DAA,
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C) Species: Agrobacterium tumefaciens
C) Species: Agrobacterium tumefaciens
C) Species: Agrobacterium tumefaciens
C) Accession: AB3143
R) Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, erage, G.; Giller, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A) Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-582 <CCL>
A;Cross-references: GB:Z82098; GB:AL123456; NID:g3261664; PIDN:CAB05045.1; PID:e280737;
A;Experimental source: strain H37Rv
C;Genetics:
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A.Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A.Reference tumber: AB2577; MUID:21608550; PMID:11743193
A.Accession:,AB3143
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A;Molecule type: DNA
A;Residues: 1-141 <CNO
A;Coss-references: GB:Ab008689; PIDN:AAL45560.1; PID:g17743275; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 VGQ---GADDNSTIEL----TQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASD 132
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50 VVTHEMAHALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 VPQWGGG--GNHNGGGNSSGPDYDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGAD
                                                        ----QYGRHNLSAVGQEGHDNYGSTTQNGNRNVAGI---
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                                                                                                                                                    110 NSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQ 150
                                                                                                                                                                                                97 -----GQFGSNHTTILTQDGNGNIAAGVQVGRGCSANVSQ
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12.0%; Score 93.5; DB 2;
Best Local Similarity 27.1%; Pred. No. 1.8;
Matches 38; Conservative 16; Mismatches 71;
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C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Species: 11.5m-2002 #sequence_revision 11.5m-2002 #text_change 18-Nov-2002
C; Accession: AD3143
E; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I. R; Wood, D.; Romero, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A; Atuthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
A; Reference number: AB2577; MUD:21608550; PMID:11743193
A; Residues: 1-145 KUR>
A; Status: preliminary
A; Molecule type: DNA
A; Status: preliminary
A; Residues: 1-145 KUR>
A; Experimental source: strain C58 (Dupont)
C; Genetics: 1-145 KUR>
A; Cross-references: GB-AE008689; PIDN:AAL45562.1; PID:g17743277; GSPDB:GN00187
A; Cone: Atu4768
A; Map position: linear chromosome
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C;Species: Agrobacterium_tumefaciens
C;Species: Agrobacterium_tumefaciens
C;Accession: H98144
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; MUID:21608551; PMID:11743194
A;Status: preliminary
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A;Cross-references: GB:AE007870; PIDN:AAK88682.1; PID:g15158413; GSPDB:GN00170 C;Genetics:
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12.2%; Score 95.5; DB 2;
Best Local Similarity 24.2%; Pred. No. 0.25;
Matches 39; Conservative 22; Mismatches 57;
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A,Gene: AGR L 228
A,Map position: linear chromosome
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                                           Best Local Similarity 26.0%; Pred. No. 0.39;
Matches 39; Conservative 22; Mismatches 63; Indels 26; Gaps
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1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
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Copyright (c) 1993 - 2004 Compugen Ltd.
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-!- FUNCTION: CURLIN 1S THE STRUCTUREL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
of Salmonella enterica serovar Typhi strains Ty2
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 21-33.
SPECIES-S enteritidis; STRAIN-27655-3B;
MEDLINE=91310566; PubMed=1677357;
Collinson S.K., Emcody L., Mueller K.-M., Trust T.J., Kay W.W.;
"Purification and characterization of thin, aggregative fimbriae from Salmonella enteritidis.";
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SPECIES=S.enteritidis; STRAIN=27655-3B;
MEDLINE=9401373; PubMed=810466.
Doran J.L., Collinson S.K., Burian J., Sarlos G., Todd E.C.D.,
Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., Kay W.W.;
"DNA-based diagnostic tests for Salmonella species targeting agfA, the Structural gene for thin, aggregative fimbriae.";
J. Clin. Microbiol. 31:2263-2273(1993).
                                                                                 SPECIES-S enteritidis; STRAIN=27655-3B; MEDILIBE-5614612; PubMed-8550497. Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W.W. "Salmonella enteritidis agfaAC operon encoding thin, aggregative
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                                  Bacteriol. 185:2330-2337(2003)
                                                                                                                                                  fimbriae.";
J. Bacteriol. 178:662-667(1996)
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nes 137; Conserv
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Salmonella enteritidis.";
J. Bacteriol. 173:4773-4781(1991).
-!- FUNCTION: CURLIN 1S THE STRUCTURE SUBUNIT OF THE CURLI. CURLI ARE COLLED SURRACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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MEDLINE-91310586; PubMed-1677357;
Collinson S.K., Emoedy L., Trust T.J., Kay W.W.;
"Purification and characterization of thin, aggregative fimbriae from
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96414468; PubMed=8817489; Hammark S.; Arriqvist A., Bian Z., Olsen A., Normark S.; Arriqvist C. Arriqvist S. Expersion of two csg operons is required for production of fibronectin- and congo red-binding curli polymers in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Moromura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.,
"A 718-kb DNA sequence of the Escherichia coli K.12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
[5]
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SEQUENCE FROM N.A.
STRAIN=K12 / W3110;
MEDLINE=93211294; PubMed=8459772;
MEDLINE=93211294; PubMed=8459772;
Olsen A., Arngvist A.;
"The RpoS sigma factor relieves H-NS-mediated transcriptional
"The RpoS sigma factor relieves H-NS-mediated transcriptional
"The RpoS sigma factor relieves H-NS-mediated transcriptional
"The RpoS sigma factor relieves H-NS-mediated transcriptional
                                                                                                                              Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                      01-OCT-1996 (Rel. 34, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Major curlin subunit precursor.
151 AA
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MEDLINE=93023873; PubMed=1357528;
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MEDLINE=97061202; PubMed=8905232;
                                                                                                                                                                      Enterobacteriaceae; Escherichia.
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STANDARD;
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STRAIN=K12 / MG1655;
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01-OCT-1996 (
28-FEB-2003 (
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STRAIN=K12 / MC4110;
MEDLINE=56414468; PubMed=8817489;
Hammar M., Ainqvist A., Bian Z., Olsen A., Normark S.;
Hammar M., Ainqvist A., Bian S., Olsen A., Normark S.;
Hammar M., Ainqvist Operons is required for production of fibronectin- and congo red-binding curli polymers in Escherichia coli
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Minor curlin subunit precursor.
CSGB OR B1041 OR Z1675 OR ECS1419.
Escherichia coli, and
Bacheria; Proteobacteria; Gammaproteobacteria; Enterobacterials Gammaproteobacteria; Escherichia, Proteobacteria; Casteria; Proteobacteria; Managroteobacteria; Casteria; Managroteobacteria; Managr
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MAJOR CURLIN SUBUNIT.
, EE2D2D94DDE91243 CRC64;
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EMBL, AE005315; AAG55788.1; -.
EMBL, AP002054; BAB34843.1; -.
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                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN-0157:H7 / Arcc 43895;
MEDLINE=21218556; PubMed=11319125;
Uhlich G.A., Keen J.E., Elder R.O.;
Whations in the Use orgo promoter associated with variations in curli expression in certain strains of Escherichia coli 0157:H7.";
Appl. Environ. Microbiol. 67:2367-2370(2001).
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Major curlin subunit precursor.
CSGA ON Z1676 OR ECS1420.
ESCHerichia coli 0157:#7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-0157.H7 / EDL933 / ATCC 700927;
MEDLINE=21074935, PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
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Pred. No. 1.7e-38;
0; Mismatches 27; Indels
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C003470D208D395F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAJOR CURLIN SUBUNIT.
     SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 NNAALVNOTASDSSVMVRQVGFGNNATANOY 151
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                                                                                                                                                                                                                                                                EMBL; 104979; AAA3616 1; -
EMBL; X90754; CAA62282.1; -
EMBL; AE000205; AA774126.1; -
EMBL; D90741; BAA35832.1; -
EMBL; D90742; BAA35840.1; -
PIR; S70788; S70788.
Ecoclene; EG11489; csgA.
Finbria; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 AA; 15049 MW;
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68.9%;
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CSGA ECO57

RESULT 3 CSGA\_ECO57

Q93U24;

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CONFLICT SEQUENCE Query Match Best Local ( Local

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EMBL; AE000205; AAC74125.1; -.

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DEPORTATION TO THE STAND OF STAND OF STRAIN COLOR THE STRAIN COLOR THE STRAIN COLOR THE STRAIN COLOR THE STRAIN COLOR THE STRAIN COLOR TO THE STRAIN C.-G., Ohtesubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H., Complete genome sequence of enterchemorrhagic Escherichia coli "Complete genome sequence of enterchemorrhagic Escherichia coli Ols7.H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                    Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arnqvist A., Olsen A., Normark S.,
"Sigma S-dependent growth-phase induction of the csgBA promoter in
Escherichia coli can be achieved in vivo by sigma 70 in the absence
of the mucleoid-associated protein H-NS.";
Mol. Microbiol. 13:1021-1032(1994).
-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI AR
COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
FIRENDECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                       SEQUENCE FROM N.A.
STRAIN=KIZ / MG1655;
MEDLINE=97426617; bubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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Nature 409:529-533(2001).
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Berna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Gortbeck B.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                         "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
                                                                                                                                                                                                   "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=0157:H7 / EDL933 / ATCC 700927;
K-12.";
Mol. Microbiol. 18:661-670(1995).
                                                                                                                                                                                                                                                                                                   MEDLINE=97061202; PubMed=8905232;
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MEDLINE=95157246; PubMed=7854117;
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                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                  Mau B.,
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EMBL; X90754; CAA62281.1; -.

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                                                                                                                                                                                                                                                                                                            70 ITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQT 129
                                                                                                                                                                                                                                                                                                                                           49 IGQAGTNNSAQLRQGGSKLLAVVAQEGSSNRAKIDQTGDYNL-AYIDQAGSANDASISQG 107
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-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF CURLIN MONOMERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Exer S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Chillingworth T., Connerton P., Feltwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagels K., Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Mhiteibad S., Barrell B.G., Complete genome sequence of a multiple drug resistant Salmonella enterica servora Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.,
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                   13.8%; Score 107.5; DB 1; Length 151; 35.4%; Pred. No. 0.012;
                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                          1, 21 F-POTENTIAL.
22 151 MINOR CURLIN SUBUNIT.
151 AA, 15882 MW, B18D266B964014B8 CRC64;
                                                                                                                                                                                                                                                                      43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSCW (2027M3) (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-CC-2003 (Rel. 42, Last annotation update)
Minor curlin subunit precursor.
CSGB OR STY1180 OR T1777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 AA.
                                                                                                                                                                                                                                                                        9; Mismatches
           EMEL, D90741; BAA338311; --
EMEL, AP005315; AA655787.1; --
EMEL, AP005254; BAB34842.1; --
PIR, C90806; C90806.
PIR, G85665; G85665.
PIR, S70787; S70787.
Fimbria; S19781; Complete protecome.
SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                  130 ASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21534947; PubMed=11677608;
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MEDLINE=22531367; PubMed=12644504;
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                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 413:848-852(2001)
                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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CSGB_SALTI
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 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                            55 MAHALQSDARKSE----TTITQSGYGNGADVGQ-GADNST-----IELTQNGFR 98
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FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI, CURLI ARE COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534949; PubMed=11677609;
MCDISINE=21534948; PubMed=11677609;
MCDISINE, SI, Spheth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES=S.typhimurium; STRAIN=SR-11;
MEDLINE=98117058; PubMed=9457880;
Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;
"Curli fibers are highly conserved between Salmonella typhimurium and
Bscherichia coli with respect to operon structure and regulation.";
J. Bacteriol. 180:722-731(1998).
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                 78 NRAKVDQ--AGNYNFAYIEQTGNANDASISQSAYGNSAAIIQKGSGNKANITQY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. SPRAIN-27655-38; SPECIES-S. enteritidis; SPRAIN-27655-38; MEDLINE-96146512; PubMed-8550497; Collinson S.K., Clouther S.C., Dovan J.L., Banser P.A., Kay W.W.; "Salmonella enteritidis agfBAC operon encoding thin, aggregative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBI_TaxID=602, 592;
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                                                                                                                                                                                                                                                                                 NNATIDQWNAKNSDIT-VGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                  13.7%; Score 106.5; DB 1; Length 151; 30.7%; Pred. No. 0.015; Live 17; Mismatches 43; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
Minor curlin subunit precursor (Fimbrin SEF17 minor subunit).
CSGB OR AGRED OR STW1143.
Salmonella typhimurium, and
Salmonella enteritidis.
                                                                                                           POTENTIAL.
MINOR CURLIN SUBUNIT.
161C54326E573495 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURLIN MONOMERS.
SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                 151 AA
                                                                 EMBL; AL627269; CAD08267.1; -.
EMBL; AE016840; AA069400.1; -.
Fimbria; Signal; Complete proteome.
SIGNAL
                                                                                                                                         151 AA; 16254 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 413:852-856(2001).
                                                                                                                                                                                                35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                               Best Local Similarity
Matches 35; Conserv
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                                                                                                                                          SEQUENCE
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CSGB_SALTY
ID _CSGB_S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 IATATUYDLARSEYNPAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISQEGGN 77
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Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.7%; Score 106.5; DB 1; Length 151; 30.7%; Pred. No. 0.015; ive 17; Mismatches 43; Indels 19.
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.larity 23.2%; Pred. No. 0.8;
Conservative 19; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Durbin R.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YKO3_CAEEL STANDARD; PRT; 401 AA.
P34231;
01-FEB-1994 (Rel. 28, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Hypothetical 43.5 kDa protein COSB5.3 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=Baristol N2;
Morthinare B.J.;
Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; C88571; C88571.
Wormbep, C0585.3; CE17369.
Hypothetical protein.
SEQUENCE 401 AA; 43472 MW; C99DF259EF6C8B55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 151 MINOR CURLIN SUBUNIT.
151 AA; 16182 MW; COFC5430E6DD361D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 MAHALQSDARKSE----TTITQSGYGNGADVGQ-GADNST----
                                                                                                                                                                                                                                                                      EMBL, AJ002301, CAA05316.1; -.
EMBL, AE008749, AAL20073.1; -.
EMBL, U43280, AAC43598.1; -.
PIR, JC66040, JC66040.
StyGene, SG10609; CSGB.
Fimbria, Signal, Complete protecome.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z32679; CAA83596.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 30.77
Matches 35, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6239;
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ω ..

Gaps

26;

Mismatches 52; Indels

Conservative

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                                                                                               90 SQSTGQINGNVPGSSSSNQQPVIYIARAGSDKYKNSEVTTSTPTPNGFNFGNGFQGQQQ 149
                                                                                                                                                 ---NSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASD 132
                                                                                                                                                                                     NTGFSSGFFNNQNQNSNQNLNQNNFQQN-----QNLGASSGFFNNQN----QNSQQ 197
                                                                           85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR (By similarity).
-!- SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a S-layer with hexagonal symmetry.
-!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
   - GGNHNGGGNSSGPDYDQLVT
                   | : | : | | | | | | : | | | | LQQYRAYAGCSSSGCVPATIVPKSSGFWPNADMIAGLQTEQRSQNQNQNGNNNPQQDDPRT
                                                                         ----MAHALQSDARKSETTI----TQSG--YGNGADVGQGA
                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
Cutface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
(rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Uchiyama 7.; "Sequencing of the gene encoding the protein rOmp B of Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rickettsia japonica.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 kDa SURFACE-EXPOSED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      japonica.";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 kDa BETA PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                           PRT; 1656 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rigreams, rigroiding, autorrans_barl; 2.
Antigen; S-layer; Cell wall.
CHAIN
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InterPro; IPR005546; Autotransporter.
LLKVAAFAAIVVSGSALAGVVPQWGG-
                                                                                                                                                                                                                         133 SSVMVRQVGFGNNATANO 150
                                                                                                                                                                                                                                                               NOVNGPISGFSNOOTSNO 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB003681; BAA20138.1; -
                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=YH;
                                                                       RVVTHE --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=35790;
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                                                                                                      104
                                                                                                                                                            602
6 VAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQSDARK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEISHMANDLYSIN.
REMOVED IN MATURE FORM (BY SIMILARITY).
ZINC (CAPALYTIC) (BY SIMILARITY).
ZINC (CAPALYTIC) (BY SIMILARITY).
ZINC (CAPALYTIC) (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                         548 ---TLILGGANIISANGGTINFQANGGTIKLTST--QNNIVVDCDLAIATDQTGVVDASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
LeishmanoLysin precursor (EC 3 4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
                                                                                                                                                                                                                                              InterPro; IPR006025, Pept M_Zn_BS.
InterPro; IPR001577; Peptidase_M8.
Promis Pro1457; Peptidase_M8. 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Glyroprotein; Metal-binding; Zinc; Signal; Cell adhesion; Glyroprotein; Lipoprotein.
                                                                                                                                                                                                            105 QWNAKNSDI -- TVGQYGGNNAAL-----VNQTASDSSVMVRQVGFGNNAT
                                                                                                      66 SETTITQSG----YGNGADVGQGADNSTIELTQNGFRNNATID-
                                                509 VLAAGAİTLDGSATI-----TGDIGNGGGGAA----LQSIT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTIVATION PEPTIDE,
                                                                                                                                                                                                                                                                                                                                                                                                     590 AA.
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MEDLINE=92107220; PubMed=1762629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M60048; AAA29244.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS; M08.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              endopeptidase)
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Mol. Biol. Evol. 10:127-139(1993).

-!- FUNCTION: Essential for biological clock functions. Determines the period length of circadian and ultradian rhythms; an increase in period length of circadian rhythms; and a decrease leads to lengthened circadian rhythms. Besential for the circadian rhythmic and a decrease leads to lengthened circadian rhythms. Essential for the circadian rhythmic component of the male courtship song that originates in rhythmic formation and nuclear localization of the TIM-PER complex. Light induces the degradation of the TIM-PER complex. Light induces the degradation of the heterodimer coordinatively regulates PER and TIM transcription through a negative feedback loop. Behaves as a negative element in circadian transcriptional loop. Does not appear to bind DNA, suggesting indirect transcriptional limibition (By similarity).

-!- SUBUNIT: Forms heterodimer with timeless (TIM); the complex then transcroase into the nucleus (By similarity).
                                                                                                                                                                                                                                                                                        241 YDQLVTRVVTHEMAHALGFSVVFFRDARILESISNVRHKDFDVPVINSSTAVAKAREQYG 300
                                                                                                                                                                                                                                                                                                                           77 NGA------DVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQ 128
                                                                                                                                                                                                                                                                                                                                               301 CGTLEYLEMEDQGGAGSAGSHIKM-----RNAQ-DELMAPASD--AGYYSALTWAIFQD 351
                                                                                                                                                                                                                                                           76
                                                                                                                                                                                                                                                         43 YDQLVTRVVTHEMAHALQ-----SDAR-------KSETTITQS--GYG
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Various strains;
MEDLINE=97357421; PubMed=9214747;
Gleason J.M., Powell J.R.;
Gleason J.M., Powell J.R.;
Interspecific and intraspecific comparisons of the period locus in the Drosophila willistoni sibling species.";
Mol. Biol. Evol. 14:741-753(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peixoto A.A., Campesan S., Costa R.H., Kyriacou C.P., "Molecular evolution of a repetitive region within the per gene of
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
BY SIMILARITY.
N LIMILARITY.
N LINKED (GLONAC. . .) (FOTENTIAL).
GPI-anchor amidated asparagine (By
                                                                                                                                                                                                                            47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neopera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7260,
                                                                                                                                                                                         Length 590;
                                                                                                                                                                                                                        Indels
                                                                                                                                                       OFB315D299659F58 CRC64;
                                                                                                                                                                                                                        39;
                                                                                                                                                                                      11.7%; Score 91.5; DB 1; 30.5%; Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PER DROWI STANDARD; PRT; 1093 AA. 003297; O18421; O18422; P91721; P91722; 01-OCT-1993 (Rel. 27, Created) 15-UL-1998 (Rel. 36, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Period circadian protein (Fragment).
                                                                                                                                                                                                                        12; Mismatches
                                                                                                                                        similarity)
                                                                                                                                                                                                                                                                                                                                                                                              129 TA---SDSSVMVRQVGFGNNA 146
                                                                                                                                                                                                                                                                                                                                                                                                                  | : : : | | | 352 LGFYQADFS-KAEEMPWGRNA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila willistoni (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 579-646 FROM N.A.
MEDLINE=93196482; PubMed=8450754;
                                                                                                                                                       62950 MW;
                                                                                                                                                                                                                        Conservative
     590 AA;
                                                                                                                                                                                                        Similarity
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Mol. Biol. E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T -> A (IN STRAIN 0811.4).
S -> F (IN STRAIN 0811.4).
G -> V (IN STRAIN 0311.4).
G -> S (IN STRAIN MANAUS.2).
G -> S (IN STRAIN MANAUS.2).
MISSING (IN STRAIN PORTO ALEGRE 3).
MISSING (IN STRAIN PORTO ALEGRE 3).
MISSING (IN STRAIN PORTO ALEGRE 3).
MISSING (IN STRAINS MANAUS.1 AND MANAUS.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ď
SUBCELLULAR LOCATION: Nuclear at specific periods of the day.
                 Substance Localization, Nuclear region about one hour before translocation into the nucleus. Interaction with Tim is required for nuclear localization (By similarity).

FOR INCHEST LOCALIZATION (BY SIMILARITY).

FOR THE STABLITY OF DER MONOMER AND IN THE FORMATION OF HETERODIMER THE STABLITY OF PER MONOMER AND IN THE FORMATION OF HETERODIMER MISCELLANBOUS: THE SECRET SHAD IN THE FORMATION OF HETERODIMER MISCELLANBOUS: THE SECRET SHOWN IS THAT OF STRAIN ATLIXCO. SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains. SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G -> V (IN STRAIN PORTO ALEGRE 4).
MISSING (IN STRAINS GUADELOUPE, MANAUS
PORTO ALEGRE 2, PORTO ALEGRE 1 AND
GUANA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biological rhythms; Repeat; Nuclear protein; Phosphorylation;
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POLY-SER.
POLY-GLY.
POLY-ALA.
POLY-ALA.
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InterPro; IPR000014; PAS domain.
                                                                                                                                                                                                                                                                                            AAB41363.1, -...
AAB41364.1, -...
AAB41365.1, -...
AAB41365.1, -...
AAB41367.1, -...
AAB41367.1, -...
                                                                                                                                                                                                                                              EMBL; U51055; AAB41360.1; -
EMBL; U51056; AAB41361.1; -
EMBL; U51057; AAB41362.1; -
TTT1058; AAB41363.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB41377.1; -.
                                                                                                                                                                                                                                                                                                                                                                    EWBL, US1064, AAB41369.1,
EWBL, US1065, AAB41370.1,
EWBL, US1065, AAB41371.1,
EWBL, US1069, AAB41372.1,
EWBL, US1069, AAB41373.1,
EWBL, US1070, AAB41374.1,
EWBL, US1070, AAB41375.1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00989; PAS; 2.
SMART; SM00091; PAS; 2.
PROSITE; PS50112; PAS; 2.
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EMBL; L06342; AAA28765.
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US1059;
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EMBL; Y00647; CAA68673.1; -. PIR; PL0221; PL0221.
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S - A (IN STRAIN GADELOUPE AND GUANA).

MISSING (IN STRAIN MANAUG 3).

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Structure 6:1035-1046(1998).

-!- FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.

-!- CATALVITA ACTIVITY: Preference for hydrophobic residues at Pl and Pl' and basic residues at P2 and P3'. A model nonapeptide is cleaved at "Ala-Tyr-|-Leu-Lys-Lys-.
                                                                                                                                                                             27 GGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGADVGQGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leishmania major.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leishmanolysin, the major surface metalloproteinase from Leishmania
                                                                                                                                                                                                                                                                                                                                         GP63_LEIMA STANDARD, PRT; 602 AA. P08148; P15906; 01-AWG-1998 (Rel. 08, Created) 01-ARP-1990 (Rel. 14, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Leishmanolysin precursor (EC 3.4.24.36) (Cell surface protease) (Major surface glycoprotein) (GP63 protein) (Promastigote surface
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Schlagenhauf E., Etges R., Metcalf P.;
"The crystal structure of the Leishmania major surface proteinase
 MISSING (IN STRAINS MANAUS 4, PORTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF 101-123.
MEDDINE-88154764; PubMed=3346625;
Button L.L., McMaster W.R.,
"Molecular cloning of the major surface antigen of leishmania.";
J. Exp. Med. 167:724-729(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schneider P., Ferguson M.A.J., McConville M.J., Mehlert A., Homans S.W., Bordier C., "Structure of the glycosyl-phosphatidylinositol membrane anchor the Leishmania major promastiqute surface protease."; J. Biol. Chem. 265:16955-16964(1990).
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Schlagenhauf E., Etges R., Metcalf P.;
"Crystallization and preliminary X-ray diffraction studies of
                                                                                                                   11.7%; Score 91; DB 1; Length 1093; 26.1%; Pred. No. 3.1; ive 8; Mismatches 46; Indels
                                                                                        115896 MW; ABGDE050267EC187 CRC64;
                                                                                                                                                                                                                                       87 NSTIELTQNGFRNNATIDQWNAKNSDITVGQY 118
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J. Exp. Med. 171:589-589(1990).
                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COPACTOR: Binds 1 zinc ion per subunit.
SUBCEDLUAR LOCATION: Attached to the membrane by a GPI-anchor.
PTM: THE PHOSPHATIDYLINOSITOL MOIETY OF THE GPI-ANCHOR CONTAINS A
FULLY SATURATED, UNBRANCHED 1-0-ALKYL CHAIN (MAINLY C24:0) AND A
MIXTURE OF FULLY SATURATED UNBRANCHED 2-0-ACYL CHAINS (C12:0,
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N-LINKED (GLCNAC. . .) (POTENTIAL).
GPI-anchor amidated asparagine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTIVATION PEPTIDE.
LEISHMANOLYSIN.
REMOVED IN MATURE FORM.
                                                                                                                                              C14:0, C16:0, AND C18:0).
SIMILARITY: Belongs to peptidase family M8.
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ZINC (CATALYTIC).
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CDTLEYLEVEDQGGAGSAGSHIKM 337

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=91352027; PubMed=1652753;

A Puckettic., Gomez C.M., Korenberg J.R., Tung H., Meier T.J.,
Chen X.N., Hood L.E.;
Chen X.N., Hood L.E.;
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Intemate receptor genes.";

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                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Glutamate receptor i precursor (GluR-1) (GluR-A) (GluR-KI) (Glutamate receptor ionotropic, AMPA 1).
GRIAI OR GLUHI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=P42261-2; Sequence=VSP_000092, VSP_000093, VSP_000094, VSP_000096; VSP_000096; TISSUE SPECIFICITY: Widely expressed in brain.
MISCELLANEOUS: This receptor binds AMPA (quisqualate) > glutamate
                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalià; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Hippocampus;
MEDLINE=2232975; PubMed=1320959;
Potier M.C., Spillantini M.G., Carter N.P.;
The human glutamate receptor cDNA Glubl: cloning, sequencing, expression and localization to chromosome 5.";
DNA Seq: 2:211-218(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=2;
                                                                       906 AA.
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IsoId=P42261-1; Sequence=Displayed;
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EMBL; M64752; AAA58613.1;
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PIR, S25852; S25852.
HSSP; P19491; 1GR2.
Genew; HGNC:4571; GRI.
                                                                                                                                                                                                       (Human)
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                                                                          HUMAN
                                          RESULT 12
GLR1_HUMAN
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Pred. No. 1.9;
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; Mismatches
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 R GO; GO:0005886; C:plasma membrane; TAS.
R GO; GO:0005866; F:glutamate receptor activity; TAS.
R GO; GO:0005207; F:kainate selective glutamate receptor activity; TAS.
GO; GO:0007269; P:synaptic transmission; TAS.
R TherPro; IPR001329; AnF receptor.
R InterPro; IPR001329; AnF receptor.
R InterPro; IPR001329; AnF receptor.
R InterPro; IPR001508; MMDA receptor.
R InterPro; IPR001508; MMDA receptor.
R InterPro; IPR001508; MMDA receptor.
R Pfam; PF01094; ANF receptor.
R Pfam; PF01094; ANF receptor.
R Pfam; PF01094; ANF receptor.
R Pfam; PF01094; ANF receptor.
R Pfam; PF01094; ANF receptor.
R Pfam; PF00107; MDDARCEPTOR.
R Pfam; PF00107; MDDARCEPTOR.
R Pfam; PF00107; MDDARCEPTOR.
R Pfam; PF00107; MDARCEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            358 KGRRINYTLHVIEMKHDSIRKIGYWNEDDKFVPAATDAQAGGDNSSVQNRTYIVTTILED 417
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 41, Last annotation update)
Outer membrane protein B precursor (168 kba surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Scas) (rompa)
(romp B) [Contains: 120 kba surface-exposed protein (Surface protein antigen) (120 kba outer membrane protein ompa); 32 kba beta peptide].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72; Gaps
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                                                                                                                                                                                                                                                                           receptor, concurrentive splicing.
SIGNAL 1 18 POTENTIAL.
CHAIN 19 906 GLUTAMATE RECEPTOR 1.
POMAIN 19 536 EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stenos J., Walker D.,

"The rickettsial outer membrane protein A and B genes of Rickettsia
"The rickettsial outer membrane protein of the spotted fever group.";

submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

-! FUNCTION: THE 120 KDB SURFACE-EXPOSED PROTEIN IS A MAJOR

STRUCTURAL PROTEIN WHITH MAY PLAY A ROLE AS A RICKETTSIAL
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by a S-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity).
-!- FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR [8P similarity].
-!- SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a SIASCELLULAR hexagonal symmetry (By similarity).
-!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P. S. A. (IN STRAIN INDIAN TICK TYPHUS).
G -> S (IN STRAIN INDIAN TICK TYPHUS).
K -> N (IN STRAIN INDIAN TICK TYPHUS).
V -> A (IN STRAIN INDIAN TICK TYPHUS).
N -> D (IN STRAIN INDIAN TICK TYPHUS).
I -> V (IN STRAIN INDIAN TICK TYPHUS).
A -> T (IN STRAIN INDIAN TICK TYPHUS).
C -> GH (IN REF. 3).
F -> S (IN REF. 3).
F -> S (IN REF. 3).
H -> R (IN REF. 3).
H -> R (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 33-1649 FROM N.A.
SEQUENCE OF 33-1649 FROM N.A.
STRAIN=Indian tick typins, and Malish 7;
MEDLINE=20395643; PubMed=10939649;
Roux V., Raoult D.;
"Phylogenetic analysis of members of the genus Rickettsia using the gene coding the outer-membrane protein römpB (ompB).";
Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
                                                                                                                                                                                                                                                                                                  "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098(2001)
                                                                                                                                                                                 MEDLINE-21442074; PubMed-11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGRPAMS; TIGRO1414; autocrans bar1; 2.
Antigen; S-layer; Cell wal1; Complete proteome.
CHAIN 1 1334 32 kDa BETA BEPTIDE.
CHAIN 1335 1655
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E -> D (IN REF. 3).

G -> S (IN REF. 3).

H -> R (IN REF. 3).

W, E49E19377D5FCE37 CRC64;
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EMBL, AF123721; AAF3114.1; --
EMBL, AF123726, AAF34129.1; --
EMBL, AF149110; AAF3553.1; --
PIR, E97835, E97835.
InterPro, IPR006315; Autotransport.
InterPro, IPR00546, Autotransporter.
Péam; PF03797; Autotransporter.
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                                                                                                                       SEQUENCE FROM N.A. STRAIN=Malish 7;
                                                          NCBI_TaxID=781;
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                                                                                                                                                                                                                                                                               Raoult D.;
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                                                                                                                                                            LVGGALAAGTITLDGSATITGDIGNAGGAAALQGIT-----LANDATK---TLTL 551
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                                                      Gaps
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SEQUENCE FROM N.A.
MEDLINE-92112918; PubMed=1370484;
Ramamoorthy R., Donelson J.E., Paetz K.E., Maybodi M., Roberts S.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
131 TaxID=44271;
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10-APR-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-90205976; PubMed-2320059;
Miller R.A., Reed S.G., Parsons M.;
"Leishmania gp63 molecule implicated in cellular adhesion lacks
Arg-Gly-Asp sequence.";
                                                        45;
Length 1655;
                                                                                                                                                                                                                  SGY----GNGADVGOGADNSTIELTQNGFRNNATID-------
                                                                                                                                                                                                                                                                                                                           DIT--VGQYGGNNAAL-----VNQTASDSSVMVRQVGFGNN 145
                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                        90;
  11.3%; Score 88.5; D 25.2%; Pred. No. 8.1; ive 17; Mismatches
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InterPro; IPR00157; Peptidase MB:
Pfam: PF01457; Peptidase MB: I
PRINTS; PR00782; LSHMANOLYSIN.
                                                   17;
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EMBL; M28527; AAA29235.1; -.
PIR; A44951; A44951.
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                               Local Similarity
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01-APR-1990
10-OCT-2003
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  Query Match
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STRAIN=Gregon-R;

MEDILINE=91293102; PubMed=1712294;

MEDILINE=91293102; PubMed=1712294;

Mevel-Nimio M.T.M., Terracol R., Kafatos F.C.;

Mevel-Nimio M.T.M., Terracol R., Kafatos F.C.;

Mevel-Nimio M.T.M., Terracol R., Kafatos F.C.;

Mevel-Nimio M.T.M., Terracol R., Kafatos F.C.;

Mevel-Nimio M.T.M., Terracol R., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kafatos A., Kaf
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Bukaryota; Mecazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 599;
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PROSITE; PS00142; ZINC_PROTEASE; 1.

Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zymogen; Signal; Cell adhesion; GPI-anchor; Lipoprotein.

SIGNAL 1 39 POTENTIAL.

PROPEP 40 97 ACTIVATION PEPTIDE.
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01-0CT-1996 (Rel. 34, Created)
10-CCT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 2.8;
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MEDLINE=95021209; PubMed=7935398;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformetics and the EMBL outstation—the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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TRANSFAC; T00669; ...
TRANSFAC; T00669; ...
Flyasee, Feguno00208; ovo.
InterPro; IRR007087; Znf C2H2.
Ffam; PF00096; zf-C2H2; 3.
SMART; SM00355; ZnF C2H2; 4.
PROSITE; PS00028 ZINC_FINGER C2H2_1; 3.
PROSITE; PS00157; ZnC_FINGER C2H2_2; 3.
Zinc-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein; Cranscription regulation.
DOMAIN 72 77 POLY-ALA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;; Score 87.5; DB 1; Length 1028;
;; Pred. No. 5.7;
11; Mismatches 58; Indels 47;
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EMBL, X59772; CAB36921.1; ALT_SEQ.
PIR; A56038; A56038.
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Best Local Similarity 25.63
Matches 40; Conservative
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969 99
647 64
1028 AA;
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Perfect score:

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Sequence:

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Minimum DB Maximum DB

Database

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SECUENCE FROM N.A. MEDLINE=98053981; PubMed=9393832; MEDLINE=98053981; PubMed=9393832; Sukupolvi S.S., Lorentz R.G., Gordon J.I., Bian Z., Pfeifer J.D., Normark; S.J., Rhen M.; "Expression of thin, aggregative fimbriae promotes interaction of Salmonella typhimurium SR-11 with mouse small intestinal epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmoneila typhimurium.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
NCBI_TaXID=602;
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EMBL, AJ000514; CAA04151.1; -.
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01-JAN-1998 (TrEMBLrel. 05, Le
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AgfA protein (Fragment).
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Q8cw63 escherichia
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Q54069 salmonla
Q9535 escherichia
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Q7x244 citrobacter
Q8eih4 shewahella
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Q80313 brigella fl
Q8cw64 escherichia
Q80ck5 bradyrhizob
Q99358 escherichia
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Q9kkb2 israeli tic Q9kb2 israeli tic Q8y106 ralstonia s Q83916 bradyrhizob Q93397 cyprinus ca Q89ev2 bradyrhizob Q8eih3 shewahella Q9vix6 drosophila P71868 mycobacteri Q7tw98 mycobacteri Q9kka8 rickettsia

Q88hgo pseudomonas Q8ev84 mycoplasma Q98ln6 rhizobium 1 Q7x238 enterobacter Q7x241 citrobacter Q8ewd6 mycoplasma Q8efu3 shewanella Q9xcj4 salmonella Q8zn57 salmonella

Q7v8s5 prochloroco Q8eyy9 leptospira Q8u6n9 agrobacteri

Q89ji5 bradyrhizob Q9vix5 drosophila O33801 salmonella Q89ji4 bradyrhizob

SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAXNSDITVGQYGG 120 61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ Gaps .; 0 Length 152; 12; Indels Score 682; DB 2; Pred. No. 1.7e-46; 4; Mismatches 12; 121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151 Query Match 87.4%; Best Local:Similarity 89.4%; Matches 135; Conservative 61 日  $\stackrel{>}{\circ}$ 엄 ò

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Result

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Q7X243; Q7X243

RESULT 2 27X243

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SDARKSETTITOSGYGNGADVGOGADNSTIELTONGFRNNATIDOWNAKNSDITVGOYGG 120
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
MEDLINE=22388234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Welch R.A., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mayhew H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKLLKVAAFAAIVVSGSALAGVVPOW-GGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHAL
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Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Enterobacter.
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Major curlin subunit precursor.
CSGA OR C1306.
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Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002)
EMBL; AE016759; AAN79779.1; -.
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STRAIN=Fec39;
Zogaj X., Bokranz W., Nimtz M., Romling
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SOGNATIVE FEC2;
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SOGNATIVE FECA:
SOGNATIVE FECA:
SOGNATIVE FECA:
SOCIATION OF CALLULOSE AND CULTI FIND TO BE SOCIATION OF CALLULOSE AND HUMAN GASTROINTESTINAL Tract.",
INFECA: IMMUN. 72:+4151-4158 (2003).
SERBL, ASSISTON, CADSSOGNAT.1;
SEQUENCE 150 AA; 15016 MW; 1D7141B8D6973DC6 CRC64;
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ZOGAIX., Bokranz W., Nimtz M., Romling U.;
ZOGAIX., Bokranz W., Nimtz M., Romling U.;
ZOGAIX., Bokranz W., Nimtz M., Romling U.;
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 72:4151-4158(2003).
EMBL; AJ515701; CAD56675.1;
SEMBL; AJ515701; CAD56675.1;
SEMBL; AJ515701; CAD56675.1;
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Last annotation update)
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(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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NNAALVNQTASDSSVMVRQVGFGNNAPANQY 151
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NCBI_TaxID=213763,
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Best Local Similarity
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"Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract."; Infect. Immun. 72:4151-4158(2003).
EMBL, AJ515702; AZ5566781; -. SEQUENCE 150 AA; 15112 MM; SD8B32D872DF15F3 CRC64;
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NGBI_TaxID=592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cox J.M., Eglezos S., Woolcock J.B.;
"Virulance of Salmonella enteritidis in chickens correlates with
colony morphology and expression of SEF17 fimbriae.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 6.6e-17;
                                                                                                                                                                                               21; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Curlin subunit monomer (Fragment).
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                                                                                                                                                 DB 2;
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1 Similarity 55.1%; Pred. No. 1.8e-26;
92; Conservative 21; Mismatches 21
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(TrEMBLrel. 01, I
(TrEMBLrel. 19, I
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NON TER 76 76
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01-NOV-1996 (TrEMBLrel. 0
01-DEC-2001 (TrEMBLrel. 1
SEF17 fimbrin (Fragment).
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1640 OFGGGGNSNGGQSWGTSSGSDWN------CÓSNVOES-TTTSSGGWGS---- 1680
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Tetrahymena thermophila.
Eukaryota, Alveolata, Ciliophora, Oligohymenophorea, Hymenostomatida,
Tetrahymenina, Tetrahymena.
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MADLINES #81898111, PubMed=3357771;

MATTINGALE D.W., Taylor F.M.;

"Multiple introns in a conjugation-specific gene from Tetrahymena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q94821 PRELIMINARY, PRT; 1748 AA.
Q94821; P92146; P92145; P92144; P92143; P92141; Q94820;
Q1-FBH-1997 (TYEMBLrel. O2, created)
Q1-FBH-1997 (TYEMBLrel. O2, Last sequence update)
Q1-OCT-2003 (TYEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40;
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MEDILIRE=940011569; PubMed=8233798;
MEDILIRE=940011569; PubMed=8233798;
Taylor F.M., Martindale D.W.;
"Retroviral-type zinc fingers and glycine-rich repeats in a gent ecrowiral-type zinc fingers and glycine-rich melosis.";
encoded by cnjB, a Tetrahymena gene active during meiosis.";
Nucleic, Acids cas, 21.4610-4614(1993);
EMBL; X06462; CAB37323.1;
EMBL; X06462; CAB37323.1;
EMBL; S0642136; S42136;
HSSP; P05888; 1AAPF.
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56 I -> N (IN REF. 1).
199624 MW; 0B03F210104008A3 CRC64;
                                                                                                                                                                                                                                                                                          Score 122, DB 2; Length.
Pred. No. 0.0042;
1; Mismatches 2; Indel
                                                                                                                                                                                                                                                     29 AA; 2789 MW; E290DFC07ABBB243 CRC64;
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Nucleic Acids Res. 16:2189-2201(1988)
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Gaps

15;

Indels

Length 151;

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Q8EIH4 RESULT 9 Q8EIH4

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52 ALSSAAQAANTSTTVQVGLVNGSSVTQNGLTNDSSSTTQIGILNGASTMQGTSSPS---- 107
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Zogaj X., Bokranz W., Nimtz M., Romling U.;
"Production of Cellulose and Curli Fimbriae by Members of the Family
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 72:4151-4158 (2003).
EMBL; AJS15700; CAD56671.1; -.
SEQUENCE 151 AA; 16158 MW; BD00AF57E1400704 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=USDA 110;
MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamurra Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watenabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
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DNA Res. 9:189-197(2002. USDA Res. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2005. USDA RES. 9:189-197(2
                                                                                                                                                                                                                                                                                                                                                                                                                                                  47 VTRVVTHEMAHALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFR----
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Enterobacteriaceae; Shigella.
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Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Bradyrhizobiaceae, Bradyrhizobium.
NCBI_TaxID=375,
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Last sequence update)
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Local Similarity 36.6%; Pred. No. 0.44;
nes 34; Conservative 10; Mismatches 39;
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                                                                                                                                                                                                                                                                                    14.2%; Score 110.5; DB
25.0%; Pred. No. 0.24;
ive 26; Mismatches
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01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
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07UCZ1
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MEDLINE-2297686; PubMed=12368813;

MEDLINE-2297686; PubMed=12368813;

Heidelberg Jr., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Sechadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam M., Lee K., Berry K., Lee C., Wueldman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; Shewanella oneidensis."
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                 1681 -SGSGNQ----TGGGWGSN---DNQQQQNBNTGGGGWGSSNS---NQTNNESS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
NCBI_TaxID=213763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36;
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SEQUENCE 502 AA; 52441 MW; D08CA23D6C46B62D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Nucleation component of curlin monomers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.5%; Score 113; DB 16; 26.0%; Pred. No. 0.64; ive 20; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 GNNAALVNQTASDSSVMVRQVGFGN----NATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348 DNNELVAFATGEDNSIEISQEGDANFAYVDATGN 381
                                                                                                                                                                                                                                                                                                                                                                              502 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nat. Biotechnol. 20:1118-1123(2002).
EMBL; AE015532; AAN53941.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conserved hypothetical protein.
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                                                                                                                                                                          1723 WGSNNQAS 1730
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                                                                                             149
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SEQUENCE FROM N.A.
STRAIN=Fec2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM N.A.
                                                                                             142 FGNNATAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=70863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IIGR; S00865; -.
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Citrobacter sp.
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70 ITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQT 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : |:|| | : | | | ::| | | ::| | | ::| | | ::| | ::| | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | ::| | | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | :
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 FAAIVVSGSALAGVVPQWGGGGNHNGGCNSSGPDYDQLVTRVVTHEMAH----ALQSDAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
                                                                                                                                                                                                                                                                               STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang V., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.
Sun D., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res: 9:189-197(2002).
EMBL; AP005963; BAC53057.1; -.
                                                                                                                                              Bacceria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
NCBL_TaxID=623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 107.5; DB 16; Length 160;
Pred. No. 0.45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bradyrhizobium japonicum.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Bradyrhizobiaceae, Bradyrhizobium.
NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1209 AA; 118292 MW; 50F97581D524EB71 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 AA; 16919 MW; 50269F5268D2A32F CRC64;
01-JUN-2003 (TrEMBLrel. 24, Created) 01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Minor curlin subunit precursor, similar ro CsgA. CSGB OR SF1035.
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Last annotation update)
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25.0%; Pred. No. 5.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Mismatches
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MEDLINE=22484998; PubMed=12597275;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 AYGNTAMIIQKGSGNKANITQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB015131; AAN42658.1; -.
Complete proteome.
SEQUENCE 160 AA; 16919 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 35.4*
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                   Shigella flexneri.
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome.
SEQUENCE 1209 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Yu J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQT 129
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                                        SEQUENCE FROM N.A.
STRAIN-24577 / ATCC 700930 / Serotype 2a;
MEDINE-25590274; PubMed-12704152.
Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
Man B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
Schwartz D.C., Blattner F.R.;
"Complete genome sequence and comparative genomics of Shigella
"Idenneri serotype 2a strain 24577";
Infect. Immun. 71:277-2786 (2003).
EMBL; AE016981; AAP16542.1;
SEQUENCE 151 AA; 15868 MW; 5D5D266B964014A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bscherichia coli 06.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
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Pred. No. 0.45;
9; Mismatches 43; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                     DB 16; Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Minor curlin subunit precursor.
CSGB OR C1305.
                                                                                                                                                                                                                                                                                                                                                                                                                                     43;
                                                                                                                                                                                                                                                                                                                                                                                  Score 107.5; DE
Pred. No. 0.42;
9; Mismatches
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segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use, of thin aggregative finbriae (SERI/TAR) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the back into the chromosome of the homologous species, replacing the native
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1 MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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genesegp2004s:*
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PA XX	(UYVI)	-) CINIA	/ VICTORI	RIA.					
PI	White	AP, D	Doran JL	0	olli	son SK,	Kay ww;		
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Y L L L	Recombii which en	nant icod use	agfA ges fore	gn	having epitope iciting	a Lox	egment replaced ) antigen, expresi wne response in	oy a foreign ses recombina animal.	DNA sequence nt AgfA
X & S	Disclo	osure;	Page 13	37; 13	39pp	; Engli	sh.		
¥88	The p	present	invention	ion de	scrib	es a	recombinant ag	agfA gene (I) whe	where a

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comprising separating an amino acid polymer comprising a recombinant Agfa protein containing a replacement segment or segments of foreign amino acid polymer comprising a recombinant Agfa protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or can be contained as a contained and introducing the complymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant Agfa protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copiess/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and incompanies the inserted epitope, and hybrid fimbriae are easy and incompanies the inserted epitope, and hybrid fimbriae are easy and incompanies the exemplification of the present invention
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0
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Best Local Similarity
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure, Page 138; 139pp; English

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The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative finbriae (SEP1/7PR) mucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant of AgfA, CsgA and AgfA.homologue fimbrin subunits, respectively, (2) directing recombination of a recombinant gene into the chromosome of the homologues species, replacing the native copy of that gene, and (4) eliciting an immune response in an animal, copy of that gene, and (4) eliciting an immune response in an animal, copy of that gene a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant AgfA protein which is useful for system the heterologues arigines are presented in high numbers (up to 500,000 copies/Cell), the hybrid finbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live function, the numbers of mortant for directing an immune response
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid finbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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89.9%; Pred. No. 3.7e-64;
ive 0; Mismatches 0; Indels
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Best Local Similarity 89.9
Matches 143; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AgfA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9425598-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-NOV-1994.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR74625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR74625
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(UYVI-) UNIV VICTORIA INNOVATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW23570 standard; protein; 151
                                                                                                                                                                                                                                                               89.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94US-00233788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 90.7
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kay WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
                                                                                                                                                                                                                                             Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collinson SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-APR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US5635617-A.
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                                                                                                                                                                                                                                                                                                                                                                                                          121
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                                                                                                                                                                                                                                                                                                                                                                                       121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                    SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                  an immune response to Salmonella - using attenuated Salmonella vector constructs, or compsns. contg. fimbrial type proteins.
                                                                                                             immunization compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                                                                                                                                  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGFDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are:
                                                                                                                                                                                                              1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                           Gaps
                                                                                                  Salmonella AgfA protein and DNA are used in vaccine and genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene replacement; fimbrin; epitope;
                                                                                                                                                                                            ..
                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella enteritidis AgfA amino acid sequence SEQ ID NO:5.
                                                                                                                                                                      Length 151;
                                                                                                                                                                                            Indels
  Doran JL;
                                                                                                                                                                      Score 689; DB 2;
Pred. No. 4.1e-62;
3; Mismatches 11;
                                                  Eliciting an immune response to Salmonella -
                                                                                                                                                                                                                                                                                                            NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kay WW;
 Clouthier SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 135; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collison SK,
                                                                                                                                                                                                                                                                                                                                                                   AAB36341 standard; protein; 151 AA
                                                                              7B; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   a; agfA; chromosomal
immune response; imm
                                                                                                                                                                      89.08;
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                                                                                                                                                                                             Conservative
 SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella enteritidis
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                    WPI; 1994-358275/44.
N-PSDB; AAQ87467.
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                                                                                                                                                                                Local Similarity
les 137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella; agfA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAC64617
                                                                                                                                                    Seguence 151 AA;
                                                                               Disclosure, Fig
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                                                                                                                                                                                                                                                                                                                                                                                        AAB36341;
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                                                             strains,
                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine;
Kay WW,
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Matches
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assembly system of strains of Salmonella, Escherichia coll and assembly system of strains of Salmonella, Escherichia coll and assembly system of strains of Salmonella, Escherichia coll and canteriaceae for the production of finbriae comprising recombinant of a recombinant gene into the chromosome of the homologous species, respectively; (2) directing recombination of a recombinant gene book into the chromosome of the homologous species, replacing the native comprising species, of the homologous species, replacing the native comprising separating an animal and separating an animal or sequence of the homologous species, replacing the native comprising separating an animo acid polymer comprising a recombinant define protein containing a replacement segment or sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequence of sequences of sequences of sequences of sequences of sequences of sequences of sequences of sequences of sequences of sequences of sequences of sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 689; DB 3;
Pred. No. 4.1e-62;
3; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella enteritidis 27655-3b agfA.
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Page 138; 139pp; English
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nes 136; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SDARK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                          Sequence 151 AA;
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                      Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                61 SDARKSETTITQSGYGNGADVQQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                 The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 2765-3b. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide proposes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                   09
                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                       1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                            Isolated Salmonella gene agfA - used for diagnosis of Salmonella or enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella, agfA, chromosomal gene replacement, fimbrin, epitope, vaccine, immune response, immunogen.
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                                                                                                                                                                                                                                                     Length 151;
                                                                                                                                                                                                                                                                          12; Indels
                                                                                                                                                                                                                                                    Score 684; DB 2;
Pred. No. 1.3e-61;
                                                                                                                                                                                                                                                                                                                                                                                            151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid sequence SEQ ID NO:28,
                                                                                                                                                                                                                                                                                                                                                                                                                   121 NNPALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                           3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB36354 standard; protein; 151
                                                                              Example 2; Fig 7; 85pp; English
                                                                                                                                                                                                                                                     88.4%;
90.1%;
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                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 90.1
Matches 136, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella enteritidis.
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           WPI; 1997-309886/28.
N-PSDB; AAT74142.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli.
Synthetic.
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N-PSDB; AAC64630.
                                                                                                                                                                                                                                 Sequence 151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB36354;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitepe or antigen. Also described are: (I) use of thin aggregative finbriae (SEP1/7RF) nucleation depended assembly system of strains of Salmonella. Escherichia coli and Enterposateriaceae for the production of finbriae comprising recombinant of a recombination of a recombinant of a recombinant gene into the chromosome of the homologous species, replacing the native comprising species, and (4) eliciting an immune response in an animal, we comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. Coli or acid sequence or sequences grown on a Salmonella, E. Coli or Enterobacteriaceae host cell. from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluter. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogens, which may be important for directing an immune response con manaled are are usually strong animal protein are are usually strong animal properties are usually strong animal properties are usually strong animal protein are passed and are presented and are passed and are passed and are passed and are passed and are passed and are passed and are passed and are passed and are passed and are passed and are passed and are passed and are passed and are passed and are passed and are passed and are passed and are passed and are passed and are passed and are passed and are passed and are passed and are passed and are passed and are passed and are passed and are pas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 WNAKNSDITVGQYGGNNAALVNQTASDSSVWVRQVGFGNNATANQY
protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.5%; Score 662; DB 3;
ilarity 81.9%; Pred. No. 2.3e-59;
Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AgfA::PT3#4 amino acid sequence SEQ ID NO:18.
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Salmonella enteritidis. Escherichia coli.

Synthetic.

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epicope or antigen. Also described are: (1) use of thin aggregative finbries (SEPI)/TAP) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Entertage and AgfA-homologue fimbrin submits, respectively; (2) directing recombinant of a recombinant gene into the chromosome of the homologue species; (3) directing recombinant gene into the chromosome of the homologue species; replacing the native comprising separating a manno acid polymer comprising recombinant gene copy of that gene; and (4) eliciting an immune response in an animal, comprising separating a replacement segment or segments of foreign amino acid solver comprising a replacement segment or segments of foreign amino acid segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino set discreting actions and introducing the polymer into the animal in conjunction with a carrier or dilutent. (I) is eliciting an immune response in an animal. In a finbrial presentation system the hererologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid finbrin protein possesses both the immunogens, which may be important for alrecting an immune response in an animal processive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                   Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GQGADNSTIELTQNGF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPD-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----YDQLVTRVVTHEMAHALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNNATIDOWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 622; DB 3;
Pred. No. 2.8e-55;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AgfA::PT3#6 amino acid sequence SEQ ID NO:22.
                                                                                 Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SDARKYDQLVTRVVTHEMAHA-------
                                                                                                                                                                                                                                                                   Disclosure, Page 136; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine; immune response; immunogen.
                                                                                 Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB36351 standard; protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                     (UYVI-) UNIV VICTORIA.
                                                                               White AP, Doran JL,
                                                                                                                       WPI; 2000-672631/65.
N-PSDB; AAC64625.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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segment of the gene has been replaced by a segment of the gene has been replaced by a segment of the gene has been replaced by a segment of the gene has been replaced by a segment of the gene has been replaced by a segment of the agreement of strains of salmonella. Then morpates of secretariates of salmonella. Becherichia coli and Buterobacteriaceae for the production of fimbriae comprising recombinant of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene in immorphism of the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene in immorphism of a recombinant gene on the chromosome of the homologous species; replacing the native copy of that gene; and (4) eliciting an immore response in an animal, comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino acid polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --YDQLVTRVVTHEMAHAGQGADNSTIELTQNGFR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKLLKVAAFPAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a recombinant agfA gene (I) where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.0%; Score 619; DB 3; Length 151; 74.6%; Pred. No. 5.6e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHA----
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                                                                                                                                                                                                                                                                                                                                                  Kay WW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Page 137; 139pp, English.
                                                                                                                                                                                                                                                                                                                                                  Collison SK,
                                                                                                                                                                                                            05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                        99US-0127888P
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Matches 129, Conservative
                                                                                                                                                                                                                                                                                                   (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                  Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-672631/65.
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                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAC64627
                                                                                                                WO200060102-A2
                                                                                                                                                                                                                                                        05-APR-1999;
                                                                                                                                                            12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                  White AP,
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x 
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                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                   Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen.
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                                                                                            AgfA::PT3#1 amino acid sequence SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                                         Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 135; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                         Collison SK,
           AAB36346 standard; protein; 151 AA
                                                                                                                                                                                                                                                                          05-APR-2000; 2000WO-CA000356.
                                                                (first entry)
                                                                                                                                                         Salmonella enteritidis.
Escherichia coli.
Synthetic.
                                                                                                                                                                                                                                                                                                                              (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                         White AP, Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-672631/65.
N-PSDB; AAC64622.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 122; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 151 AA;
                                                                                                                                                                                                                    WO200060102-A2.
                                                                                                                                                                                                                                                                                                    05-APR-1999;
                                                                 26-FEB-2001
                                                                                                                                                                                                                                               12-OCT-2000.
                                      AAB36346;
AAB36346
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1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative fimbriae (SET17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and the construction of strains of strains of the production of fimbriae compirating recombinant Garecting recombinant gene into the chromosome of the homologous species, respectively; (2) directing recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA comprising separating an amino acid polymer comprising a recombinant AgfA comprising containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or and sequence or sequences grown on a Salmonella, E. coli or colymer into the animal in confidention with a carrier of diluter. (I) is useful for the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid finbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier finbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response capainst the inserted epitope, and hybrid finbriae are essually strong incurpansive to purify in large amount. The present sequence is given in
                                                  61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQXGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella, agfA, chromosomal gene replacement, fimbrin, epitope; vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AgfA::PT3#2 amino acid sequence SEQ ID NO:14.
                                                                                                                                                                                           121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                            121 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 136; 139pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB36347 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-APR-2000; 2000WO-CA000356.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella enteritidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAC64623.
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WO200060102-A2
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                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                 SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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SDARKSETTIIQSGYGNGADVGQGADNSTIELIQNGFRNNATIDQWNAKNSDIIVGQYDQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CSBA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the homologous species; (3) directing recombinant of a recombinant gene.
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                                                                                                1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                        1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                        gene replacement; fimbrin; epitope;
                                                                        .;
                                               Length 151;
                                                                       22; Indels
                                               Score 609; DB 3;
Pred. No. 5.8e-54;
6; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                AgfA::PT3#7 amino acid sequence SEQ ID NO:24.
the exemplification of the present invention
                                                                                                                                                                                                  121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kay
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                                                                                                                                                                                                                                                                                                                                                                                                     vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Collison SK,
                                                                                                                                                                                                                                                                                       AAB36352 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                        agfA; chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-APR-2000; 2000WO-CA000356
                                               78.7%;
81.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0127888P
                                                                                                                                                                                                                                                                                                                                        (first entry)
                                              Query Match 78.7
Best Local Similarity 81.5
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000-672631/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli
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N-PSDB; AAC64628.
                         Sequence 151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) useful for the expression of recombinant AgrA protein which is useful eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 'copies/cell', the hybrid fimbrin protein possesses both the immunogénicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 606; DB 3; Length 151;
Pred. No. 1.2e-53;
5; Mismatches 22; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine; immune response; immunogen.
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82.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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N-PSDB; AAC64624.
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cc (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterbacteriaese for the production of fimbriae comprising recombinant of Enterbacteriaese for the production subunits, respectively, (2) directing recombination of a recombination of a recombinant gene (5) adirecting recombination of a recombinant gene (5) back into the chromosome of the homologous species, replacing the native (5) back into the chromosome of the homologous species, replacing the native (5) back into the draman and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino cof sequence or sequences grown on a Salmonella, E. coli or Enterbacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for celliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to copies/cell), the hybrid fimbrin protein see usually strong communogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response cagainst the inserted epicope, and hybrid fimbriae are easy and income constitution of the present invention
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O
                                                                                                                                                                                                                                                                                                                                                                                77.1%; Score 597; DB 3; Length 151; 81.5%; Pred. No. 9.8e-53; ive 5; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AgfA::PT3#3 amino acid sequence SEQ ID NO:16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 NNAALVNOTASDSSVMVRQVGFGNNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kay ww;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 81.5'
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-672631/65.
                                                                                                                                                                                                                                                                                                                                                      Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200060102-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     White AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA comparison encoded by a segment of the gene has been replaced by a segment of a foreign DNA comparison to the modes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbrise (SETI/TAF) nucleation depended assembly system of strains of Salmonella. Escherichia coli and consequent of the production of fimbrise compirating recombinant consequences for the production of fimbrise compirating recombination of a recombination of a recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino conteining a replacement segment or segments of foreign amino conteining a replacement segment or segments of foreign amino conteining a replacement segment or segments of foreign amino conteining a replacement segment or segments of introducing the protein conteining a replacement segment or segments of foreign amino conteining a replacement segment or segments of foreign amino conteining an immune response in an animal. In a finbrial presentation system the heterologous antigens are presented in high numbers (up to concine, the carrier finbrial submit protein possesses both the immunogens, which may be important for directing an immune response in any immune response in any immune response in any immune response in any immune response in any immune response in any immune response in any immune response in any immune response in any immune response in any immune response in any immune response in any immune response in expression of the present invention requence is given in the exemplification of the present invention present sequence is given in
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella, agfA; chromosomal gene replacement; fimbrin; epitope;
vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli CsgA amino acid sequence SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 574; DB 3;
Pred. No. 2.2e-50;
6; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                               Disclosure, Page 136; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ź
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.2%;
ilarity 80.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 122; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200060102-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epicope or anigen. Also described are: (1) use of thin aggregative fimbries (SEPI/TAP) nucleation depended assembly system of strains of Salmonella Escherichia coli and Entertobacteriaceae for the production of fimbriae comprising recombinant of Entertobacteriaceae for the production of fimbriae comprising recombination of a recombinant gene into the chromosome of the homologue species; (3) directing recombinant gene into the chromosome of the homologue species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the coliciting an immune response in an animal. In a fimbrial presentation system the heterologus antigens are presented in high numbers (Up to 500,000 copies/cell), the hybrid fimbrin protein sare usually strong immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial submit protein are usually strong against the inserted epitope, and hybrid fimbriae are easy and much in the exemplification of the present invention
                                                                                                                                                                                                                                     Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                               Kay WW;
                                                                                                                                                                                                                                                                                                                           Disclosure; Page 135; 139pp; English.
                                                                                                                               Collison SK,
05-APR-2000; 2000WO-CA000356
                                         99US-0127888P
                                                                                   (UYVI-) UNIV VICTORIA
                                                                                                                               Doran JL,
                                                                                                                                                                      WPI; 2000-672631/65.
N-PSDB; AAC64619.
                                            05-APR-1999;
                                                                                                                               White AP,
```

0; Gaps 68.2%; Score 528; DB 3; Length 151; 68.9%; Pred. No. 1.1e-45; Live 20; Mismatches 27; Indels Best Local Similarity 68.99 Matches 104; Conservative Sequence 151 AA; Query Match

120 09 9 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ ò d à

SDARKYDOLVTRVVTHEMAHAGOGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 61

> d ð

120

121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151 

RESULT 15 ABR82651

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ABR82651 standard; protein; 151

ABR82651;

(first entry) 04-DEC-2003

subunit 15 kDa protein. E. coli CsgA XEXEXEX

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The invention relates to an isolated peptide capable of binding a mammalian plasma protein or of generating an immune response in a mammal selected from sequences shown in ABREAGE4. ABREAGE48.49. The peptide or antibody is useful for treating a bacterial infection in a human or animal or in the manufacture of a medicament for the prophylactic treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infection. The peptide that is immobilized on a solid support is also useful as a reagent for determining the ability of a plasma protein to bind to bacteria. The present sequence represents an E. coli
                                                                                                                                                                                                                                                                                                                                        New isolated peptide capable of binding a mammalian plasma protein, useful in the manufacture of a medicament for the prevention and/or treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infections.
Plasma protein; immune response; antibacterial; vaccine; gene therapy
                                                                                                                                                                                                                                                       Herwald H;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 41-42; 42pp; English.
                                                                                                                                                                                                                                                       Wikstroem M,
                                                                                                                                               30-JAN-2003; 2003WO-EP000943
                                                                                                                                                                                  31-JAN-2002; 2002GB-00002275
                                                                                                                                                                                                                      (HANS-) HANSA MEDICAL RES AB.
                                                                                                                                                                                                                                                     Bjoerck L, Olsen A,
                                                                                                                                                                                                                                                                                            WPI; 2003-646136/61.
                                      Escherichia coli.
                                                                                                                                                                                                                                                                                                               N-PSDB; ACF36153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 151 AA;
                                                                         WO200306446-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 kDa protein
                                                                                                            07-AUG-2003
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SDARKYDOLVŢRVVŢHEMAHAGOGADNSTIELTONGFRŅNATIDOWNAKNSDITVGQYGG 120 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ Gaps 0 67.6%; Score 523; DB 7; Length 151; 68.2%; Pred. No. 3.4e-45; ive 20; Mismatches 28; Indels 121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151 Query Match Best Local Similarity 68.2 Matches 103; Conservative -19 61 9 d 8 8 ò

9

completed: August 2, 2004, 14:48:26 : 45.9 secs Search co

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AFFLICANT: Clouthier, Sharon C.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Seed and Berry
STREES: Seed and Berry
STREES: Seed and Berry
STREES: Washington
CONTRY: Seattle
STATE: Washington
CONTRY: US.A.
ZIP: 98104-7092
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATENIA SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 35,570
TELECOMMUNICATION INFORMATION:
NAME: KING, JOSHUA
REJESTAATION NUMBER: 35,570
TELECOMMUNICATION NUMBER: 35,570
TELECOMMUNICATION NUMBER: 920043.403C2
TELECOMMUNICATION NUMBER: 920043.403C2
TELECOMMUNICATION NUMBER: 920043.403C2
TELECOMMUNICATION NUMBER: 920043.403C3
TELECOMMUNICATION NUMBER: 920043.403C3
TELECHANCE CHARACTERISTICS:
LENGTH 151 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: Amino acids
TYPE: Amino acids
TYPE: Amino acids
TYPE: Amino acids
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774
1 MKLIKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           389414 segs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

7-851-976B-8 8-291-609-8 8-401-136-8 8-850-554-8 8-276-852-34 8-322-34 8-332-011-16 8-332-013-16 8-382-619-16 8-899-575-34 8-899-575-34 8-899-575-34 8-899-575-34 8-899-575-34 8-899-575-34 8-899-575-34 8-899-575-34 8-899-575-34 8-899-575-34 8-383-619-16 8-899-575-34 8-383-619-16 8-899-575-34 8-383-619-16 8-383-619-16 9-425-880A-26 8-438-745-4								
74:5 9.6 304 1 US-08-29-609-8 74:5 9.6 304 1 US-08-401-136-8 73:5 9.6 304 3 US-08-401-136-8 73:5 9.5 211 1 US-08-270-534 73:5 9.5 211 1 US-08-132-716 73:5 9.5 211 1 US-08-38-77-16 73:5 9.5 211 1 US-08-38-77-16 73:5 9.5 211 1 US-08-38-619-16 73:5 9.5 211 1 US-08-99-575-34 73:5 9.5 211 1 US-08-99-575-34 73:5 9.5 211 1 US-08-99-575-34 73:5 9.5 211 1 US-08-99-575-34 73:5 9.5 211 1 US-08-99-575-34 73:5 9.5 211 1 US-08-99-575-34 73:5 9.5 211 2 US-08-90-475-89 73:5 9.5 211 2 US-08-99-575-34 73:5 9.5 211 3 US-09-975-39-16 73:5 9.5 211 4 US-09-495-880A-42 73:5 9.5 238 4 US-09-495-880A-42 73:5 9.5 238 4 US-09-495-880A-42 73:5 9.5 238 4 US-09-495-880A-42 73:5 9.5 238 4 US-09-495-880A-42 73:5 9.5 238 4 US-09-495-880A-42 73:5 9.5 238 4 US-09-495-880A-42 73:5 9.5 238 4 US-09-495-880A-42 73:5 9.5 238 4 US-09-495-880A-16 73:5 0.5 2386 4 US-09-495-880A-16 73:5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.	28	74:5	٠.	304	1	07-851-976B-		
74:5 9.6 304 1 US-08-401-136-8 73:5 9.5 211 1 US-08-554-8 73:5 9.5 211 1 US-08-137-011-16 73:5 9.5 211 1 US-08-137-011-16 73:5 9.5 211 1 US-08-37-91-16 73:5 9.5 211 1 US-08-387-874-16 73:5 9.5 211 1 US-08-383-619-16 73:5 9.5 211 1 US-08-383-619-16 73:5 9.5 211 2 US-08-383-619-16 73:5 9.5 211 2 US-08-383-619-16 73:5 9.5 211 2 US-08-383-619-16 73:5 9.5 211 2 US-08-383-619-16 73:5 9.5 211 5 PCT-US95-0874-3-34 73:5 9.5 211 5 PCT-US95-0874-3-34 73:5 9.5 211 5 US-09-495-880A-26 73:5 9.5 293 3 US-08-438-745-4 73:5 9.5 293 3 US-08-438-745-4 73:5 9.5 293 3 US-08-438-745-4 73:5 9.5 293 3 US-08-438-745-4 73:5 US-08-438-745-8 73:5 US-08-438-745-8 73:5 US-08-438-745-8 73:5 US-08-438-745-8 73:5 US-08-438-745-8 73:5 US-08-438-745-8 73:5 US-08-438-745-8 73:5 US-08-438-745-8 73:5 US-08-438-745-8 73:5 US-08-438-745-8 73:5 US-08-438-745-8 73:5 US-08-438-74	29	74:5		304	Н	-08-291-609-	ω	
74.5 9.6 304 3 US-08-850-554-8 73.5 9.5 211 1 US-08-176-852-34 73.5 9.5 211 1 US-08-176-852-34 73.5 9.5 211 1 US-08-322-730A-16 73.5 9.5 211 1 US-08-382-730A-16 73.5 9.5 211 1 US-08-899-575-34 73.5 9.5 211 1 US-08-899-575-34 73.5 9.5 211 1 US-08-899-575-34 73.5 9.5 211 1 US-08-899-575-34 73.5 9.5 211 1 US-08-899-575-34 73.5 9.5 211 1 US-08-899-575-34 73.5 9.5 211 2 US-08-99-575-34 73.5 9.5 211 4 US-09-729-597-16 73.5 9.5 211 4 US-09-495-880A-42 73.5 9.5 211 5 PCT-US93-0834-16 87 73.5 9.5 212 5 US-08-495-880A-26 73.5 9.5 293 3 US-08-495-880A-26 859, Application US/08233788A No. 5633617 ICANT: Doran, James L. ICANT: Ray, William W. ICANT: Collinson, Karen S. ICANT: Cloubier, Sharon C.	30	74:5		304	Н	-08-401-136-	æ	
73.5 9.5 211 1 US-08-276-852-34 73.5 9.5 211 1 US-08-133-011-16 73.5 9.5 211 1 US-08-133-011-16 73.5 9.5 211 1 US-08-387-974-16 73.5 9.5 211 1 US-08-387-874-16 73.5 9.5 211 1 US-08-899-575-34 73.5 9.5 211 1 US-08-999-575-34 73.5 9.5 211 2 US-08-999-575-34 73.5 9.5 211 2 US-08-997-75-34 73.5 9.5 211 2 US-08-997-75-34 73.5 9.5 211 4 US-09-787-08 73.5 9.5 211 5 PCT US9-08364-16 73.5 9.5 211 5 PCT US9-08364-16 73.5 9.5 211 5 PCT US9-08364-16 73.5 9.5 211 5 PCT US9-08364-16 73.5 9.5 238 4 US-09-495-880A-26 73.5 9.5 286 4 US-09-495-880A-26 73.5 9.5 238 4 US-09-495-880A-26 73.6 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5	31	74.5		304	m	-08-850-554-	œ	
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73 5 9.5 211 1 US-08-38-874-16 73 5 9.5 211 1 US-08-899-575-34 73 5 9.5 211 1 US-08-899-575-34 73 5 9.5 211 2 US-08-389-575-34 73 5 9.5 211 2 US-08-38-619-16 73 5 9.5 211 2 US-08-997-739-16 73 5 9.5 211 4 US-09-97-16 73 5 9.5 211 5 PCT-US93-08364-16 73 5 9.5 211 5 PCT-US93-08364-16 73 5 9.5 211 5 PCT-US93-08364-16 73 5 9.5 211 5 PCT-US93-08364-16 73 5 9.5 238 4 US-09-495-880A-42 73 5 9.5 238 4 US-09-495-880A-26 73 5 9.5 293 3 US-08-438-745-4 73 5 9.5 293 3 US-08-438-745-4 73 5 9.5 293 3 US-08-438-745-4 74 5 9.5 238-745-880A-26 75 75 75 75 75 75 75 75 75 75 75 75 75 7	2.5	73.5		211	н	-08-322-730A-1	16	
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73:5 9.5 211 1 US-08-899-575-34 73:5 9.5 211 2 US-08-839-575-34 73:5 9.5 211 3 US-08-937-739-16 73:5 9.5 211 4 US-09-720-597-16 73:5 9.5 211 5 PCT-US93-08164-16 73:5 9.5 211 5 PCT-US93-08164-2 73:5 9.5 211 5 PCT-US93-08164-16 73:5 9.5 211 5 PCT-US93-0816-2 73:5 9.5 211 5 PCT-US93-0816-2 73:5 9.5 238 4 US-09-495-880A-42 73:5 9.5 293 3 US-08-438-745-4 80.5533617 80.5533617 80.5533617 80.5533617 80.5533617 80.5533617 80.5533617 80.5533617 80.553617 80.553617 80.553788 80.553788 80.55378 80.553788 80.5	36	73.5		211	Н	38-899-575-3	34	
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73:5 9.5 211 4 US-09-720-537-16 73:5 9.5 211 5 PCT-US93-08364-16 73:5 9.5 211 5 PCT-US93-08743-34 73:5 9.5 218 4 US-09-495-880A-26 73:5 9.5 238 4 US-09-495-880A-26 73:5 9.5 293 3 US-08-438-745-4 873:5 9.5 293 3 US-08-438-745-4 873:5 9.5 293 3 US-08-438-745-4 88A-59 8 59, Application US/08233788A No.5633617 1CANT: Doran, James L. 1CANT: Ray, William W. 1CANT: Collinson, Karen S. 1CANT: Collinson, Karen S.	66	73:5		211	m	08-907-739-1	16	
73 5 9.5 211 5 PCT US93-08364-16 5 73.5 9.5 211 5 PCT US93-08364-16 5 73.5 9.5 218 4 US-09-495-880A-42 5 3 8 4 US-09-495-880A-42 5 5 238 4 US-09-495-880A-26 73.5 9.5 293 3 US-08-438-745-4 8 120APT S 10 S 293 3 US-08-438-745-4 8 11 USAPT Doran, James L. LICANT: Ray, William W. ICANT: Ray, William W. ICANT: Collinson, Karen S. ICANT: Collinson, Karen S. ICANT: Cluthier, Sharon C.	0.4	73.5		211	4	19-729-597-1	equence 16	
73:5 9.5 211 5 PCT US95-08743-34 873.5 9.5 238 4 US-08-495-880A-42 873.5 9.5 238 4 US-08-495-880A-26 873.5 9.5 293 3 US-08-438-745-4 843.5 9.5 293 3 US-08-438-745-4 853.5 9.5 293 3 US-08-438-745-4 853.5 9.5 293 3 US-08-438-745-4 853.5 9.5 293 3 US-08-438-745-4 853.5 9.5 293 3 US-08-438-745-4 853.5 9.5 293 3 US-08-438-745-4 853.5 9.5 293 3 US-08-438-745-4 853.5 9.5 293 3 US-08-438-745-4 853.5 9.5 9.5 293 3 US-08-438-745-4 853.5 9.5 9.5 9.5 9.5 9.5 9.5 9.5 9.5 9.5 9	4.	73.5		211	ın	-US93-08364-1	equence 16	
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73.5 9.5 293 3 US-08-438-745-4 S ALIGNMENTS ALIGNMENTS -788A-59 -59, Application US/08233788A No.5635617 LINFORMATION: LICHNIT Edsy, William W. LCANT: Collinoor Karen S. LCANT: Collinoor Karen S. LCANT: Collinoor Karen S.	4 4	73.5		266	4	-495-880A-2	e 26,	
ALIGNMENTS -788A-59 e 59, Application US/08233788A No.:563567 LICANT: Doran, James L. ICANT: Kay, William W. ICANT: Collinson, Karen S. ICANT: Collinson, Sharon C.	45	73.5		293	m	08-438-745-	Sequence 4, Appli	
ALIGNMENTS -788A-59 e 59, Application US/08233788A No. 5635617 LCANT: Doran, James L. ICANT: Kay, William W. ICANT: Collinson, Karen S. ICANT: Collinson, Karen C.								
-788A-59 e 59, Application US/08233788A No.:563567 LCANT: Doran, James L. ICANT: Kay, William W. ICANT: Collinson, Karen S. ICANT: Collinson, Karen C.						ALIGNMENTS		
788A-59 e 59, Application US/08233788A No.:5633517 ICANT: Doran, James L. ICANT: Kay, William W. ICANT: Collinson, Karen S. ICANT: Collinson, Raren C.		٠						
788A-59 6 59, Application US/08233788A 6 15.5635617 L INFORMATION: LONNT: Doran, James L. ICANT: Politinson, Karen S. ICANT: Collinson, Sharon C.								
-788A-59 e 59, Application US/08233788A NO.:5635617 NO.:5635617 ICANT: Doran, James L. ICANT: Ray, William W. ICANT: Ray, William W. ICANT: Collinson, Karen S. ICANT: Clouthier, Sharon C.	PESIILT							
e 59, Application US/08233788A No.:Se35617 LICANT: Doran, James L. ICANT: Ray, William W. ICANT: Collinson, Karen S. ICANT: Collinson, Karen C.	US-08-	233-788A-	o,					
Parent No. 5635617 GENERAL INFORMATION: APPLICANT: Dozan, James L. APPLICANT: Kay, William W. APPLICANT: Collinson, Karen S. APPLICANT: Clouthier, Sharon C.	: Seaut	ance 59, 7	Applicat	tion US	/08	233788A		
		1t No. 56	35617					
villiam W. Milliam W. Aszen S. Aszen, S. Aszen C.	GENE	SRAL INFO	RMATION					
: Kay, William W. : Collinson, Karen S. : Clouthier, Sharon C.	, AI	PPLICANT:	Doran	, James	ŗ.			
: Collinson, Karen S. : Clouthier, Sharon C.	, Ai	PPLICANT:	Kay,	William	3			
: Clouthier, Sharon C.	, A!	PPLICANT:	Collin	nson, K	are			
ECC	, Al	PPLICANT:	Clout	_	har	Ö.		

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TOPOLOGY: linear MOLECULE TYPE: protein

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                                                   61 SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                            61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Coran, James L.
APPLICANT: Collinson, Karen S.
APPLICANT: Collinson, Karen S.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TITLE OF INVENTION: OF SALMONELLA
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
CITY: Seattle
CONDITRY: U.S.A.
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,788A
                                                                                                                                                       NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                121 NNPALVNQTASDSSVMVRQVGFGNNATANOY 151
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CLASSIFCATION: 415
TORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REPERBNOE/POCKET NUMBER: 920043.403C2
TELEPANICATION INFORMATION:
TELEPANICATION INFORMATION:
TELEFAX: (206) 622-4900
TELEFAX: (206) 622-6931
TELEFAX: (216) 622-6931
TELEFAX: 1218346 SEEDANBERRY:
INFORMATION FOR SEQ ID NO: 57: SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                             Sequence 57, Application US/08233788A Patent No. 5635617 GENERAL INFORMATION:
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Sequence 27661, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:

RESULT 3 US-09-252-991A-27661

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Kunio NAKASHIMA et al.
FUNTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
FENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
FENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
FENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
FENTION: TO SAID POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 LFAVAAL-GLLFAGSTLLPGELSPVGSAYAKGGNGGGNGGGHSGGKGGSHGGNLGGHSSK 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 LLKVAAFAAIVVSGSAL-----LSIY 48
                                                                                                                                                                                                                                                                                                                                                                                                                                           15; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 QYGSANAALALQSDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQN 95
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM-TYPES Diskete, 3.50 inch, 1.44 MB storage COMPUTER: Diskete, 3.50 inch, 1.44 MB storage COMPUTER: IEM Comparible OPERATING SYSTEM: Microsoft Windows 95 SOFTWARE: Word Perfect 6.1 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 08 184459 FILING DATE: 15-July-1996 ATTORESY AGENT INFORMATION: NAME: C. Bruce Hamburg REGISTRATION NUMBER: 22.389 REGISTRATION NUMBER: F-5610 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEPHONE: (212)986-2340
                                                                                                                                                                                                                                                                                                                                                                                                                                           49;
                                                                                                                                                                                                                                                                                                                                                                                           ch 10.8%; Score 83.5; DB 4; 1. Similarity 29.0%; Pred. No. 0.35; 31; Conservative 12; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08864038A Patent No. 6001592 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Isshinden CITY: Tsu-city STATE: Mis-no-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
CONTITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mie-préfecture
: JAPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                 US-09-252-991A-27661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            514-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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279 NGTGDSG-VSALGGSGNGSGDGAGNGIASGNGEHNYGIGNG----NGDDVDITAPITGVL 333
                                                                                                                                                                                                                                                                                                                                                                                                                              75 THE-----MAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQ 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEE: No. 5667990o No. 5667990disk of No. 5667990th America, Inc.: 405 Lexington Avenue
New York
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                         334 NISGNSFTLIGNSSSSSVNTAPTTTSNTVNDNDTID--NGNSGCTGSGSGNGSGDGLLNG 391
                                                                                                                                                                                                                                                                                                                                           15 SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKYDQLVTRVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                      BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                        Length 975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Berka, Randy M.
APPLICANT: Yoder, Wendy
APPLICANT: Takagi, Shinobu
APPLICANT: Boominathan, Karuppan C.
AITLE OF INVENTION: ASPERGILLUS EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/458,023B
FILING DATE: 01-JUN-1995
CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28;
                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.1%; Score 78; DB 1
30.7%; Pred. No. 2.9;
cive 13; Mismatches
                                                                                                                                                                                                                                                                                                 19; Mismatches
                                                                                                                                                                                                                                                        10.3%; Score 79.5;
25.0%; Pred. No. 8;
TITLE OF ENVENTION: BAUMANNII FOR DIAGNOS.
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
ERQ ID NO 4764
LENGTH: 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08458023B
Patent No. 5667990
                                                                                                                                                                     TYPE: PRT ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Lowney Dr., Karen A.
REGISTRATION NUMBER: 31,274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TASDSSVMVRQVGFGN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     392 AASGNGEHNYGIGNGN 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 363 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
INFORTH: 363 mmino acidi
                                                                                                                                                                                                                                                                                                   34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                          Best Local Similarity Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Berka,
                                                                                                                                                                                                                US-09-328-352-4764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18, Application US/09498520A

Batent No. 661353

GENERAL INFORMATION:
APPLICANT: Rock, Charles O
APPLICANT: Heath, Richard J
TITLE OF INVENTION: No. 661353el Enoyl Reductases and Methods of Use Thereof
FILE REFERENCE: SJ-0022
CURRENT APPLICATION NUMBER: US/09/498,520A
CURRENT FILE OF DINOS: 62
NUMBER OF SD ID NOS: 62
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                      ARKYDQL----VTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 LKAAGLKVMVVCGAVKHAVKAEQAGCDAVICQGGEGGGHTGLVGTLPLVAQAVEAVKIPV 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216 AADEDTVRTRCYSGKPMRVKKNPYVDDWEARPGDIQPFPQQAMVSIRNGAMGGIGGQIEG 275
                                                                                                                                                                                                                                                                                                                                             419 LLKSSASASASASASASAG-----GGGGGGNGGGNGGGGG------GGAGALAALAA 465
                                                                                                                                                                                                                                                                                                                                                                                                                              ----- GGL 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 VAAGGLHDG------RGLA-AALALGAQG---VWMGTRFIASHEAHAGDLYRQAVVE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 GADNSTIEL-TQNG----FRNNATIDQMNAKNSDITV------GQYGGNNAALVN 127
                                                                                                                                                                                                                                                                                                   LLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD
                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                           Indels 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69;
                                                                                                                                                                                                                Length 738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                              466 AGAGGGIGGGGGGALAAALAAAGAGG------GGFGGLGGL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGNNAALVNQTASDSS-----VMVRQVGFGNNATA 148
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                                                                                                                                                                                                                                                           26;
                                                                                                                                                                                                                DB 3;
                                                                                                                                                                                                                Query Match
10.8%; Score 83.5; Di
Best Local Similarity 27.7%; Pred. No. 2;
Matches 44; Conservative 12; Mismatches
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Conservative 15; Mismatcher
                                                                                                         NAME/KEY: peptide
LOCATION: from 1 to 738
IDENTIFICATION METHOD: E (by experiment)
                      ORIGINAL SOURCE:
ORGANISM: Pinctada fucata
CELL TYPE: mantle epithelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caulobacter crescentus
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Best Local Similarity
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US-09-498-520A-18
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US-09-498-520A-18
                                                                                                                                                                        US-08-864-038A-3
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TYPE: PRT
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                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Welinder, Karen
APPLICANT: Andersen, Morten B
APPLICANT: Andersen, Morten B
APPLICANT: Andersen, Morten B
APPLICANT: Andersen, Morten B
TITLE OF INVENTION: PEROXIDASE VARIANTS WITH IMPROVED
TITLE OF INVENTION: HYDROGEN PEROXIDE STABILITY
NUMBER OF SEQUENCES:
ADDRESSEE: No. 58518110 No. 5851811disk of No. 5851811th America, Inc.
STREET: New York
STREE: New York
-----PDSTLSI 47
                        58 YQ-GS-----KCESPVRK----ILRIVFHDAIGFSPALTAAGQFGGGADGSII 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90
                                                                                  48 YQYGSANAALALQSDARKXDQLVTRVVTHE------MAHAGQ----GADNSTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 YQYGSANAALALQSDARKYDQLVTRVVTHE-----MAHAGQ----GADNSTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38;
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNH---NGGGNSSG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUW TYPE: FLOSDY disk
COMPUTER: IBM PC COMPATIDLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,515A
FILING DATE: U1-NOV-1994
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/POCKET NUMBER: 38,711
REFERENCE/COCKET NUMBER: 3769.204-US
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09168406A
Patent No. 6258769
GENERAL INFORMATION:
APPLICANT: Wellinder, Karen G.
APPLICANT: Andersen, Morten B.
TITLE OF INVENTION: Peroxidase Variants With Improved
TITLE OF INVENTION: Hydrogen Peroxidase Stability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
10.1%; Score 78; DB 2
Best Local Similarity 30.7%; Pred. No. 3.8;
Matches 35; Conservative 13; Mismatches
                                                                                                                                                                                                           US-08-331-515A-2; Sequence 2, Application US/08331515A; Patent No. 5851811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-331-515A-2
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US-09-168-406A-2
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APPLICANT: Caughey, Byron W
APPLICANT: Chabry, Joseffe
APPLICANT: Chabry, Josefte
APPLICANT: Priola, Susette
TITLE OF INVENTION: Inhibitors of Formation of Protease Resistant Prion
FITLE OF INVENTION: Protein
FITLE OF TAPPLICATION NUMBER: US/09/128,450
CURRENT APPLICATION NUMBER: US/09/128,450
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 MKLSLLSTFAAVIIGALA---PQGPGGGGSVTCPGGQSTSNSQCCVWFDVLDDLQTNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
10.1%; Score 78; DB 3; Length 435;
Best Local Similarity 30.7%; Pred. No. 3.8;
Matches 35; Conservative 13; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNH----NGGGNSSG-
FILE REFERENCE: 3769.214-US
CURRENT APPLICATION NUMBER: 08/9168,406A
FRIOR APPLICATION NUMBER: 08/311,515
PRIOR PILING DATE: 1994-11-01
PRIOR PILING DATE: 1994-11-01
PRIOR PILING DATE: 1994-00-01
PRIOR PILING DATE: 1993-06-01
PRIOR PREDICATION NUMBER: 0792/92
PRIOR PREDICE SEQ ID NOS: 43
NUMBER OF SEQ ID NOS: 43
LENGTH: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1)...(435)
OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 26, Application US/09128450 Patent No. 6211149 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              ORGANISM: Coprinus cinereus FEATURE:
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TYPE: PRT
ORGANISM: Hamster sp.
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Matches 32, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: VARIANT
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US-09-128-450-26
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REGISTRATION NUMBER: 26591
REPERENCE/DOCKET NUMBER: 94
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3067
                                                                                                                                            TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 30.4%;
Matches 35; Conservative 1.
                                                                                                                                                                                                                                                                                            LENGTH: 364 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
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amino acid
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Best Local Similarity 26.2
Matches 37; Conservative
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MOLECULE TYPE: peptide
US-07-792-259-17
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US-09-056-556-204
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US-09-056-556-204
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GENERAL GENERAL GENERAL
TITLE OF INVENTION:
FOLIA
CURRENT FILING DATE:
CURRENT FILING DATE:
GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENER
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Patent No. 5286638

Patent INFORMATION:
APPLICANT: TANAKA, YOSHIKAZU
APPLICANT: ASHIKARI, TOSHIKAZU
APPLICANT: HATANAKA, HARUYO
APPLICANT: SHIBANO, YUJI
APPLICANT: SHIBANO, YUJI
APPLICANT: NAKAYAMA, TORU
APPLICANT: NAKAYAMA, TORU
APPLICANT: NAKAYAMA, TORU
APPLICANT: SUMIDA, MOTOO
TITLE OF INVENTION: PEROXIDE GENE OF MICROBIAL ORIGIN
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATEN: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/792,259
FILING DATE: 19911115
CLESSIFICATION: 43.5
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WAISON T.
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                                                                      Sequence 26, Application US/09823494 Patent No. 6355610
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ORGANISM: Hamster sp.
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                                      US-09-823-494-26
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US-07-792-259-17
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LENGTH: 254
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1 MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHN----GGGNSSG------PDSTLS 46
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Patent No. 6350456
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39;
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STATE: Washington
CONTRY: USA
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;; Pred. No. 3.3;
13; Mismatches
9437/93433
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TREAT

16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAA--LALQSDARKYDQLVT 71

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TYPE: PRT
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Job time
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464 GSGNIGVFNVGSGSLGNYNIGSGN-----LGIYNIGFGNVGDYNVGFGNAGDFNQGFA 516
                                              72 RVVTHEMAHAGQGADNSTIELT---QNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQ 128
                                                                                        517 NTGNNNIGFANTGNNNIGIGLSGDNQQGFN---IASGWNSGTGNSGLFNSGTNNVGIFNA 573
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 9.9%; Score 77; DB 4; Length 943; Best Local Similarity 26.2%; Pred. No. 14; Matches 37; Conservative 14; Mismatches 66; Indels
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COUNTRY: Washington

COUNTRY: USA

ZOMP: 98104-7092

COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Bub PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION MARER: US/09/072,596
FILING DATE: 0-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKY, DATA: 392
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELEPOWNICATION INFORMATION:
TELEPRACE (206) 622-4900
TELEPRACE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                              Sequence 199, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                         129 TASDSSVMVRQVGFGNNATAN 149
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RESULT 15

US-09-47-135A-131

US-09-47-135A-131

Sequence 131, Application US/09477135A

Patent No. 6572865

GENERAL INFORMATION:
MINIOR FRANCE

FILE OF INVENTION:
MINIOR PRINCE 2000-01-03

FILE OF INVENTION:
MINIOR PRINCE 1099-01-215

PRINCE APPLICATION NUMBER: US/09/477,135A

PRINCE PRINCE DATE: 1099-01-215

PRINCE APPLICATION NUMBER: US/09/477,135A

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US-90-411-80-43-64-4

Sequence 4; Application US/09741873B

Publication No. US20020081722A1

SEQUENCE 4: Application No. US20020081722A1

APPLICANT: Olsen, Arne
APPLICANT: Olsen, Arne
CURRENT FILMS DATE: US-08-084

CURRENT FILMS DATE: US-08-084

CURRENT FILMS DATE: US-08-064

PRIOR APPLICATION NUMBER: US 8801723-1

PRIOR APPLICATION NUMBER: US 08/978,878

PRIOR PRILING DATE: 1990-05-06

PRIOR FILING DATE: 1990-05-06

PRIOR FILING DATE: 1990-05-06

PRIOR PRIOR PRILING DATE: 1991-11-06

PRIOR FILING DATE: 1991-11-06

PRIOR FILING DATE: 1992-11-03

PRIOR FILING DATE: 1992-11-03

PRIOR FILING DATE: 1994-10-05

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NUMBER OF: SEQ ID NOS: 10

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SOFTWARB: VARIABE: US-08-06 06

SOFTWARB: VARIABE: US-08-06 06

SOFTWARB: VARIABE: US-08-06 06

SOFTWARB: VARIABE: US
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67.8%; Score 525; DB 12; Length 15
Best Local Similarity 68.2%; Pred. No. 6e-46;
Matches 103; Conservative 21; Mismatches 27; Indels
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GENERAL INFORMATION: Staffan
APPLICANT: Normark, Staffan
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084
CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR PILING DATE: 1999-05-04
PRIOR FILING DATE: 1991-11-03
PRIOR FILING DATE: 1994-11-03
PRIOR FILING DATE: 1994-01-28
PRIOR PELING DATE: 1994-01-28
PRIOR PELING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Version 3.0
SSEQ ID NO 2
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Best Local Similarity 64.9%; Pred. No. 5.2e-38;
Matches 85; Conservative 20; Mismatches 26;
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PRIOR APPLICATION NUMBER: SE 8801/23-1
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR PILING DATE: 1989-05-04
PRIOR PILING DATE: 1980-05-04
PRIOR PILING DATE: 1991-11-06
PRIOR PILING DATE: 1991-11-06
PRIOR PILING DATE: 1991-11-06
PRIOR PILING DATE: 1991-11-06
PRIOR PILING DATE: 1991-11-06
PRIOR FILING DATE: 1992-11-03
PRIOR FILING DATE: 1992-11-03
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-01-05
NUMBER OF SEQ ID NOS: 10
SORTWARE: PALENTIN VERSION 3.0
SORTWARE: PALENTIN VERSION 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Escherichia coli
US-09-741-873B-2
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US-US-141-8/18-4
US-US-141-8/18-4

Sequence 4, Application US/09741873B

Publication No. US20040096965A9

GENERAL INPORMATION:
APPLICANT: Olsen, Arme
APPLICANT: Olsen, Arme

TILE OF INVENTION: Elbronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012689-084

CURRENT FILING DATE: 2003-04-04

PRIOR APPLICATION NUMBER: US 08/978,878

PRIOR APPLICATION NUMBER: US 08/978,878

PRIOR APPLICATION NUMBER: US 07/347,189

PRIOR APPLICATION NUMBER: US 07/789,437

PRIOR FILING DATE: 1999-11-06

PRIOR FILING DATE: 1991-11-06

PRIOR FILING DATE: 1991-11-03

PRIOR FILING DATE: 1991-11-06

PRIOR FILING DATE: 1991-11-03

PRIOR FILING DATE: 1991-11-03

PRIOR FILING DATE: 1991-11-03

PRIOR FILING DATE: 1991-11-03

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APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 01289-004
CURRENT APPLICATION NUMBER: US/09/741,873B
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                 1 MKLLKVAAIAAIVESGSAVAGVVPQYGGGNHGGGGNNSGPNSELNIYQYGGGGNSALALQ 60
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Best Local Similarity 68.2%; Pred. No. 6e-46;
Matches 103; Conservative 21; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                         121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
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US-09-741-873B-2
, Sequence 2, Application US/09741873B
; Publication No. US20020081722A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---LOSDARKYDQ-----LVTRVVTHEMAHAGGGADNSTIELTON-GFRN 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 33;
                                                                                                                                                                                                                                                                                                                                                                                 DB 14; Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                 46; Indels
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12.2%; Score 94.5; DB
Best Local Similarity 25.9%; Pred. No. 0.39;
Matches 37; Conservative 27; Mismatches
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
SPRIOR FILING DATE: 2001-08-02
NUMBER OF:SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 49412, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 TGALLPWDAKNFD----KIGGKD 131
                                                                                                                                                                                                                                                                               ; TYPE: PRT;
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9343
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Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
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Yamamoto, Robert
Forsyth, R.
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US-10-282-122A-49412
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APPLICANT
TITLE OF I
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Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Hinkle, Gregory J.

APPLICANT: Gater, Yorgwei

APPLICANT: Gladman, Barry S.

APPLICANT: Gladman, Barry S.

APPLICANT: Gladman, Barry S.

APPLICANT: Gladman, Warleng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES

FILE REFREENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

SEQ ID NOS: 47374
                                                                                                                                                                                                       61 VGQGSDDSSIDLTQRGFGRSATLDQWNGRQNSEWTVKQFGGGGRGAAVDQTASNSSVNVTQV 120
                                                                                                                                                                               81 AGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQV 140
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                                                                             21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKYDQLVTRVVTHEMAH 80
                                                                                                             7 AAFAA-----IVVSGSALAGVVPQWGGGG-----GNSSGPDSTLSIYQY 50
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  Best Local Similarity 64.9%; Pred. No. 5.2e-38;
Matches 85; Conservative 20; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (1)..(445)
COTHER INFORMATION: unsure at all Xaa locations US-10-369-493-20638
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Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: HORIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: HATTORI, WASAHIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Rhodopseudomonas palustris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 26.vv
                                                                                                                                                                                                                                                                               141 GEGNNATANOY 151
                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
US-10-369-493-20638
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US-10-156-761-9343
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ORGANISM: Yersinia pestis
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE OF INVENTION: ELITRA.034A
CURRENT APPLICATION NUMBER: 0/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PELING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,727
PRIOR APPLICATION NUMBER: 60/2030,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PRIOR PAPLICATION NUMBER: 60/267,636
PRIOR PLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PLING DATE: 2000-12-20
PRIOR PRIOR DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 PA------DKAITLATVPAGSLASAGAVAGTSNPTDLQLSLTGCTGTATKAIARFENG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSS----GPDSTLSIYQYGSANAA 56
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 49412
LENGTH: 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 ATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                    Length 186;
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
11.8%; Score 91; DB 12; Length 186
Best Local Similarity 29.6%; Pred. No. 0.3;
Matches 50; Conservative 17; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 77944, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:
APPLICANT: Manor, Carlos
APPLICANT: Malone, Carlos
APPLICANT: Malone, Carlos
APPLICANT: Tamadio, Carlos
APPLICANT: Anone, Carlos
APPLICANT: Anone, Carlos
APPLICANT: Anone, Carlos
APPLICANT: Carro, Grant
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, Grant
APPLICANT: Yamanoco, Robert
APPLICANT: Yamanoco, Robert
APPLICANT: Yamanoco, Robert
APPLICANT: Yamanoco, Robert
APPLICANT: Yamanoco, Robert
APPLICANT: Yamanoco, Robert
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                                                                                                                                                                                                                                                                                                                    US-10-282-122A-49412
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1354 ILNGVSESIANVLSGVAGSTVDIIGGADTALTAN---NSGFLGQYALAGNSKLTV---- 1405
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                                                                                                                                                                                                         10 AAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKYDQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                       44; Gaps
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 67793
LENGTH: 6310
                                                                     DB 12; Length 3705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 6310;
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11.0%; Score 85; DB 12; Length 631
Best Local Similarity 23.7%; Pred. No. 1.1e+02;
Matches 40; Conservative 19; Mismatches 58; Indels
                                                                                                                                       55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1406 ---ASTNNLGASSSVALAGAGDTLSLSGFNGTFGNSVTGS 1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 NNAALVNQTASDSSVMVRQVG------FGNNATAN 149
                                                                 Query Match 11.0%; Score 85; DB 1
Best Local Similarity 23.8%; Pred. No. 57;
Matches 38; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 67793, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT AFFLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR ELLING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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US-10-282-122A-67793
US-10-282-122A-77944
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US-10-282-122A-67793
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82 -GNGSVATQVNSTAFGNLSTAAGTSATA-LGPGAHAMGDGSTAVGINAQATGVDSASLGV 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 AFAAIVVSGSALAGVVP------QWGGGGNHN-GGGNSSGPDSTLSIYQYG 51
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,930
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 QAIGSGAYSVAIGNISSATQSGAVAMGSGAAATGVAAIGIGNNAFASGQY 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
10.9%; Score 84; DB 12; Length 1129;
Best Local Similarity 27.1%; Pred. No. 16;
Matches 46; Conservative 20; Mismatches 72; Indels 3:
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APPLICANT Lu, Guihua
APPLICANT Zhang, Lingur
TITLE OF INVENTION: of Use
FILE REPRENCE: 1183
CURRENT APPLICATION NUMBER: US/09/810,264
CURRENT PILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: US 60/190,467
PRIOR APPLICATION NUMBER: US 60/190,467
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 278;
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Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 28, Application US/09810264; Patent No. US20020076775A1; Patent No. INFORMATION: APPLICANT! Crane, Virginia C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM Burkholderia cepacia
US-10-282-122A-48048
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20.8%;
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Famodu, Omolayo O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , OKGANISM: Triticum aestivum
US-09-810-264-28
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Best Local Similarity
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LENGTH: 1129
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US-09-810-264-28
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APPLICANT
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APPLICANT: I.M.S.E.R.M.
TITLE OF INVENTION: Polymucleotides which are of nature B2/D+ A- and which are isolat TITLE OF INVENTION: E.coli, and biological uses of these polymucleotides and of their FILE REFERENCE: BLANDINE US/10/238,075
CURRENT APPLICATION WINBER: US/10/238,075
CURRENT FILING DATE: 2002-09-10
PRIOR APPLICATION WINBER: 0003145
FRIOR FILING DATE: 2000-0310
NUMBER OF SEQ ID NOS: 1576
SOFTWARE: Patentin version 3.1
LENGTH: 1778
TYPE: PRI
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                                                                                                                                                                                                              55 AALALQSDARKYDQLVTRVVTHEMAHAGQGADNSTIEL-------TQNGFRNN 100
                                                                                                                                                                                                                                                                                                 -----APÁTPIDLLVS---PDGLRLTGRGEAGTTVNIRDAAGNLIGSGTVGADGNFNVT 207
                                                    AAIVVSGSALAGVVPQW-----GGGG----NHNGGGNSSG---PDSTLSIYQYGSAN 54
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APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 KVAAFAAIVVSGSALAGVVPQW----GGGGNHNGGGNSSGPDSTLSIYQYGSANAALAL-
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                                                                                                                               111 AGIGTAĞSAM----PTWALAGLSLLĞVĞĞAAAAADNĞĞĞĞSSĞĞSDPDTS----
                                                                                                                                                                                                                                                                                                                                                                                101 ATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATAN 149
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10.9%; Score 84.5; DE
Best Local Similarity 26.8%; Pred. No. 25;
Matches 40; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1020 LYGVSDYIADALGGN--AVVN---TDGSI 1043
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; Sequence 48048, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 749, Application US/10238075
Publication No. US20030148324A1
GENERAL INFORMATION:
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Olisen, Kari
APPLICANT: Olisen, Kari
APPLICANT: Eyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Fawick, John
APPLICANT: Fawick, John
APPLICANT: Fawick, John
APPLICANT: Fawick, John
APPLICANT: Fawigh, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Escherichia coli
US-10-238-075-749
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119 GGNNAALVNQTASDSSVMVRQVGFGNN 145
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                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
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Publication No. US20030119013A1
GENERAL INFORMATION:
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                                                                         Carr, Grant
Yamamoto, Robert
Forsyth, R.
                              Frawick, John
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US-10-128-714-3213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        404 -----TNTGFGNAGFFNMGIGNAGNEDMGVGNGGSFNVGVGN--AGNOS-----VGFG 449
                                                                                                                                                                                                                                                                                                                   120 -HGDNEGSSGGTGACVKPVREPRLVVQTLSDIDILDDGFRWRKYGQKVVKGNPNPRSYYK 178
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                                                                         SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKYDQLVTRVV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Skeiky, Yasir
APPLICANT: Ovendale, Pamela
APPLICANT: Jen, Shyian
APPLICANT: Lodes, Michael
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
TITLE OF INVENTION: Of Tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                         --NNATIDQWNAKNS-DITVGQYGGNNAALVNQTASDSSVMV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                         | | | ::|||||: ::|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| :|| | :|| | :|| | :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| 
Gaps
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                                                                                                                                              71 NSSGCAAVIAE----DHINGSEHSGPIPENSSVIFGDDEADNGAEPEIKREKE
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67;
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51; Indels
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23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 014038-008740US
CURRENT APPLICATION NUMBER: US/09/793,306
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US 60/185,037
PRIOR APPLICATION NUMBER: US 60/223,828
PRIOR PILING DATE: 2000-08-08
PRIOR FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 164
SOFTWARE: PatentIN Ver. 2.1
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; Publication No. US20040029129Al
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 146, Application US/09793306
Patent No. US20020098200A1
GENERAL INFORMATION:
APPLICANT: Campos-Neto, Antonio
APPLICANT: Skeiky, Yasir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
    37; Conservative
                                                                                                                                                                                                                                              75 TH---EMAHAGQGA
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Best Local Similarity
Matches 34; Conserv
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LENGTH: 597
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    Matches
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APPLICANT: Jiang, Bo
APPLICANT: Tishkeff, Daniel
APPLICANT: Tishkeff, Daniel
APPLICANT: Tishkeff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Methods of Use
FILE REFERRINCE: 10182-018-999
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
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TILE OF INVENTION: AND IDENTIFICATION OF Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-20 PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308 GGGNTGNSNFGFGNTGNVNFGNGNTGDTNFGSGNLGSGNIGFGNKG------S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614 SOFTWARE: PatentIn version 3.1 SEQ ID NO 64573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 678;
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                                                                                                                                                                                                                                                                                                                                                                                                Query Match
10.7%; Score 82.5; DB 14; Length 435;
Best Local Similarity 19.6%; Pred. No. 6.6;
Matches 31; Conservative 30; Mismatches 66; Indels 31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 AKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|| : : || | : 388 PENSTKPIARLLGHQKEVNHVTFSPDMAYIASAGFDNH 425
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR PILING DATE: 2001-04-27
PRIOR PILING DATE: 2001-06-05
PRIOR PILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/305,890
PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR PILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
SOFTWARE: PATENTH VETSION 3.1
LENGTH: 435
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; ORGANISM: Aspergillus fumigatus
US-10-128-714-3213
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Sequence 5834, Apples Sequence 5834, Apples Sequence 5834, Apples Sequence 2, Appli Sequence 37, Apples Sequence 37, Apples Sequence 39, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8854, Apples Sequence 8
                                              Sequence 5, Ar
Sequence 57, Ar
Sequence 28, A
Sequence 22, A
Sequence 22, A
Sequence 14, A
Sequence 14, A
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Sequence 4, P
Sequence 4, P
Sequence 2, P
Sequence 2, P
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GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES;
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543.407
CURRENT FILICALION NUMBER: US/09/543.407
CURRENT FILICALION NOWES OF US ON O'4-05
NUMBER OF SEQ ID NOS: 59
                                                                                                                                                                                                                                                 Sequence 3
Sequence 3
Sequence 1
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19 US-09-543-407-20

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US-08-233-642A-57-20

US-08-233-642A-57-20

US-08-233-642A-57-20

US-09-543-407-12

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US-09-573-655B-667
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ORGANISM: Artificial Sequence
PEATURE:
          US-09-543-407-20
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                                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            6019581 seqs, 976053577 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                       using sw model
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Match Length DB
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Score

Result Š.

8854, Ap 8854, Ap 20638, A 7657, Ap 7656, Ap 7655, Ap 7946, Ap 7946, Ap 7946, Ap 7946, Ap

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Washington
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Matches 136; Conserv
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ZIP: 98104-7092
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STATE: Washing
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                                                                                                                           TYPE: PRT
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                                                                                                                                                                                               1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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                                                                                                                                                  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                   Gaps
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Sol, Miliam W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGGUS PEPTIDE SEQUENCES
FILE REFERENCE: 920493.407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                 Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 91.6%; Score 709; DB 19; Length 151; Best Local Similarity 89.9%; Pred. No. 3.8e-68; Matches 143; Conservative 0; Mismatches 0; Indels 1
                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 ITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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APPLICANT: White, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPFILE REPERBUCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
                                               Query Match 100.0%; Score 774; DB 19; Best Local Similarity 100.0%; Pred. No. 3.3e-75; Matches 151; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                 121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                         121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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US-09-543-407-20
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LENGTH: 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Clouthier, Sharon C.
APPLICANT: Doran, James L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: BASED VACCINES
NUMBER OF SEQUENCES: 58
NUMBER OF SEQUENCES: -
CORRESPONDENCE ADDRESS: -
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.4%; Score 684; DB 6; Length 151;
ilarity 90.1%; Pred. No. 1.9e-65;
Conservative 3; Mismatches 12; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/233,642A

FILING DATE: 26-APR-1994

CLASSIFICATION: 424

ATTONREY/AGENT INFORMATION:

NAME: King, Joshmation:

REPERENCE/DOCKET NUMBER: 35.570

REPERENCE/DOCKET NUMBER: 35.570

TELEPRANICATION INFORMATION:

TELEPRANICATION INFORMATION:

TELEPRANICATION INFORMATION:

TELEPRANICATION INFORMATION:

TELEPRANICATION INFORMATION:

TELERA 3336 SEEDABBERRY

INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                Score 689; DB 19;
Pred, No. 5.6e-66;
3; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 57, Application US/08233642A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                  ORGANISM: Salmonella enteritidis
US-09-543-407-5
                                                                                                                                                                                                                                                                   89.0%;
ilarity 90.7%;
Conservative
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--YDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQ 105
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                                                                                                           61 SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                       SDARKSETTITQSGYGNGADVGQGADNSTIELIQNGFRNNATIDQWNAKNSDITVGQYGG 120
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09
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Sequence 28, Application US/09543407

Sequence 28, Application US/09543407

APPLICANT: White, Aaron P.

APPLICANT: Orian, James L.

APPLICANT: Colinson, S. Karen

APPLICANT: Colinson, S. William W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: BACTERIAL PIMBRIAL SYSTEM FOR

TITLE OF INVENTION: BACTERIAL PIMBRIAL SYSTEM FOR

TITLE OF INVENTION: BACTERIAL PIMBRIAL SYSTEM FOR

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

: ENGIN: 151
  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                         MKLIKVAAFAAIVVSGSALAGVVPOWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALAQ
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APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BATERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.405
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PASISEQ for Windows Version 4.0
LENGTH: 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.5%; Score 662; DB 19; Length 151;
81.9%; Pred. No. 4.7e-63;
iive 0; Mismatches 0; Indels 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 WNAKNSDITVGQYGGNNAALVNQTASDSSVWVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                      121 NNPALVNQTASDSSVMVRQVGFGNNATANQY 151
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US-09-543-407-18
Sequence 18, Application US/09543407
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 81.9
Matches 136, Conservative
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US-09-543-407-28
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SGUENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

TITLE OF INVENTION: BRESENTALION OF HETEROLOGOUS PEPTIDE SEQUENCES

TITLE OF INVENTION: BRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

TITLE OF INVENTION: BRESENTATION OF HETEROLOGOUS

CURRENT APPLICANTON

CURRENT PELING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 22

LENGTH: 151
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                                                                                                                                                                                                                                                                                                                                                                                                           98 RNNATIDOWNAKNSDITVGOYGGNNAALVNOTASDSSVMVRQVGFGNNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                   -----DQWNAKNSDITVGQYGGNNAALVNQTASDSSVWVRQVGFGNNATANQY 151
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TYPE: PRT
CRGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
US-09-543-407-18
                                                                                                                                                         Length 151;
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                                                                                                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPD-
                                                                                                                                                         80.4%; Score 622; DB 19;
73.6%; Pred. No. 1e-58;
tive 0; Mismatches 0;
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Pred. No. 2.2e-58;
0; Mismatches 0;
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US-08-243-40'-12
Sequence 12, Application US/09543407
GENERAL INFORMATION:
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Best Local Similarity 74.6'
Matches 129; Conservative
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                                                                                                                                                                                 1].Similarity 73.6
128; Conservative
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US-09-543-407-22
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Best Local
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US-09-543-407-14
i Sequence 14, Application US/09543407
i GENERAL INFORMATION:
APPLICANT: Mitce, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Milam W.
ITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 20004-406
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 151
LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BRACESTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
SOFTWARE: Fast SEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 78.9%; Score 611; DB 19; Length 151; Best Local Similarity 80.8%; Pred. No. 1.6e-57; Matches 122; Conservative 7; Mismatches 22; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.78; Score 609; DB 19; Length 151; Conservative 6; Mismatches ... ...
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                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 123; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                   US-09-543-407-12
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US-09-543-407-14
                                                                                                                                                                                                           SEQ ID NO 12
LENGTH: 151
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                                                                                                                                                                                                                                                                                                           FEATURE:
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61 SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                Sequence 24, Application US/09543407

GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Solver APPLICATION NUMBER: US/09/543,407

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOCTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 24
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William BESTIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
CURRENT PRILICATION NUMBER: US/09/543,407
CURRENT APPLICATION NUMBER: US/09/543,407
NUMBER OF SEG ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0

LENTH: 13
LENTH: 13
TYPE: PRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE: OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 78.3%; Score 606; DB 19; Length 151; Local Similarity 82.1%; Pred. No. 5.7e-57; les 124; Conservative 5; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 131;
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89.3%; Pred. No. 1.3e-56;
                           121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151
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121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
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; ORGANISM: Salmonella enteritidis
US-09-543-407-31
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ORGANISM: Artificial Sequence
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Best Local Similarity
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US-09-543-407-24
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Matches 1
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21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKYDQLVTRVVTHEMAH 80

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61 SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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APPLICANT: NORMARK, Staffan
APPLICANT: OLSEN, Arne
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS ITS PREPARATION
FILE REFERENCE: 012889-081
CURRENT APPLICATION NUMBER: US/08/978,878
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: SE 8801723-1
                                                                                                                                                                                                                                                  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTERIAL FIMBRIAL SYSTEM FOR PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
                Recombinant Salmonella enteritidis 3b afgA sequence containing the replacement fragment encoding PT3 from GP63 of Leishmania major.
                                                                                                                                Length 151;
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                                                                                                                                                                          Indels
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                                                                                                                                74.2%; Score 574; DB 19; 80.8%; Pred. No. 1.7e-53;
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                                                                                                                                                                                                                                                                                                                                                                                                NNAALVNOTASDSSVMVROVGFGNNATANQY 151
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                                                                                                                                                                            6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT White, Aaron P.
APPLICANT COLLINSON, S. Karen
APPLICANT COLLINSON, S. Karen
APPLICANT KAY, WILLIAM W.
TITLE OF INVENTION: BACTERAL FIMBRIAL SYSTER
TITLE OF INVENTION: PRESENTATION OF HETEROLK
FILE REPREBNCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE FRASESQ for Windows Version 4.0
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US-09-543-407-7
                                                                                                                                                  Best Local Similarity 80.8 Matches 122; Conservative
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Matches 104; Conservative
                    OTHER INFORMATION:
OTHER INFORMATION:
                                                                     ; OTHER INFORMA
US-09-543-407-16
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                                                                                                                                  Query Match
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  FEATURE:
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                                                                 81 AGGGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQV 140
                                                                                          61 VGQGADNSTIELIQNGFRNNATIDQWNAKONSDITVGQYGGNNAALVNQTASDSSVMVRQV 120
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Sequence 16, Application US/09543407;
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: COllinson, S. Karen
APPLICANT: Collinson, S. Karen
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BRESENICATION OF HETEROLOGOUS PEPTIDE SEQUENCES
TITLE OF INVENTION: UNMER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 151
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Callinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT FILING DATE: 2000-04-05
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 5.4e-56;
5; Mismatches 23;
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                                                                                                                                                                                                                                                                                                          Sequence 30, Application US/09543407 GENERAL INFORMATION:
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Best Local Similarity 81.5%;
Matches 123; Conservative
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ORGANISM: Artificial Sequence
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                                                                                                                                                       GFGNNATANOY 151
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LENGTH: 151
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Search completed: August 2, 2004, 15:26:44 Job time : 168.9 secs

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Sequence 2, Appli
Sequence 7907, Ap
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Sequence 7905, Ap
Sequence 7905, Ap
Sequence 7906, Ap
Sequence 7906, Ap
Sequence 7306, Ap
Sequence 7306, Ap
Sequence 7306, Ap
Sequence 7377, Ap
Sequence 1695, Ap
Sequence 1695, Ap
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Sequence 17559, A
Sequence 35514, A
Sequence 7973, Ap
Sequence 7973, Ap
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
                                                                                                                       August 2, 2004, 14:49:38 ; Search time 17.8 Seconds (without alignments) 888.146 Million cell updates/sec
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1. /cgn2 6/ptodata/2/paa/USO6 NEW COMB.pep:*

2. /cgn2 6/ptodata/2/paa/USO6 NEW COMB.pep:*

3. /cgn2 6/ptodata/2/paa/USO8 NEW COMB.pep:*

4. /cgn2 6/ptodata/2/paa/USO8 NEW COMB.pep:*

5. /cgn2 6/ptodata/2/paa/USO8 NEW COMB.pep:*

5. /cgn2 6/ptodata/2/paa/USO8 NEW COMB.pep:*

5. /cgn2 6/ptodata/2/paa/USO8 NEW COMB.pep:*

7. /cgn2 6/ptodata/2/paa/USO8 NEW COMB.pep:*

7. /cgn2 6/ptodata/2/paa/USO8 NEW COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-741-873C-4
US-60-56-612-7907
US-60-579-062-7907
US-60-579-062-7905
US-60-579-062-7905
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US-10-10-205E-35515
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US-10-170-205E-3551
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Match Length
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	Αb	Sequence 273, App	129, Ap	O	Sequence 339993,	Seguence 280, App	ý		Sequence 11867, A	7	Sequence 346132,	Sequence 8923, Ap	Sequence 8923, Ap	Sequence 9813, Ap	Sequence 553, App	Seguence 343835,	Sequence 22578, A	Sequence 9640, Ap	Sequence 13, Appl	
	US-10-872-769-5	PCT-US03-24982A-273	US-10-482-706-129	US-10-425-115-242035	US-10-425-115-339993	US-09-490-324-280	US-60-563-858-16	PCT-US04-10229-38	US-60-556-841-11867	US-09-248-796A-25337	US-10-425-115-346132	US-60-565-632-8923	US-60-579-062-8923	US-60-581-351-9813	PCT-US04-07096-553	US-10-425-115-343835	US-09-248-796A-22578	US-60-556-841-9640	US-10-490-953-13	
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	27	28	O.	30	31	32	93	3.4	35	36	37	88	68	40	41	4.2	4.3	44	45	

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APPLICANT: NOTHER, STETIAN
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084
CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 1998-05-06
FRIOR APPLICATION NUMBER: US 8801723-1
PRIOR PILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR PILING DATE: 1997-11-26
PRIOR PEDICATION NUMBER: US 07/347,189
PRIOR PEDICATION NUMBER: US 07/789,437
PRIOR PEDICATION NUMBER: US 07/789,437
PRIOR PEDICATION NUMBER: US 08/970,846
PRIOR FILING DATE: 1992-11-03
PRIOR PEDICATION NUMBER: US 08/318,519
PRIOR PEDICATION NUMBER: US 08/318,519
PRIOR FILING DATE: 1994-10-05
NUMBER: OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.0
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Best Local Similarity 68.2%; Pred. No. 8.3e-40;
Matches 103; Conservative 21; Mismatches 27; Indels
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                 Sequence 4, Application US/09741873C; GENERAL INFORMATION: APPLICANT: Normark, Staffan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Escherichia coli
US-09-741-873C-4
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APPLICANT: Roberts, James K
APPLICANT: Roberts, James K
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Alarg, Bal
APPLICANT: Alarg, Bal
TITLE OF INVENTION: Compositions thereof
TITLE OF INVENTION: Compositions thereof
TITLE OF INVENTION: Compositions thereof
TITLE OF INVENTION: Compositions thereof
TITLE OF INVENTION: 0201 (5340) C
TITLE OF INVENTION: 2016-05-11
NUMBER OF SEQ ID NOS: 41445
SOFTWARE: Patentin version 3.2
SEQ ID NO 7907
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GENERAL INFORMATION
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yinua
APPLICANT: Cao, Yongwai
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REPERRICE: 38-21(5322) B
CURRENT APPLICATION NUMBER: US/10/425,115
                                                                                                                                                                                                                                                                                                                                                                             300 AAQGTDNGAAAENTGNADPAQGNDNGAAAENSGNENGTAAENNANADVQNDAAQVNDNGA 359
                                                                                                                                                                                                                                              241 GNENGTGAENNANADAQTDVAQ-GSTNEANAENNANADVQNDAAQANENGAAAENSGNAD 299
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                                                                                                                                                                                     --- LOSDARKYDQLVTRVVTHEMAH 80
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                                                                                                                            Gaps
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                                                            7; Length 573;
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11.2%; Score 87; DB 7; Length 573;
Best Local Similarity 24.9%; Pred. No. 9.5;
Matches 42; Conservative 15; Mismatches 62; Indels
                                                                                                                            62; Indels
                                                            DB 7
                                                            ; Score 87; DB
; Pred. No. 9.5;
15; Mismatches
                                                                                                                                                                                     30 GNHNGGG--NSSGPDSTLSIYQYGSANAALA---
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APPLICANT: Kovalic, David K
APPLICANT: Larosa, Thomas J
APPLICANT: Lu, Maclong
APPLICANT: Munyikwa, Tichifa R.
APPLICANT: Roberts, James K
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US-60-579-062-7907
                                                            11.2%;
24.9%;
                                                                                                                     Conservative
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                                                     Query Match
Best Local Similarity
Matches 42; Conserv
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US-10-425-115-193207
US-60-565-632-7907
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APPLICANT: Larosa, Thomas J.
APPLICANT: Larosa, Thomas J.
APPLICANT: Larosa, Thomas J.
APPLICANT: Larosa, Thomis B.
APPLICANT: Larosa, Thomis R.
APPLICANT: Larosa, James R.
APPLICANT: Laros, James R.
APPLICANT: Roberts, James R.
APPLICANT: Roberts, James R.
APPLICANT: Chang, Bei
TITLE OF INVENTION: Compositions Thereof
FILE REPERENCE: 38-21(53403)B
CURRENT APPLICATION WUMBER: US/60/565,632
CURRENT FILING DATE: 2004-04-27
NUMBER OF SEQ ID NOS: 15449
SOFTWARE: Patentin version 3.2
LENGTH: 573
LENGTH: 573
                                                                                                                                  APPLICANT: Olsen, Arne
TITLE OLSEN, Arne
TITLE OLSEN, Arne
TITLE OLSEN, Arne
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64.9%; Pred. No. 7.1e-33;
Live 20; Mismatches 26; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baum, James A.
Kovalic, David K.
Larcsa, Thomas J.
Lu, Maolong
Munyikwa, Tichifa R. I.
Roberts, James K.
                                                  Sequence 2, Application US/09741873C
GENERAL INFORMATION:
APPLICANT: Normark, Staffan
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ORGANISM: Diabrotica virgifera
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SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 131
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Best Local Similarity 64.94
Matches 85; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GFGNNATANOY 151
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APPLICANT: Lu, Maclong
APPLICANT: Lu, Maclong
APPLICANT: Runytkwa, Tichifa R. I.
APPLICANT: Roberts, James K
APPLICANT: Wu, Weis,
APPLICANT: Roberts, James K
APPLICANT: Stangy, Weis,
Taris, Or INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
TITLE OF INVENTION: Compositions thereof
FILE REPRENEUS: 82-15-3403, C
CURRENT APPLICATION NUMBER: US/60/579,062
CURRENT APPLICATION NUMBER: US/60/579,062
CURRENT FILING DATE: 2004-06-11
NUMBER OF SEQ ID NOS: 41445
SOFTWARE: PatentIn version 3.2
SEQ ID NO 7905
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Sequence 7906, Application US/60565632

GENERAL INFORMATION:
APPLICANT: Baum, James A

APPLICANT: Baum, James A

APPLICANT: Baum, James A

APPLICANT: Larosa, Thomas J.

APPLICANT: Munyikwa, Tichifa R. I.

APPLICANT: Roberts, James K.

APPLICANT: Wu, Wei

APPLICANT: Wu, Wei

APPLICANT: APPLICANT: Wu, Wei

TITLE OF INVENTION: Compositions Thereof

TITLE OF INVENTION: Compositions Thereof

FILE REFERENCE: 38-21(53403)B

CURRENT APPLICATION NUMBER: US/60/565,632

CURRENT FILING DATE: 2004-04-27
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NAMMEKEY: misc feature
LOCATION: (392)...(392)
COTHER INFORMATION: Xaa can be any naturally occurring amino US-60-579-062-7905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Length 412;
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                                          204 AAENNGNADAAQSNDNGAAAENNTNADAQNDAAQ-GTANEANA 245
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108 --AKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATA 148
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11.0%; Score 85; DB 'Best Local Similarity 26.4%; Pred. No. 9.6; Matches 43; Conservative 12; Mismatches
                                                                                                                                                                                                                    US-60-579-062-7905; Sequence 7905, Application US/60579062; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                        APPLICANT Baum, James A
APPLICANT Kovalic, David K
APPLICANT Larosa, Thomas J
APPLICANT LU, Maolong
APPLICANT Munyikwa, Tichifa R. I.
APPLICANT Roberts, James K
APPLICANT RU, Wei
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ORGANISM: Diabrotica virgifera
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US-60-565-632-7906
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| Sequence 7905, Application US/60565632
| Sequence 7905, Application US/60565632
| APPLICANT: Monsanto Technology, LLC
| APPLICANT: Baum, James A
| APPLICANT: Larcea, Thomas J
| APPLICANT: Larcea, Thomas J
| APPLICANT: Larcea, Tichifa R. I.
| APPLICANT: Munyikwa, Tichifa R. I.
| APPLICANT: Roberts, James K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 ARKYDOLVTRVVTHEMAHAGOGADNSTIELTONGFRNNATIDOWNAKNSDITVGOYGGNN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----RPITGLLGNIYNGQVPFARPIGFSAPRNGVAIPNANGQ-----VPTYNGNT 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 AAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQY----GSANAALALQSD 62
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LOCATION: (369)...(369)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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LOCATION: (392)..(392)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 24.6%; Pred. No. 2.8;
Matches 35; Conservative 18; Mismatches 63; Indels
                                                                                                                                                                                                                                       ; CTHER INFORMATION: Clone ID: MRT4577_107790C.1.pep
US-10-425-115-193207
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Matches 43; Conserva
       CURRENT FILING DATE:
NUMBER OF SEQ ID NOS:
SEQ ID NO 193207
LENGTH: 147
                                                                                                                                                          TYPE: PRT
ORGANISM: Zea mays
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                                                                                                                                                                                                                               FEATURE:
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Sequence 7536, Application US/60581351
Sequence 7536, Application US/60581351
GENERAL INFORMATION:
APPLICANT: Laurie, Cathy C
TITLE OF INFORMORIC: Acid Molecules Associated With Protein In Plants
TITLE OF INFORMORIC: 38-21(53372)B
CURRENT FILING DATE: 2004-06-17
PRIOR APPLICATION NUMBER: US 60/479,962
PROR APPLICATION UMBER: US 60/479,962
PROR FILING DATE: 2003-06-19
NUMBER: OF SEQ ID NOS: 13980
SOFTWARE: PatentIn version 3.2
SEQ ID NO 7636
LENGTH: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   416 HHLQLNTQSINNEKGH--MSADTVDINTHQQGLNNTAGLIVAERNMILRTGELLNRQGSV 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 GGGAGGGGSSVAGNGIAMTANHNQQHSAAEAAGLLAIARS------GGDLAQSGQGG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 KVAAPPAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
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                                                                                                         Sequence 7377, Application US/60579902
Sequence 7377, Application US/60579902
APPLICANT: Goldman, Barry S.
APPLICANT: Krascomil-Osterfeld, Karina C.
APPLICANT: Wu, Wei
TITLE OF INVENTION: Nucleotide and Amino Acid Sequences from Xenorhabdus
TITLE OF INVENTION: and Uses thereof
FILE REFERENCE: 38-21 (53444) A
CURRENT APPLICATION NUMBER: US/60/579,902
CURRENT FILING DATE: 2004-06-15
NUMBER OF SEQ ID NOS: 14985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   370 QLLASKSLVVSASAI-----DNRQGKITSSGGDITLTTGQLDNLSGKIA----GQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -TIDQWNAKNS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23; Gaps
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---TANSSDLVEGEHGGGEHGGGGHNQQDSQVL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 DNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVM 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 ----DITVGOYG-----GNNAALVNQTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        474 RSGQDLTLNTHGNQLDNRDSGLQGGLFSQGA-----MHLNTGYLNNQSGH 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 26.1%; Pred. No. 21;
Matches 29; Conservative 16; Mismatches 43; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 11.0%; Score 85; DB 7; Length 2663; Local Similarity 24.7%; Pred. No. 91; les 42; Conservative 23; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 KYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNA
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US-10-425-115-320950
; Sequence 320950, Application US/10425115
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US-60-581-351-7636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Xenorhabdus bovienii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : ::| :
128 RGNLLDLHSD----
                                                          RESULT 10
US-60-579-902-7377
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US-60-581-351-7636
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                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 737
LENGTH: 266
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Matches
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TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
TITLE OF INVENTION: Methods thereof
TITLE OF INVENTION: Methods thereof
FILE REFERENCE: 38-21 (53403) C
CURRENT APPLICATION WUMBER: US/60/579,062
NUMBER OF SEQ ID NOS: 41445
SOFTWARE: Patentin Version 3.2
SOFTWARE: Patentin Version 3.2
LENGTH: 841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 GNENGTGAENNANADAQTDAAQ-GSTNEANAENNANADVQNDAAQANENGAAAENSGNAD 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 AGQGADN-STIELTQN-----GFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSS 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                            30 GNHNGGG--NSSGPDSTLSIYQYGSANAALA-----LQSDARKYDQLVTRVVTHEMAH
                                                                                                                                                                                          NAME/KEY: misc_feature
    LoCATION: (810)
    OTHER INFORMATION: Xaa can be any naturally occurring amino acid
    US-60-565-632-7906
                                                                                                                                                                                                                                                                                                                                                                                           26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) NAME/KEY: misc_feature

) LOCATION: (810)

) OTHER INFORMATION: Xaa can be any naturally occurring amino acid

US-60-579-062-7906
                                                                                                                                                                                                                                                                                                                             Query Match
11.0%; Score 85; DB 7; Length 841;
Best Local Similarity 30.7%; Pred. No. 23;
Matches 42; Conservative 13; Mismatches 56; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7906, Application US/60579062
GENERAL INFORMATION:
APPLICANT: Baum, James A
APPLICANT: Larosa, Thomas J
APPLICANT: Larosa, Thomas J
APPLICANT: Lu, Maclong
APPLICANT: Muslong
APPLICANT: When Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 VMVRQVGFG--NNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      380 AQVNDNGTAAENNGNAD 396
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                                                                                                                                         ORGANISM: Diabrotica virgifera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Diabrotica virgifera
NUMBER OF SEQ ID NOS: 15449
SOFTWARE: Patentin version 3.2
SEQ ID NO 7906
LENGTH: 841
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Best Local Similarity
Matches 42; Conserv
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                                                                                                                 PRT
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242 VSLYPLAGGATQAFAXENNQKAYXETYGVSHITRHDMLQIPKQQQNEKYQVPQ---FDQS 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 TIKNIESAKGLDVWDSWPLQNADGTVAEYNGYHVVFALAGSPKDADDTSIYMFYQKVGDN 358
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PRIOR FILING DATE: 2002-03-14
PRIOR PLING DATE: 2002-12-12
PRIOR PLING DATE: 2001-12-12
PRIOR PLING DATE: 2001-12-12
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-04-25
PRIOR PLING DATE: 2000-04-25
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PRIOR PLING DATE: 2000-01-21
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PRIOR PLING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: US 99/491,404
PRIOR PLING DATE: 2000-01-25
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PRIOR PRIOR APPLICATION NUMBER: US 99/491,404
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PRIOR PLING DATE
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TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides FILE REFERENCE: 822
CURRENT APPLICATION UNBER: US/10/389,559
CURRENT FILING DATE: 2003-03-14
PRIOR PRELICATION NUMBER: US 60/365,264
PRIOR FILING DATE: 2002-03-14
PRIOR FILING DATE: 2002-03-14
PRIOR FILING DATE: 2001-12-12
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22.3%; Pred. No. 41;
+ive 25; Mismatches
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Goodrich, Ryle W.
Chen, Rui-hong
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Ma, Yunging
Ghosh, Malabika
Xue, Aidong J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity 22.3 27; Conservative
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Wang, Jian-rui
Zhang, Jie
Ren, Feiyan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhao, Qing A.
Wang, Dunrui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wehrman, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weng, Gezhi
Wang, Zhiwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-07412-1695
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Best Local S:
Matches 27
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                            APPLICANT: La Rosa, Thomas J.
APPLICANT: La Vovalic, David K.
APPLICANT: Sovalic, David K.
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APPLICANT: Drmanc, Radoje T.
TITLE OP INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 822CIP/PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70;
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US-10-425-115-320950
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LOCATION: (1)..(511)
PHER INFORMATION: unsure at all Xaa locations
FEATURE:
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20.8%; Pred. No. 32;
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SEQUENCE INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Zhang, Jian-rui
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
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Goodrich, Ryle W.
Chen, Rui-hong
Wehrman, Tom
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Ma, Yunging
Ghosh, Malabika
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Zhao, Qing A.
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Wang, Zhiwei
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Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Zea mays
                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 TAN 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 TI-----DQWNAKNSDITVGQYGGNNAALV----NQTASDSSVMVRQVGFGNN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 VAAGGLHDG------RGLA-AALALGAQG---VWMGTRFIASHEAHAGDLYRQAVVE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 LKAAGLKVMVVCGAVKHAVKAEQAGCDAVICQGGEGGGHTGLVGTLPLVAQAVEAVKIPV 168
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                                 FRIOR APPLICATION NUMBER: US 09/552,317

PRIOR APPLICATION NUMBER: US 09/488,725

PRIOR FILING DATE: 2000-04-21

PRIOR FILING DATE: 2000-01-21

PRIOR PELING DATE: 2000-01-21

PRIOR PELING DATE: 2001-01-25

PRIOR FILING DATE: 2000-01-25

PRIOR FILING DATE: 2000-01-25

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PRIOR PELING DATE: 2000-01-26

PRIOR PELING DATE: 2000-04-27

PRIOR PILING DATE: 2000-02-03

PRIOR PILING DATE: 1000-02-03

PRIOR PILING DATE: 1000-02-03

PRIOR PILING DATE: 2000-02-03

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Sequence 11319, Application US/60556841
Sequence 11319, Application US/60556841
Sequence 11319, Application US/60556841
Sequence 11319
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)
CURRENT APPLICATION UNBER: US/60/556,841
CURRENT FILING DATE: 2004-03-25
SEQ ID NOS: 12463
SEQ ID NO 11319
APPLICATION NUMBER: PCT/US00/35017
FILING DATE: 2000-12-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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Oy 128 GTASDSSVMVRQVGFG 143

Db 276 LDAAKSCFAMGGSAGG 291

Search completed: August 2, 2004, 15:29:5
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Search completed: August 2, 2004, 15:29:53 Job time : 18.8 secs

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August 2, 2004, 14:39:53; Search time 9.4 Seconds (without alignments) 1545.204 Million cell updates/sec US-09-543-407-20 774 1 MKLIKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151 GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM protein - protein search, using sw model BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table: Run on:

283366 Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	protein	úrlin c	-ri	major sub	ga]	l hyg	hypothetical prote	prote	n nuclea	urlir	curlin minor chain	hypothetical glyci	at:	بن	eishmanoly	PE pr	eishmanolysin	probable homeobox	probable homeobox	probable disease r	cell surface antig	fimbrin protein ag	nucleation compone	adhesin	e adhesin	lysin (E	eishmanolysi	shmanolysin (E	leishmanolysin (EC
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	S35327	S42136	AI0452	T35789	E70663	E96590	AD0123	YQECF2	JC2143	JQ0188	T15502	F87494	T20847	E70946	A70762	T13828	
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	30	31	32	33	3.4		36	3.7	æ	3.9	4	4.1	24	4.3	44	45	

	ALIGNMENTS	
K 24000K	RESULT 1 JC6039 fimbrin protein agfA precursor - Salmonella enteritidis C,Species: Salmonella enteritidis C,Species: Salmonella enteritidis C,Date: 31-Dec-1996 #sequence revision 31-Dec-1996 #text_change 08-Oct-1999 C,Accession: JC6039; PC6015; Ā44898 R;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.	
DAAAA	J. Bacteriol: 178, 662-667, 1996 A,Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fimbriae A,Reference number: JC6039; MUID:96146512; PMID:8550497 A;Accession:JC6039 A;Molecule type: DNA	ае.
दिदद	A;Residues: 1-151 <col/> A;Residues: 1-151 <col/> A;Cross-references: GB:U43280; NID:g1184712; PIDN:AAC43599.1; PID:g1184714 A;Accession: PG6015 A;Molecule type: protein	
дадк	A; Residues: 21-52 <cc2> A; Experimental source: strain 27655-3b A; Note: the authors translated the codon ACG for residue 44 as Ile B; Collinson, S.K.; Emody, L.; Muller, K.H.; Trust, T.J.; Kay, W.W.</cc2>	
סממ, מי	U. Bacteriol: 173, 4/13-4/31. A; Title: Purification and Characterization of thin, aggregative fimbriae from S. A; Reference number: A44898; MUID:91310586; PMID:1677357 A; Contents: 27655	Salmonell
. 4 4 4 4 0 4	A, Arcession: Arabolomery A, Status: profilminary A, Molecule type: protein A, Residues: 21-33 <co3> A, Note: sequence extracted from NCBI backbone (NCBIP:45936) A, Genetics: A, Genetics: A, Genetics:</co3>	
	C;Function: A;Description: major component of thin aggregative fimbriae A;Description: major component of thin aggregative fimbriae A;Note: fimbriae bind to fibronectin, plasminogen, tissue plasminogen activator C;Keywords: fimbria F;1-20/Domain: signal sequence #status predicted <sig> F;1-20/Domain: signal sequence #status predicted <aig> F;21-151/Product: fimbrin protein agfA #status experimental <mai></mai></aig></sig>	V.
	Query Match Best Local.Similarity 90.7%; Pred. No. 3.1e-51; Matches 137; Conservative 3; Mismatches 11; Indels 0; Gaps 0;	
0 1	Qy 1 MKLLKVAAFAAIVVSGSALAGVVEOWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60	
0 1	Qy 61 SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQMNAKNSDITVGQYGG 120	
	Qy 121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151	

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A)Description: major component of wild-type curli, interaction between CsgA and CsgB tri
A)Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli that
and H-kininogen, in the absence of CsgA, CsgB can self-assemble into polymers
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-151/Product: curlin #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: D90806
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gend
A;Reference number: A99629; MUID:21156231; PMID:11258796
     transcriptional repression of csg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          curlin major subunit CsgA [imported] - Escherichia coli (strain O157:H7, substrain RIMD
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A,Status: preliminary
A,Molecule type: DNA
A,Robedues: 1-152 - CHMY>
A,Excestreferences: GB:BA000007; PIDN:BAB34843.1; PID:g13360880; GSPDB:GN00154
A,Excestrimental source: strain 0157:H7, substrain RIMD 0509952
A,Gene: ECS1420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 OSDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG 119
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                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-133, RQRDSGWLW' <0LS3>
A;Cross_references: EMBL:L04979; NID:9290424; PIDN:AAA23616.1; PID:9290425
A;Experimental source: strain K-12, substrain W3110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKLLKVAALAAIVFSGSALAGVVPQYGGGGNHGGGGGNNSGPNSELNIYQYGGGNSALALQ
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  A;Title: The RpoS sigma factor relieves H-NS-mediated tr
A;Reference number: S31202; MUID:93211294; PMID:8459772
A;Accession: S31202
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68.9%; Pred. No. 1.2e-37;
tive 20; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 65.4%; Score 506.5; DB 2
Best Local Similarity 67.1%; Pred. No. 7.7e-36;
Matches 102; Conservative 21; Mismatches 28
                                                                       A,Molecule type: DNA
A,Residues: 1-6,'V', 8-151 < OLS1>
A,Cross-references: EMBL:L04979
A,Ancession: 334560
A,Molecule type: protein
A,Residues: 21-42;44-50 < OLS2>
R;Olsen, A.N.; Armqvist, A.M.
Submitted to the EMBL Data Library, October 1992
A,Reference number: 834559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 104; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 23.15
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                                                                                                           major curlin chain precursor [imported] - Salmonella enterica subsp. enterica subsp. enterica subsp. enterica serovar Typhi
G.Species: Salmonella enterica subsp. enterica serovar Typhi
G.Date: Ob-Nov-2001 #sequence_revision ob-Nov-2001 #text_change 18-Nov-2002
G.Accession: A10635
R.Parkhill, G.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gacra, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUD:21534947; PMID:1167608
A;Accession: A10635
A;Accession: A10635
A;Cross-references: GB:AL513382; PIDN:CAD08268.1; PID:g16502315; GSPDB:GN00176
C;Genetics:
A;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 689; DB 2;
Pred. No. 3.1e-51;
3; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151
     151
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  NNAALVNOTASDSSVMVRQVGFGNNATANQY
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ilarity 90.7%;
Conservative
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Best Local Similarity
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121
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Matches
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H98144

hypothetical protein AGR L 228 [imported] - Agrobacterium tumefaciens (strain C58, Cere Species and Agrobacterium Tumefaciens
C; percis 22-oct-2001 #sequence_revision 22-oct-2001 #text_change 18-Nov-2002
C; Accession; H98144
R; Coodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B. Science 294, 2323-2328, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium two A; Accession: H98144
A; Status: préliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C86266

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                                                                                                                                                        56 ALALQSDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A) Cross-references: GB: AE007870, PIDN: AAK88682.1; PID: 915158413; GSPDB: GN00170
                                                  1 MIRKSFIASALVALVGLSAAAPAMANDVRIEQYGWSNSAGGAQEGYGNRIRTYQNGGYNR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 ALALQSDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: prėliminary
A;Molecule type: DNA
A;Residues: 1-573 <STO>
A;Cross-references: GB:AE005172; NID:g4850402; PIDN:AAD31072.1; GSPDB:GN00141
C;Genetics:
               ----GGNHNGGGNSSGPDSTLSIYQYGSANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --GGNHNGGGNSSGPDSTLSIYQYGSANA
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                                                                                                                                                                                                           61 IVGHQ-----YGR-----HNLSAVGQEGHDNYGSTTQNGNRNVAGI
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13.6%; Score 105.5; DB 2;
Best Local Similarity 23.2%; Pred. No. 0.049;
Matches 36; Conservative 27; Mismatches 61;
                                                                                                                                                                                                                                                                                                     GOYGGNNAALVNOTASDSSVMVROVGFGNNATANO 150
                                                                                                                                                                                                                                                                                                                                                       116 GOYGGNNAALVNQTASDSSVMVRQVGFGNNATANQ 150
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           LLKVAAFAAIVVSGSALAGVVPQWGG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: AGR L 228
A;Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-145 < KUR>
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A; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A; Accession: AD3143
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Status: C58.
A; Coss-references: G3.AE008689; PIDN:AAL45562.1; PID:g17743277; GSPDB:GN00187
C; Genetics:
A; Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                       hypochetical protein csgA [imported] - Escherichia coli (strain O157:H7, substrain EDL93 (Species: Escherichia coli imported] - Escherichia coli (species: Bscherichia coli imported] - Escherichia coli imported] - C;Species: Escherichia coli #sequence_revision 16-Peb-2001 #text_change 14-Sep-2001 C;Accession: #85665 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001 A;Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.

A, Pitle: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.

A, Reference number: A88480; MUID:21074935; PMID:11206551
A, Scatus: proliminary
A, Scatus: proliminary
A, Setatus: proliminary
A, Rolecule type: DNA
A, Setatus: DNA
A, Cross-references: GB:AB:O05174; NID:g12514574; PIDN:AAG55788.1; GSPDB:GN00145; UWGP:Z16
C, Genetics: A; Gene: csgA
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QSDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 QADARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQMNGKDSHMTVKQFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
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13.6%; Score 105.5; DB 2;
Best Local Similarity 23.2%; Pred. No. 0.049;
Matches 36; Conservative 27; Mismatches 61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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C,Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: E95965
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernar
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9884, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R.Perna, N. T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhev iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85665
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A;Molecule type: DNA
A;Residues: 1-151 <HAY>
A;Residues: 1-151 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34842.1; PID:G13360879; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: G85665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 SSGPDSTLSIYQYGSANAALALQSDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 AAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98 RNNATIDOWNAKNSDITVGOYGGNNAALVNOTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-151 <CTO.
A;Cross-references: GB:AE005174; NID:g12514573; PIDN:AAG55787.1;
A;Experimental source: strain O157:H7, substrain EDL933
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Best Local Similarity 28.1%
Matches 32, Conservative
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Best Local Similarity
Matches 32; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sylvian nucleator protein csgB precursor - Bscherichia coli (strain K-12)

NyAlternate names: csgB protein; curlin nucleation component; minor curlin protein
C;Species: Escherichia coli
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 01-Mar-2002
C;Accession: S70787; F64846

R;Hammar, M.; Arnqvist, A.; Blan, Z.; Olsen, A.; Normark, S.

Mol. Microbiol. 18, 661-670, 1995
A;Reference number: S70783; MUID:96414468; PMID:8817489
A;Reference number: S70783; MUID:96414468; PMID:8817489
A;Accession: S70787
A;Status: nucleic acid sequence not shown; translation not shown
A;Residues: 1-151 cHAM>
A;Residues: 1-151 cHAM>
A;Residues: 1-151 cHAM>
A;Residues: 1-151 cHAM>
A;Residues: 1-151 cHAM>
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A;Residues: 1-151 cHAM>
A;Residues: 1-151 cHAM>
A;Residues: 1-151 cHAM>
A;Residues: 1-151 cHAM>
A;Reference number: R:; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278533
A;Reference number: A64720; MUID:97426617; PMID:927855; PIDN:AAC74125.1; PID:q1787278;
A;Reference nucleotide acid sequence ont shown; translation not shown
A;Molecule type: DNA
A;References: CR:AFRENCES:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE000205; GB:U00096; NID:91787265; PIDN:AAC74125.1; PID:91787278; A;Experimental source: strain K-12, substrain MG1655
A;Experimental source: strain K-12, substrain MG1655
A;Genetics:
A;Genetics:
A;Map position: 23.15
A;Map position: 23.15
A;Map position: A;Map position: A;Map position: Mild-type curli; interaction between CsgA and CsgB trip. A;Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli that A;Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli that A;Note: curli are thin, sequence destatus predicted cslGs
F;1-21/Domain: signal sequence #status predicted cslGs
F;2-151/Product: minor curlin chain #status predicted cMAT>
                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ςį
                                                                                                                                                                                                                                                                                                            127
                                                                                                                                                                                                                                                                                                                                                                                                                                              128 IQSNKIAQQG----STTVVLNNHGFSGNAVNVPEMPVHNSYGAPPQGAQQIPVSQMSVNP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97
                                                                                                                                                                                                                                         13 VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKYDQLVTR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 AAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
12.5%; Score 96.5; DB 2; Length 151;
Best Local Similarity 28.1%; Pred. No. 0.29;
Matches 32; Conservative 15; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                          DB 2; Length 573;
0.81;
                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                               73 VVTHEMAHAGOGADNSTIELTQNGFRNNA-TIDQWNAKNS-
                                                                                                                                                                                24; Mismatches
                                                                                                             12.8%; Score 99; 25.4%; Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 AALVNOTASDSSVM 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 NVMMNKSPTQSFVV 197
                                                                                                             Query Match
Best Local Similarity 25.43
Matches 34; Conservative
                                                 A; Map position: 1
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residues 100-407,412-498
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N'Alternate names: promastigote surface proteinase; surface endopeptidase glycoprotein
C'Species: Leishmania major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between two hydrophobic residu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leishmania as
                                                                                                                                                                                                              Sequence similarity
ice nucleation protein inaA - Erwinia ananas
C;Species: Erwinia ananas
C;Date: 30-Sép-1991 #sequence_revision 30-Sep-1991 #text_change 26-Aug-1999
C;Accession: 50703
C;Accession: 50703
B;Abe, K.; Watabe, S.; Emori, Y.; Watanabe, M.; Arai, S.
FEBS Lett. 258, 297-300, 1989
A;Title: An ice nucleation active gene of Erwinia ananas. Sequence similarit
A;Reference number: S07053; MUID:90092494; PMID:2599095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 15-Sep-2000 C;Accession: PL0221; A27598; A60648 R;Button, L.; Masster, W.R. A.7 Exp. Med.:171, 589, 1990 A;Reference number: PL0221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QNGFRNNATIDQWNAKNSDITVGQYG----GNNAALV-----NQTASDSSVMVRQVGFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGNSSGPDSTLSIYQYGSANAALALQSDARKYDQLVTRVVTHEMAHAGQGADNSTIELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSTSTAGPDSSL-IAGYGSTQTA-----GYNSILT------AGYGS----T
                                                                                                                                                                                                                                                                                           A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-132 AABB;
A;Cross-references: GB:X17316; NID:g296095; PIDN:CAA35194.1; PID:g296096
C;Superfamily: ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leishmania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Residues: 1-602 <BUT>
A, Cross-references: GB:Y00647; NID:99554; PIDN:CAA68673.1; PID:99555
A, Note: this is a review to the sequence from reference A27598
A, Note: this is a review w.R.
J. Exp. Med. 167, 724-729, 1988
A, Title: Molecular cloning of the major surface antigen of Leishmania A, Reference number: A27598; MUID:88154764; PMID:3346625
A, Accession: A27598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49,
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A,Molecule type: DNA
R,Bouvier, J.; Bordier, C.; Vogel, H.; Reichelt, R.; Etges, R.
Mol. Biochem, Parasitol. 37, 235-246, 1989
A,Title: Characterization of the promastigote surface protease of A,Reference number: A66648; MUID:90114330; PMID:2608099
A,Accession: A66648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Modecule type: protein
A; Residues: 101, E', 103-118, 'SV', 121-123 <BOU>
A; Residues: 101, 'E', 103-118, 'SV', 121-123 <BOU>
A; Experimental source: strain LEM513.
K; Schlagenhauf, E, E Eges, R.; Metcalf, P.
submitted to the Brookhaven Protein Data Bank, March 1997
A; Reference number: A68135; PDB:LLML
A; Contents: annotation; X-ray crystallography, 1.86 angstroms, A; Note: strain LRC-L119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Description: catalyzes the hydrolysis of peptide bonds b:
A,Note: the activated form can activate the proenzyme form
C,Superfamily: leishmanolysin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.8%; Score 91.5; DB
ilarity 29.1%; Pred. No. 8.9;
Conservative 19; Mismatches
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1014 SSQTARE 1020
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les 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-602 <BUT>
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                                                                                                             A; Modecule Type: DNA
A; Residues: 1-2174 (KUR)
A; Residues: 1-2174 (KUR)
A; Residues: 1-2174 (KUR)
A; Experimental source: strain 1021, megaplasmid psymB
A; Cross-references: GB:AL591985; PIDN:CAC49389.1; PID:g15140875; GSPDB:GN00167
A; Experimental source: strain 1021, megaplasmid psymB
B; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Brian, R.W.; Jones, T.
L; Hyman, R.W.; Jones, T.
Science 293 668-672, 2001
A; Alautons: Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.A; Reference number: A96039; MUID:21368234; PMID:11474104
C; Genetics: annotation
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inax from Xanthomonas campestri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -LALQSDARKYDQLVTRVVTHEMAHAGQGADNSTIBLTQNGFRNNATIDQWNAKNSDITV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STITAGYGSTQTAQEGSRLTSGYGSTATSGSDSAVI----SGYGSTQTAGSESSLTAGYG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 -DQWNAKNSDITVGQYG----GNNAALV-----NQTASDSSVMVRQVGFGNNATANQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STÇTARKGSDITAG-YGSTGTAGSDSALIAGYGSTQTAGSESSLT--AGYGSTQTARK 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Xanthomonas campestris
Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 26-Aug-1999
Accession: S11672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 VYGSTLTGADQSRLVAGYGSTETAGDHSDLIAGYGSTGTAGSDSSI-LAGYGSTQTAAGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 VSGSALAG-----VVPQWGG---GGNHN-----GGGNSSGPDSTLSIYQYGSANAALAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 AIVVSGSALAGVVPQ--WGGGGNHNGGGNSSGPDSTLSIYQYGS-----ANAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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A;Residues: 1-1567 <2HA>
A;Cross-references: EMBL:X52970; NID:g48531; PIDN:CAA37140.1; PID:g48532
C;Superfamily: ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 OSDARKYDQLVT----RVVTHEMAHAGQGADNSTIELTQNGFRNNATI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.4%; Score 96; DB 2; Length 2174; 27.0%; Pred. No. 6.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      750 GLTLTTQGSHAAGIVAQSV-----GGGGGTGGTASSYSAGIGFTAS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Xanthomonas campestris
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_C;Accession: S11672
C;Accession: S11672
R;Zhao, J; Orser, C.S.
Mol. Gen. Genet. 223, 163-166, 1990
A;Title: Conserved repetition in the ice nucleation gene
A;Reference number: S11672; MUID:91080859; PMID:2259339
A;Status: preliminary
                             A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: E95965
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54;
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(7)
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25.8%; Pred. No. 8.9;
ive 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ice nucleation protein - Xanthomonas campestris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GQYGGNNAA - - LVNQTASDSSVMVRQVG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | | | | | | | GGTGGNGGAGGEVSVSLTDSAIRTGQGG 821
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Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 40: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: SMb21548
A;Genome: plasmid
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C;Keywords: blocked carboxyl end; cell adhesion; glycoprotein; homodimer; hydrolase; lip F;1-39/Domain: signal sequence #status predicted <SIG>F;40-100/Domain: activation peptide #status predicted <ATP>F;40-100/Domain: activation peptide #status predicted <ATP>F;40-100/Domain: activation peptide #status seperimental <AMT>F;578-602/Domain: carboxyl-terminal propeptide #status predicted <CTP>F;58-662/Domain: carboxyl-terminal propeptide #status predicted <CTP>F;58-662/Domain: carboxyl-terminal propeptide #status predicted <CTP>F;58-642/Se8,334/Binding site: val-val (autolytic) #status experimental F;25-142,191-230,314-386,333-455,406-425,415-489,466-510,515-565,535-558/Disulfide bond F;265/Active site: Glu #status predicted F;265/Active site: Glu #status predicted F;300,407/Binding site: carbohydrate (Asn) (covalent) #status experimental F;577/Wodified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature form
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
11.8%; Score 91; DB 1; Length 602;
Best Local Similarity 37.5%; Pred. No. 4;
Matches 27; Conservative 6; Mismatches 15; Indels 24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: August 2, 2004, 14:56:23 Job time : 9.4 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 2, 2004, 14:36:12; Search time 5.3 Seconds (without alignments)
1483.508 Million cell updates/sec
Title: US-09-543-407-20
Perfect score: 774
Sequence: 1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters: 14168

141681 segs, 52070155 residues

Searched:

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No, is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	scription	P55225 salmonella		a)		×	_		Q8z7m3 salmonella		٠.									arthrobac	drosc	,ς	Ŋ	Н	P09815 pseudomonas	bacillus a	E	caulobacte	ဗ	mes	art		O86343 mycobacteri	
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	Q06981 salmonella	Q8in81 drosophila	Q8vxp3 chlamydomon	Q60506 cricetulus	Q47112 escherichia	033479 pseudomonas	P07184 drosophila	Q99tc9 staphylococ	P39442 natronomona	Q9y834 penicillium	009112 mus musculu	P75780 escherichia	
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## ALIGNMENTS

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                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
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Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W.W.;
"Salmonella enteritidis agfBAC operon encoding thin, aggregative
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 21-151 FROM N.A.

SPECIES-S. enteritidis, STRAIN=27655-3B;

MEDLINE=94013, PubMed=8104955;

Doran J.L., Collinson S.K., Butian J., Sarlos G., Todd E.C.D.,

Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., Kay W.W.;

Musc C.K., Kay C.M., Salmonella species targeting agfA, the structural gene for thin, aggregative fimbriae.";

J. Clin. Microbiol. 31:2263-2273(1993).
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B7DAC0D16B621359 CRC64;
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                                                                                                                    SEQUENCE FROM N.A.
SPECIES=S.enteritidis; STRAIN=27655-3B;
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                                                               Bacteriol. 185:2330-2337(2003).
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MEDLINE=96414468; PubMed=8817489; Hammar M., Arnqvist A., Blan Z., Olsen A., Normark S.; Hammar M., Arnqvist A., Blan Z., olsen A., production of Expression of two csg operons is required for production of fibronectin- and congo red-binding curli polymers in Escherichia coli
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"Purification and characterization of thin, aggregative fimbriae from
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Olsen A., Arnqvist A.,
"The RpoS signa factor relieves H-NS-mediated transcriptional repression of cggA, the subunit gene of fibronectin-binding curli in
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MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMett G. III, Bloch C.A., Perna N.T., Burland V., Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
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Last annotation update)
151 AA.
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MEDLINE=97061202; PubMed=8905232;
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01-OCT-1996 (Rel. 34, Last seqn
28-FEB-2003 (Rel. 41, Last anno
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STRAIN=K12 / MC4100;
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                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=2128556; PubMed=113125;
Whlich G.A., Keen J.E., Elder R.O.;
"Mutations in the csgD promoter associated with variations in curli expression in certain strains of Escherichia coli O157:H7.";
pppl. Briton. Microbiol. 67:2367-2370(2001).
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MEDLINE-21074935, PubMed-11206551,
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Grosfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
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"Genome sequence of entrchaemorrhagic Escherichia coli 0157:H7.",
Nature 409:529-533 (2001).
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C003470D208D395F CRC64;
  -!- SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Major curlin subunit precursor.
ESGA OR 21676 OR ECS1420.
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EMBL; D90741; BAA35832.1; -.
EMBL; D90742; BAA35840.1; -.
EMBL; D90748; S70788.
ECOGene; EG11489; csgA.
Fimbria; Signal; Complete proteome.
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STRAIN=KL2 / MC4100;
MEDLINE=96414468; PubMed=8817489;
Hammar M., Anrqvist A., Bian Z., Olsen A., Normark S.;
"Expression of two csg operons is required for production of fibronectin- and congo red-binding curli polymers in Escherichia coli
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MAJOR CURLIN SUBUNIT.
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01-077-1996 (Rel. 31, Created)
01-077-1996 (Rel. 34, Last sequence up
28-FBB-2003 (Rel. 41, Last annotation
CSGB OR B1041 OR Z1675 OR ECS1419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AF275733; AAK53212.1; -.
EMBL, AB005315; AAG55788.1; -.
EMBL, AP005254; BAB34843.1; -.
PIR, D90806; D90806.
PIR, H85665; H85665.
Fimbria; Signal; Complete proteome.
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15099 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 67.1%
Watches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli, and Escherichia coli 0157:H7.
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NCBI_TaxID=562, 83334;
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                                                                                                                                                                                                                                                                                                          FIBRONECTIN.
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12 151 MINOR CURLIN SUBUNIT.
151 AA, 15882 MW, B18D266B964014B8 CRC64;
EMBL; AE000205; AAC74125.1; -...
EMBL; D90741; BAA3831.1; -...
EMBL; AE005315; AAG5577.1; -...
EMBL; AP002554; BAB34842.1; -...
EMBL; C90806; C90806.
PTR; C90806; C90806.
PTR; S70787; S70787.
ECOGene; EG12621; csgB.
Finbria; Signal; Complete proteome.
Finbria; Signal; Complete Proteome.
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HSSP; P06620; 11NA.
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Best Local Similarity 28.1<sup>§</sup>
Matches 32; Conservative
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P18127;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
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"Sigma S-dependent growth-phase induction of the csgBA promoter in
Escherichia coli can be achieved in vivo by sigma 70 in the absence
of the mucleoid-associated protein H-NS.";
Mol. Microbiol. 13:1021-1032(1994).
-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI AR
COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                      STRAIN=K12 / M01655,
MEDLINB=9742661; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=0157:H7, EDL933 / ATCC 700927;

MEDLINE=21074935; PubMed=11206551;

MEDLINE=21074935; PubMed=11206551;

MEDLINE=21074935; PubMed=11206551;

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpattick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;

"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.", DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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MEDLINE=97061202; PubMed=8905232;
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STRAIN=K12;
MEDLINE=95157246; Pubmed=7854117;
                                                           Mol. Microbiol. 18:661-670(1995)
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EMBL; X90754; CAA62281.1; -.

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                                                                              97
                                                                                                                  16
                                                                              38 SSGPDSTLSIYQYGSANAALALQSDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGF
                                                                                                                       21 AAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Conserved repetition in the ice nucleation gene inax from
Xanthomonas campestris pv. translucens.";
Mol. Genet. 223:163-166(1990).
-!- FUNCTION: Loe nucleation proteins enable bacteria to nucleate
crystallization in supercooled water.
-!- SUBCELLULAR LOCATION: Outer membrane (By similarity).
-!- DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS
OCTAPEPTIDE A-G-Y-G-T-L-T; FURTHER ON A 16-RESIDUB AND A
REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
-!- MISCELLANGOUS: A STRUCTHAR MODEL IS SUGGESTED IN WHICH THE ICE
NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
-!- SIMILARITY: Belongs to the bacterial ice nucleation protein
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                                                                                                                                                              98 RNNATIDOWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                               Xanthomonas campestris (pv. translucens).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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DB 1; Length 151;
                                       Indels
                                         62;
                 0.097;
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01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                         15; Mismatches
  12.5%; Score 96.5; 28.1%; Pred. No. 0.
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PRINTS; PR00327: ICENUCLEATION; 57.
PROSITE; P800314; ICE NUCLEATION; 57.
Ice nucleation; Repeat; Outer membrane.
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Matches

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----GNNAALV-----NQTASDSSVMVRQVGFG 143
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-!-EUNCTION: Has an integral role during the infection of macrophages in the mammalian host.

-!-CATALYTIC ACTIVITY: Preference for hydrophobic residues at Pl and pl' and basic residues at P2 and P3'. A model nonapeptide is cleaved at Ala-Tyr-|-Leu-Lys-Lys-.

-!-COFACTOR: Binds 1 zinc ion per subunit.

-!-COFACTOR: Binds 1 zinc ion per subunit.

-!-FULLY SATURATED, UNBRANCHED 1-0-ALKYL CHAIN (MAINLY C24:0) AND A MIXTURE OF FULLY SATURATED UNBRANCHED 2-0-ACYL CHAINS (C12:0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-95406217; PubMed=7675788; Schlagenhauf E., Etges R., Metcalf P.; "Crystallization and preliminary X-ray diffraction studies of leishmanolysin, the major surface metalloproteinase from Leishmania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (1.86 ANGSTROMS).
MEDLINE=98416698; PubMed=9739094;
Schlagephauf E., Etges R., Metcalf P.;
"The crystal structure of the Leishmania major surface proteinase leishmanolysin.";
                                                                                                                                                                                                                                                                                                                                                   01.APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmaholysin precursor (EC 3.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 101-123.
MEDLINE 8154764; PubMed=3346625;
Butcon L.L., Modaster W.R.,
"Molecular cloning of the major surface antigen of leishmania.";
J. Exp. Med. 167:724-729(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIJINE=91009116; PubMed=2145267; Schneider P., Ferguson M.A.J., McConville M.J., Mehle Schneider P., Ferguson M.A.J., McConville M.J., Mehle Homans S.W., Bordier C.; Structure of the glycosyl-phosphatidylinositol membi
                                                                                                                                                                                                                                                                                           602 AA
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                                                          ONGFRINATIDOWNAKNSDITVGQYG
               GSTSTAGPDSSL-IAGYGSTQTA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Button L.L., McMaster W.R.;
J. Exp.; Med. 171:589-589(1990)
                                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                                                                                                                             STANDARD;
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01-AUG-1988 (Rel. 08,
01-APR-1990 (Rel. 14,
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1014 SSQTARE 1020
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                                                                                                                                                    STLTAGYGSTQTAQEGSRLTSGYGSTATSGSDSAVI----SGYGSTQTAGSESSLTAGYG 319
                                                                                                                                                                                                          QSDARKYDOLVT-----RVVTHEMAHAGQGADNSTIELTQNGFRNNATI------ 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93
                                                                                                                           14 VSGSALAG-----VVPQWGG---GGNHN-----GGGNSSGPDSTLSIYQYGSANAALAL 59
                                                                                                                                                                                                                                                                                             104 -DQWNAKNSDITVGQYG-----GNNAALV-----NQTASDSSVMVRQVGFGNNATANQ 150
                                                                                                                                                                                                                                                                                                                        STOTARKGSDITAG-YGSTGTAGSDSALLAGYGSTOTAGSESSLT--AGYGSTQTARK 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 GGGNSSGPDSTLSIYQYGSANAALALQSDARKYDQLVTRVVTHEMAHAGQGADNSTIELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M [1]

**SEQUENCE FROM N.A.*

**REDINNE=90092494; PubMed=2599095;

**A BE K., Watcabe S., Emori Y., Watanabe M., Arai S.;

**Abe K., Watcabe S., Emori Y., Watanabe M., Arai S.;

**Abe K., Watcabe S., Emori Y., Watanabe M., Arai S.;

**Abe K., Watcabe S., Emori Y., Watanabe M., Arai S.;

**Abe K., Watcabe S., Emori Y., Watanabe M., Arai S.;

**Abe K., Watcabe S., Emori Y., Watcabe Of Erwinia ananas. Sequence similarity

**In to those of Pseudomonas species and regions required for ice

**Included on activity.";

**PERSIONAL Tochnology Outer membrane (By similarity).

**Included on the Contains Many IMPERFECT REPRATS OF THE CONSENSUS

**OCTAPEPTIDE A.G.Y-G.-Y-T.Y. PURTHER ON A 16-RESIDUE AND A

**REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity
                                                                                   Gaps
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49;
                                                                                   49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 1322;
                                        Length 1567;
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NW; 89B0EE24AA837039 CRC64;
                                                                                   Indels
  152548 MW; C8B451D959ECAD63 CRC64;
                                                                                   56;
                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 17, Created)
(Rel. 17, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.8%; Score 91.5; D 29.1%; Pred. No. 3.1; ive 19; Mismatches
                                        ; Score 92.5; D; Pred. No. 3.1; 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ice nucleation, Repeat, Outer membrane.
COMAIN 162 1281
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Pfam. PF00818; Ice_nucleation; 69.
PRINTS; PR00337; ICENUCLEATN.
PROSITE; PS00314; ICE_NUCLEATION; 49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131094 MW;
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25.8%;
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NCBI_TaxID=553;
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                                                                                       Conservative
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HSSP; P06620; 11NA.
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  1567 AA;
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16-OCT-2001 (
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Best Local S
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SEQUENCE
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RESULT

membrane anchor of

This SWISS-PROT entry is copyright. It is produced through a collaboration SIMILARITY: Belongs to peptidase family M8

Best Loca Matches

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63 ARKYDQLVTRVVTHEMAHA----GQGADNSTIELTQNGFRNNATIDQWNAKNSDITV---
                                                                                                                                                                                                                                                                                                                                                                                                           24; Gaps
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Pred. No. 1.4;
6; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                               63953 MW; 982EF3245D87C43E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSGB SALTI
1D CSGB SALTI
AC QGZTM3:
CQGB SALTI
STANDARD; PRT; 151 AA
AC QGZTM3:
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
11.8%;
Best Local Similarity 37.5%;
Matches 27; Conservative
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602 AA;
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NREACPS; MOROGOS; Pept M. Zn. BS.

DR InterPro; IPRO01577; Peptidase_M8.

DR Pfain; PRO1457; Peptidase M8. 1.

DR PRINTS; PRO0782; LSHAMNOLYSIN.

PROSITE; PSO0142; ZINC_PROTBASE; 1.

RW Hydrolase; Metalloprocease; Glycoprotein; Metal-binding; Zinc;

KW Zymogen; Signal; Cell adhesion; GPI-anchor; 3D-structure; Lipoprotein.

FT SIGNAL

T SIGNAL

T CHAIN 101 57 LEISHMANOLYSIN.

FT CHAIN 101 570 LEISHMANOLYSIN.

FT PROPEP 578 602 REMOVED IN MATURE FORM.

FT PROPEP 578 602 REMOVED IN MATURE FORM.
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
GPI-anchor amidated asparagine.
                                                                                                                                                                          (CATALYTIC)
(CATALYTIC)
                                                                                                                                                                          ZINC
                                                 EMBL, Y00647, CAA68673.1; -. PIR; PL0221, PL0221. PDB; 1LML, 17-SEP-97.
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'n 115 (Fimbrin SEF17 minor

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precursor
Minor curlin subunit precure
CSGB OR AGFB OR STM1143.
Salmonella typhimurium, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 413:852-856(2001).
                                                                                                     NCBI_TaxID=602, 592;
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CURLIN MONOMERS
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                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-TY2 / ATCC 700911;

STRAIN-TY2 / ATCC 700911;

MEDLINE-22531367; PubMed=12644504;

MEDLINE-22531367; PubMed=12644504;

Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;

"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";

J. Bacteriol. 185:2330-2337(2003).

-! FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COILED SUREACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
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                                                                                                                                                                         MEDLINE=21554947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holzroy S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of a multiple drug resistant Salmonella anterica serovar Tvohi CT18."
                                                                     Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 151 MINOR CURLIN SUBUNIT.
151 AA; 16254 MW; 161C54326E573495 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
 10-OCT-2003 (Rel. 42, Last annotation update)
Minor curlin subunit precursor.
CSGB OR STY1180 OR T1777.
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Pred. No. 0.
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                                                                   Bacteria; Proteobacteria; Gamma
Enterobacteriaceae; Salmonella.
NCBI_TaxID=601;
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                                                                                                                                                                                                                                                                                                                                                            CT18.";
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                                                                                                                                                                                                                                                                                                                                                          enterica serovar Typhi CT
Nature 413:848-852(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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(Rel. 34, I
(Rel. 41, I
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SEQUENCE FROM N.A.
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28-FEB-2003
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ID CSGB_SALTY
AC P55226;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SPECIES=S.enteritidis, STRAIN=27655-3B;
MEDLINE=96146512; PubMed=8550497;
Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W.W.;
Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W.W.;
"Salmonella enteritidis agfBAC operon encoding thin, aggregative
finbriae.";
J. Bacteriol. 178:662-667(1996).
-!- PUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE
COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
FIRENDECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES : LYPAINMLIUM; STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDLINE=21534948; PubMed=11677609; MCDLINE=21534948; PubMed=11677609; MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan B., Sun H., Flores L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; "Complete genome sequence of Salmonella enterica serovar Typhimurium"
                                                                                                                                                                                                                          SPECIES S. typhimurium, STRAIN-SR-11;
MEDLINE=98117058; PubMed=9457880;
Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;
"Curli fibers are highly conserved between Salmonella typhimurium and Escherichia coli with respect to operon structure and regulation.";
J. Bacteriol. 180:722-731(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                             Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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MINOR CURLIN SUBUNIT.
; COFC5430E6DD361D CRC64;
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Pred. No. 0.48;
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EMBL, AE008749; AAL20073.1, -.
EMBL, U43280; AAC43598.1; -.
EMBL, TG6040; TG6040.
Stydene, S010609; csgB.
Fimbria; Signal; Complete proteome.
                                                                           Enterobacteriaceae; Salmonella
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31.0%;
Salmonella enteritidis.
Bacteria; Proteobacteria;
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Conservative

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RESULT 11
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                                                                                                                                                                                                                                           Webb J.R., Button L.L., McMaster R.W.;
"Heterrogeneity of the genes encoding the major surface glycoprotein of Leishmania donovani.",
"Of Leishmania donovani.",
Mol. Biochem. Parasitol. 48:173-184(1991).
-!- FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.
-!- CATALYTIC ACTIVITY: Preference for hydrophobic residues at P1 and P1' and basic residues at P2 and P3'. A model nonapeptide is cleaved at -Ala-Tyr-|-leu-Lvs-Lvs-.
-!- COFACTOR: Blinds I zinc ion per subunit (By similarity).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
-!- SIMILARITY: Belongs to peptidase family M8.
                                                                                                                                                              Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania
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ZINC (CATALYTIC) (BY SIMILARITY)
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                                                  01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
01-NOV-12003 (Rel. 42, Last annotation update)
Ledshmanolysin precursor (RC 3.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
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InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR001577; Peptldase_MS.
Pfam; PF01457; Peptldase_MS. 1.
PRINTS; PR00782; LSHMANOLYSIN.
PROSITE; PS00142; ZINC_PS0TEASE; 1.
Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc; Zymogen; Signal; Cell adhesion; GPI-anchor; Lipoprotein.
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                          GP63 LEIDO
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Score 88; DB 1; Length 590; Pred. No. 2.5;

11.4%; 89.5%;

Best Local Similarity

Query Match

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NCBI_TaxID=44271;
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REMOVED IN MATURE FORM (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ramamoorthy R., Donelson J.E., Paetz K.E., Maybodi M., Roberts S.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90205976; PubMed=2320059;
Miller R.A., Read S.G., Parsons M.;
"Leishmania gp63 molecule implicated in cellular adhesion lacks an Arg-Gly-Asp sequence.";
                                                                                                                                                                                                                                             01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
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InterPro; IPR01577; Peptidase_MB.
Pfam; PF01457; Peptidase_MB.
Pfam; PF01457; Peptidase_MB.
PRINTS; PF00162; ISRCANOLYSIN.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PHYdrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc; Zymogen; Signal; Cell adhesion; GPI-anchor; Lipoprotein.
SIGNAL
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                                               238 ASRYDOLVTRVVTHEMAHA 256
63 ARKYDQLVTRVVTHEMAHA 81
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HSSP; P08148; 1LML.
MEROPS; M08.001; -.
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Leishmania mexicana.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5665;
                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin C1 precursor (EC 3.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
ZINC (CATALYTIC) (BY SIMILARITY).

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N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

GPI = anchor a midated asparagine (By contacts).
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                                                                                                                                                                       Score 88; DB 1; Length 599;
Pred. No. 2.6;
.; Mismatches 1; Indels
                                                                                                                                                    746730AE8E2A2E7C CRC64;
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                                                                                                                                                                                                                                                                                              646 AA
                                                                                                                                           similarity)
                                                                                                                                                                                                                                                                                              PRT;
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InterPro; IPR006625; Pept M Zn BS.
InterPro; IPR001577; Peptidase_M8.
Pfan; PF01457, Peptidase_M8, 1.
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                                                                                                                                                     63848 MW;
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Best Local Similarity 89.5'
Matches 17; Conservative
                                                                                                                                                                                                                                                                                              STANDARD;
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562
555
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HSSP; P08148; 1LML.
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SEQUENCE FROM N.A.
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Bacterià; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Phosphate-binding protein 3 precursor (PBP-3) (PstS-3)
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1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69054 MW;
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                                                                                                       646 AA;
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NCBI_TaxID=553;
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Q47879;
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STRAIN=06.HI / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
MEDLINE=22388234; PubMed=12471157;
MEDLINE=22388234; PubMed=12471157;
MEDLINE=22388234; PubMed=12471157;
MEDLINE=22388234; PubMed=12471157;
MEDLINE=22388234; PubMed=12471157;
MEDLINE=22388234; PubMed=12471157;
MEDLINE=22388234; PubMed=12471157;
MEDLINE=22388234; PubMed=12471160 S.R. Boutin A., Hackett J., Stroud D., Mayhew G.F., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli."
"Extensive mosaic scherichia coli."
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
-!- FUNCTION: Fimbriae (also called pili), polar filaments radiating from the surface of the bacterium to a length of 0:5-1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            van Die I., Bergmans H.;
"Nucleotide sequence of the gene encoding the F72 fimbrial subunit of
Nucleotide sequence of the gene encoding the F72 fimbrial subunit of
Gene 32:83-90(1984).
                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                           PHOSPHATE-BINDING PROTEIN 3.
N-palmatroyl Cysteine (Potential).
Schiacylglycerol cysteine (Potential).
CBOEAOAC108463EC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE=92040048; PubMed=1682251;
Denich K., Blyn L.B., Craiu A., Braaten B.A., Hardy J., Low D.A.,
O'Hanley P.D.;
                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                    Pfam; PF01547; SBP bac 1; 1."
PR05TIT; PS00013; PR0XAR LIPOPROTEIN; 1.
Phosphate transport; Transport; Membrane; Lipoprotein; Signal;
Palmitate.
                                                                                                                                                                                                                                                                                                         369;
                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                  21; Mismatches 49;
                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-701-1986 (Rel. 01, Created)
21-701-1986 (Rel. 01, Last sequence update)
21-701-1986 (Rel. 01, Last sequence update)
77-2 fimbrial protein precursor (F7-2 pilin).
F7-2 OR PAPA OR C3592.
Escherichia coll, and
Escherichia coll, 06.
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                                                                                                                                                                                                                                                                                                       11.2%; Score 86.5; 27.8%; Pred. No. 2;
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                                                                                                                                                                           POTENTIAL.
EMBL, AF137360; AAF74819.1; -.
HSSP: P06128; 1A54.
InterPro; IPR000437; Prok lipoprot_S.
InterPro; IPR006059; SBP_Dac_I.
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MEDLINE=85155489; PubMed=6152241;
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Enterobacteriaceae, Escherichia.
NCBI_TaxID=562, 217992,
                                                                                                                                                                                                                                                              37225 MW;
                                                                                                                                                                                                                                                                                                                                                  35; Conservative
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369 AA;
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Best Local Similarity
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-: SUBCELLULAR LOCATION: Outer membrane.
-:- DOMAIN: CONTAINS INPERFECT REPEATS OF A CONSENSUS OCTAPEPTIDE A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE PRIODICITY IS SUPERINPOSED.
-:- MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE NUCLEATION PROTEIN DISBLAYS A SYMMETRY RELATED TO THAT OF ICE.
-:- SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 ANAALALQSDA----RKYD-QLVTRVVTH-EMAHAGQGADNSTIELTQNGFRNNATIDQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 --SKLFLENDGESQPKSFDIKLINCDITNFKKAAGGGGAKTGTVSLTFSGVPSGPQSDML
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micrometers and numbering 100-300 per cell, enable bacteria to colonize the epithelium of specific host organs. SIMILARITY: BELONGS TO THE FIMA/PAPA FAMILY OF FIMBRIA PROTEINS.
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae, Pantoea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.9%; Score 84.5; DB 1; Length 188; 25.0%; Pred. No. 1.4; ive 26; Mismatches 76; Indels 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROBABLE.
0EEF750CFD843157 CRC64;
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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InterPro; IPR008966; Adhes bact.
InterPro; IPR000259; Fimbrial.
Pfam; PF00419; Fimbrial; 1.
Fimbria; Signal; Complete proteome.
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MEDLINE-94264407; PubMed=7764866;
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Best Local Similarity
Matches 45; Conserv
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EMBL, D14992, BAA03636.1; -..

DR PIR, JCZ143; JCZ143.

BR HSSP; P66620, IINA.

DR PIR, JCZ0143; LCE nucleatn.

DR PIRTS; PR00125; ICE nucleatn.

DR PRINTS; PR00126; ICE nucleation; 51.

DR PRINTS; PR00124, ICE NUCLEATN.

DR PRINTS; PR00124, ICE NUCLEATN.

DR PROSITS; PR00134, ICE NUCLEATN.

DR PROSITS; PR00134, ICE NUCLEATN.

DR PROSITS; PR00134, ICE NUCLEATION; 34.

FT DOMAIN 162 993 OCTAMBEPTIDE PERIODICITY.

SEQUENCE 1034 AA; 103378 MW; FA222523D333EADD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 EESSQWAGYGSTQTGMKGSDLTAGYGSTGTAGDDSSL-IAGYGSTQTAGEDSSLTAGYGS 278
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10.9%; Score 84.5; DB 1; Length 1034;
Best Local Similarity 26.9%; Pred. No. 9.6;
Matches 45; Conservative 17; Mismatches 66; Indels 39; Gaps
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Search completed: August 2, 2004, 14:49:30 Job time : 6.3 secs

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August 2, 2004, 14:39:17; Search time 29.7 Seconds (without alignments) 1604.150 Million cell updates/sec
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774
1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

scrip	033802 salmonella Q7x243 citrobacter	Q7x240 citrobacter Q8cw63 escherichia	Q7x237 enterobacte Q54069 salmonella	Q9s3j5 escherichia		Qsein4 snewanella Qsu6n9 agrobacteri	Q89ji6 bradyrhizob O9saf2 arabidopsis	ß	Q7v8s5 prochloroco	Q88hg0 pseudomonas
SUMMARIES	033802 Q7X243	~	Q7X237 Q54069	Q983J5	COSTINA COSTINA COSTINA	Q8U6N9	089JI6 09SAF2	QBOULS	07V8S5	088HG0
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## ALIGNMENTS

RESULT 1 033802 AC 033802 DT 01-JAN DT 01-DEC DE AGFA D GG AGFA. OC Bacter OC Bacter OC Bacter OC Bacter OC Bacter CO Bacter C	PRELIMINARY, PRT; 152 AA.	J.) 1988 (TrEMBLrel. 05, Created) N-1998 (TrEMBLrel. 05, Last sequence update) C-2001 (TrEMBLrel. 19, Last annotation update) protein (Fragment).	AGGRA. Salmonella typhimurium. Bacterià; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella.	SEQUENCE FROM N.A. MEDLINE-98053981; PubMed=9393832; Sukupolvi S.S., Lorentz R.G., Gordon J.I., Bian Z., Pfeifer J.D.,	VENTRARY.S.U., KHOPN M.; "Expression of thin, aggregative fimbriae promotes interaction of Salmonella typhimurium SR-11 with mouse small intestinal epithelial	Gells."; Infect. Immun. 65:5320-5325(1997). BMBL; AU000514; CAA04151.1; NON TER 152 152 SEQÜENCE 152 AA; 15401 MW; 9DA7DADC2364B006 CRC64;	Query Match Best Local Similarity 89.4%; Pred. No. 2.38-48; Matches 135; Conservative 4; Mismatches 12; Indels 0; Gaps 0;	1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGRHNGGGNSSGPDSTLSIYQYGSANAALALQ 60	61 SDARKYDQLVTRVVTHEMAHAQQADNSTIELTQNGFRNNATIDQMNAKNSDITVQQYGG 120	
380 380 380 380 4at		SSS c	ella typhii ia; Proteol bacteriace axID=602;	SE FROM N. S=98053981 Ivi S.S.,	ssion of the	. Immun. 6. AJ000514; R 152 ZE 152 AJ	ch   Similari  35; Cons			

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Q7X243; Q7X243 RESULT 2 Q7X243

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61 SDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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1 MKLLKVAAFPAAIVVSGSALAGVVPQW--GGNHHGGGSNYGPDSSLSIYQYGSNNSANALQ 58
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STRAIN=C6:HI / CFT073 / ATCC 700928;
MEDINE=22388234; PubMed=12471157;
MEDINE=22388234; PubMed=12471157;
MEDINE=22388234; PubMed=12471157;
MeDINE=2388234; PubMed=12471157;
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
Mobley H.L.T., Acad. Structure revealed by the complete genome sequence of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Enterobacter.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Major curlin subunit precursor.
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Last annotation update)
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67.1%; Pred. No. 7.1e-34;
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Zogaj X., Bokranz W., Nimtz M., Romling U.;
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SEQUENCE 152 AA;
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                                                                                                                                                                                                                                                                                                                                            Zogaj X., Bokranz W., Nimtz M., Romling U.;
"Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract."; Infect. Immun. 72:4151-4156(2003).
EMBL; AJ515701; CAD566751; -. SEQUENCE 149 AA; 15260 MW; 946DD52017F648FD CRC64;
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Bacteria, Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
file TaxID=213763;
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Citrobacter freundii.
Citrobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriacae, Citrobacter.
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121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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Matches 119, Conservative
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   NCBI_TaxID=562;
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"Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract."; Infect. Immun. 72:4151-4158(2003).
EMBL, AJ515702; CAD56678.1; -. SEQUENCE ISO AA; 15112 MW; 5D8BB2D872DF15F3 CRC64;
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBL_TaxID=592;
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
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STRAIN-SE30;
Cox J.M., Eglezos S., Woolcock J.B.;
Cox J.M., Eglezos S., Woolcock J.B.;
colony morphology and expression of SEF17 fimbriae.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U53207; AAA98671.1;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Curlin subunit monomer (Fragment).
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58.9%; Pred. No. 6.9e-28;
tive 27; Mismatches 34
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01-NOV-1996 (TrEMBLrel. 01, G.
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01-DEC-2001 (TrEMBLrel. 19, L.
SEF17 fimbrin (Fragment).
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                                                                               MEDLINE 99314153; PubMed=10386375;
La Ragione R.M., Collighan R.J., Woodward M.J.;
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Landerdiation of Escherichia coll 078:K80 isolates associated with
ISI inserti on in csgB and reduced persistence in poultry infection.";
FEMS Microbiol. Lett. 175:247-253 (1999).
BMBL; AJ31765, CAB45380.1;
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EMBL; AP005954; BAC50564:1; -.
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Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bradyrhizobium japonicum.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Bradyrhizobiaceae, Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 122; DB 2; Length 29;
Pred. No. 0.0019;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48; Indels
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130 Aa; 12699 MW; ACFB2D66A48D260F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNTATTLOTGS-----LLTVNTAVTGOGGTTAT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 ITVGOYGGNNAALVNQTASDSSVMVRQVGFGNNATANQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKLLKVAAIAAIVFSGSALAGVVPQYGGG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
SEQUENCE FROM N.A.
TRANSPOSON=Insertion sequence IS1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 89.7%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24,
24,
24,
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Query Match
Best Local Similarity
Matches 40; Conserv
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                             39 SGPDSTLSIYQYGSANAALALQSDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFR 98
                                                                                                                                                                                                                                                                                                                                                                                                           Heidelberg U.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., Madupu R., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.C., Medalyun T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M., "Genome sequence of the dissimilatory metal ion-reducing bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-22297686; PubMed=12368813;
Heidelberg J.F., Paulsen I.T., Nelson K.B., Gaidos E.J., Nelson W.C.,
Heidelberg J.F., Paulsen I.T., Nelson K.B., Gaidos E.J., Nelson W.C.,
Read T.D., Eisen J.A., Scott J., Beanan M., Brinkac L., Daugherty S.A.,
DeBoy R.T., Dodson R.J., Haft D.H., Kolonay J.F.,
Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
Mueller J., Khouri H., Gill J., Uttersback T.R., MoDonald L.A.,
Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.;
"Genome sequence of the dissimilatory metal ion-reducing bacterium
                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
                                                                                                                                                                                                                                                                                                                                                                      24;
                                                                                                                                                                                                                                                                                                                                          14.2%; Score 110; DB 16; Length 139; 28.3%; Pred. No. 0.13; ive 18; Mismatches 34; Indels 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 NNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGN 144
                                                                                                                                                                                                                                                                                                                    139 AA; 14811 MW; 41EC1CFA76957920 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .1 protein; Complete proteome.
502 AA; 52441 MW; D08CA23D6C46B62D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     502 AA
                                                                                                                                                                                                                                                      Shewanella oneidensis.";
Nat. Biotechnol. 20:1118-1123(2002).
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EMBL; AE015532; AAN53941.1; -.
  יבי בשניבר בטטט (TremBirel, 23, Last am
Minor curlin subunit CsgB, putative
פחמפר Spaner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                   STRAIN=MR-1;
MEDLINE=22297686; PubMed=12368813;
                                                                                                                                                                                                                                                                              EMBL; AE015532; AAN53942.1; -.
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                      Shewanella oneidensis.
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                                                                                                                                                                                                                                                                                                        Complete proteome.
SEQUENCE 139 AA;
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Matches 30; Conserv
                                                                                                     SEQUENCE FROM N.A.
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                                                                            NCBI_TaxID=70863;
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SEQUENCE 50
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QBEIH4
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                                                                                                                                                                                   222
                                                                                                                                                                                                                                                                                                         223 NSVDIYQKGDNHTGFVYALAGSENDISMEQEGSNNTAYLSMTTGDDNTVDITQDGDSNTV 282
                                                                                                                            42
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                                                                                                                            --GNHNG-----SGDS----SGBD
                                                                                                                                                                                163 AVFRVEGDNNDGDIKQYGNNNQAGLIALDLSANVGNNNDVSVEQIGNNNFGAAKGIAGND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=2160851; PubMed=11743194; Miller N., Blanchard M., Goodner B., Hinkle Gattung S., Miller N., Blanchard M., Goodner B., Hinkle B., Gattung S., Miller N., Halling C., Mullin L., Houmtel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Grone sequence of the plant pathogen and biotechnology agent Science 294:2223-2228 (2001).
                                                                                                                                                                                                                                                 43 STLSIYQYGSANAALALQSDARKYDQLVTRVVTHEMAHAGQ-GADNSTIELTQNGFRN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LLKVAAFAAIVVSGSALAGVVPQWGG-----GGNHNGGGNSSGPDSTLSIYQYGSANA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE_CIGORSO, PubMed=11743193,
MEDLINE_CIGORSO, FubMed=11743193,
Mood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Kutyavin T., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
Nester E.W.
                                                                                                                                                                                                                                                                                                                                                                    100 -NATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                              31;
                                                                                                                                                                                                                                                                                                                                                                                                              Length 145;
   DB 16; Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhizobiaceae, Rhizobium/Agrobacterium group, Agrobacterium,
NCBI_TaxID=176299;
                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61; Indels
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984 MW; DEDC870E1713D51A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-UN-2002 (TrEMBLrel. 21, Created)
01-UN-2002 (TrEMBLrel. 21, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Atu4768
ATU4768 OR AGR L 228.
Agrobacterium tumefaciens (strain CS8 / ATCC 33970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 16;
                                                          72;
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13.8%; Score 106.5; D 23.1%; Pred. No. 1.2; cive 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                            10 AAIVVSGSALAGVVPQWGGG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AE009405; AAL45562.1; -. EMBL, AE008209; AAK88682.1; -. PIR, AD3143; AD3143.
PIR, H98144; H98144.
Hypothetical protein; Complete SEQUENCE 145 AA; 14984 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 294:2317-2323(2001).
                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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73 VVTHEMAHAGOGADNSTIELTQNGFRNNA-TIDQWNAKNS------DITVGQYGGNN 122
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Nguyen M., Southwick A., Tripp M., Palm C.J., Jones T., Wu T.,

Nguyen M., Southwick A., Tripp M., Chang C.H., Dale J.N.,

Land J., Khen H., Cheuk K., Chan M.M., Chang C.H., Dale J.N.,

Leng J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida J., Kamiya A.,

Kawai J., Kim C.J., Narusaka M., Onodera C.S., Quach H.L., Sakurai T.,

Satou M., Seki M., Shinn P., Tang C.C., Toroumi M., Wong C., Wu H.C.,

Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J., Theologis A.,

Davis R.W.,

Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
Altafi H., Araujo R., Chao Q., Conn L., Conway A.B., Dunn P., Eansen N., Huizar L., Kim C., Palm C., Rowley D., Shinn P., Walker M., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.; "Arabidopsis thaliana chromosome I BAC F3F19 sequence."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKYDQLVTR
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kaniya A., Kawai Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakuraii T., Satoun M., Seki M., Shinn P., Yamada K., Shinozaki K., Bcker J., Theologis A., Davis R.W.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30;
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Bradyrhizobiaceae; Bradyrhizobium.
NCBI TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 573;
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                                                                                                                                                                                                                                                                                                                                                         to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
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Last annotation update)
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PROSITE: PSS0102, RRM; 1.
Hypothetical protein.
SEQUENCE 573 AA; 61400 MW; 0DIC10384B86C2BC
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5.9;
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EMBL; AYC62527; AAL32605.1; --
EMBL; BY002575; AAC00935.1; --
PIR; C86266; C86266.
GO: 0003676; F: nucleic acid binding; IEA.
IllierPro: IPR000504; RNa_rec_mot.
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Pred. No.
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184 NVMMNKSPTQSFVV 197
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01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
B115298 protein.
                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=cv. Columbia, Theologis A.; Submitted (MAY-1999)
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SEQUENCE FROM N.A.
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            ALALQSDARKYDQLVTRVVTHEMAHAGQGADNSTIELTQNGFRNNATIDQWNAKNSDITV 115
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Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kobara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
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01-MAY-2000 (TEMBLrel. 13, Last sequence update)
01-MCT-2003 (TEMBLrel. 25, Last annotation update)
01-OCT-2003 (TEMBLrel. 25, Last annotation update)
F3F19.21 protein (Hypothetical protein).
F3F19.21 OR ATIG13190, F3F19.21 OR ATIG13190.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Etreptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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DNA Res. 9:189-197(2002).
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Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Bradyrhizobiaceae, Bradyrhizobium.
                                                              55; Indels
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(TremBlrel. 24, Last sequence update)
(TremBlrel. 24, Last annotation update)
                                                                                                                                                                                                               ||:||:||:||:||:||GQFGSNHTTILTQDGNGNIAAGVQVGRGCSANVSQ 131
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STRAND=cv. Columbia,
Vysotskaia V.S., Schwartz J.R., Yu G.,
Liu S., Li J., Kremenetskaia I., Luros
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EMBL; AP005954; BAC50562.1; -.

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CsGB OR BLL5297.
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01-JUN-2003
01-JUN-2003
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                      MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.,
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EMBL, BX572055; CAE20431.1; --
                                                                                                                                                                                                     "Complete genomic sequence of nitrogen-fixing symbiotic bacterium tradyrhicobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
EMBL; AP005954; BAC50563.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
12.7%; Score 98.5; DB 16; Length 154;
Best Local Similarity 36.8%; Pred. No. 1.3;
Matches 25; Conservative 12; Mismatches 28; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prochlorococcus marinus (strain MIT 9313).
Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hemolysin-type calcium-binding region:RTX N-terminal domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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SEQUENCE 1765 AA; 187603 MW; 817CE4F5007580CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       9D698D711E2EED19 CRC64;
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12.6%; Score 97.5; DB 16;
Best Local Similarity 28.7%; Pred. No. 31;
Matches 41; Conservative 21; Mismatches 50;
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                                                                                                                                                                                                                                                                                                                                                                                       15420 MW;
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                                                                                                                                                                                                                                                                                                                                                                                               154 AA;
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SEQUENCE FROM N.A.
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NCBI_TaxID=74547;
                                                                                                                                                                                                                                                                                                                                                             Complete proteome
STRAIN=USDA 110;
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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Q7V8S5
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Search completed: August 2, 2004, 14:54:39 Job time: 30.7 secs

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aab36351 AgfA::PT3	Aab36354 AgfA::PT3	1625	Aab36341 Salmonell	3570	33	5350	5352		5347	5353	5349	48	343	걾	Aar62761 AgfA segu	59 Salmo	Fibi	63 FN		18 Sal	N	39 Salmone	Sal	44 E. Coli
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æ	Query Match Le	100.0	91.8	87.9	87.9	87.2	84.7	79.8	78.5	77.8	77.6	77.4	77.3	73.1	67.1	66.5	64.0	64.0	57.1	47.8	18.8	17.0	14.8	•	•	4
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copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant Agfa protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant Agfa protein which is useful for the expression of recombinant Agfa protein which is useful for useful for the expression of recombinant post on this animal in a system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogens(city and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response immunogens, in inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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0
                                                                                                                                                                                                                                                                                                                                                                                   Length 151;
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                                                                                                                                                                                                                                                                                                                                                                                 Score 776; DB 3;
Pred. No. 9.5e-68;
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100.0%; Pred. No. 9.5
ive 0; Mismatches
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Best Local Similarity 100.
Matches 151; Conservative
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N-PSDB; AAC64630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli.
                                                                                                                                                                                                                                                                                                                                             Sequence 151 AA;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative finbriae (SEPI/TAPE) mucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterbacteriaceae for the production of fimbriae comprising recombinant of a recombinant gene into the chromosome of the C AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologus species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, copy of that gene; and maino acid polymer comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the copy of the animal in conjunction with a carrier or diluent. (I) is cuseful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heerologus antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogens, which may be important for directing an immunogense or purify in large amount. The present sequence is given in the example first and adhesion properties relevant for an efficient incomplement the example fimbrial subunit proteins are easy and consense the example finbrial invention invention.
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Pred. No. 1.7e-61;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the exemplification of the present invention
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Best Local Similarity 91.1%;
Matches 144; Conservative
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26-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .0-NOV-1994.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR74625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYVI-)
(KING/)
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g
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cc thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and content of Strains of Salmonella, Escherichia coli and Strains of Strains of Fimbriae comprising recombinant of directing recombination submits, respectively; (2) directing recombination of a recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA comprising separating an amino acid polymer comprising a recombinant of protein containing a replacement segment or segments of foreign amino cortaining a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or cortained home or sequences grown on a Salmonella, E. coli or cortained home or sequences grown on a Salmonella, C. coli or cortained home or sequences grown and salmonella, E. coli or cortained home or sequences grown and salmonella, E. coli or cortained home or sequence in an animal. In a fimbrial presentation electricing an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to concine, the carrier fimbrial submit protein sequence in the carrier fimbrial submit proteins are usually strong immunopensive to purify in large amount. The present sequence is given in concine, the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDARKSETTITOSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKLLKVAAFAAI VVSGSALAGVV PQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 682; DB 3;
Pred. No. 1.4e-58;
2; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNAALVNOTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123
/note= "Encoded by GCC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella enteritidis 27655-3b agfA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ā
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93US-00054452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94US-00233788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.7
Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kay WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Collinson SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5635617-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-JUN-1997.
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29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW23570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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AAW23570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDARKSETTITOSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are:
                                                                                                                                                                                                                                               immunization compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKLILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                      Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                             Salmonella AgfA protein and DNA are used in vaccine and genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen.
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                                                                                                                                                                                                                                                                                                                                                                        Score 682; DB 2; Length 151;
Pred. No. 1.4e-58;
2; Mismatches 12; Indels
                     Doran JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNAALVNQTASDSSVMVRQVGFGNNATANQY
                   Clouthier SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 135; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB36341 standard; protein; 151 AA
                                                                                                                                                                                    7B; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 7
                                                                                                                                                                                                                                                                                                                                                                            87.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                     SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYVI-) UNIV VICTORIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-672631/65.
N-PSDB; AAC64617.
                                                             WPI; 1994-358275/44.
                   Collinson
                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                  Sequence 151 AA;
                                                                                   N-PSDB; AAQ87467
                                                                                                                                                                                    Disclosure; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200060102-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            White AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB36341;
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                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                        Kay
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Gaps

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back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, copy of that gene; and (4) eliciting an immune response in an animal, protein containing a replacement segment or segments of foreign animal protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, B. coli or fine the mainterpolate animal in colination with a carrier or diluent. (I) is believed animal in colination with a carrier or diluent. (I) is useful for the expression of recombinant Agfa protein which is useful for the expression of recombinant Agfa protein which is useful for system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid finbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHA-- 118
                                                                          The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative fimbriae (SETI//TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA. CsgA and AgfA-homologue filmbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into a recombinant gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosomal gene replacement; fimbrin; epitope; ssponse; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -------GGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
    protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.7%; Score 657; DB 3;
81.9%; Pred. No. 4e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4gfA::PT3#5 amino acid sequence SEQ ID NO:20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 4e-5
0; Mismatches
                                          Disclosure; Page 139; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDARKSETTITQSGYGNGADVGQGADN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB36350 standard; protein; 151 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 136; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agfA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200060102-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-OCT-2000
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      рp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG 120
                                                                                                                                                                  The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 27655-3b. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella acid molecules from greater than 99% of Salmonella acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDAKKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                          Isolated Salmonella gene agfA - used for diagnosis of Salmonella or enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 677; DB 2;
Pred. No. 4.4e-58;
2; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ID NO:30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NNPALVNOTASDSSVMVROVGFGNNATANOY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AgfA::PT3#10 amino acid sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SK,
                                                                                                                                Example 2; Fig 7; 85pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB36355 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Doran JL,
                    WPI; 1997-309886/28
N-PSDB; AAT74142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-672631/65.
N-PSDB; AAC64631.
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200060102-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-OCT-2000
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셤
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Length 151; Indels

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09 9 --YDQLVTRVVTHEMAHADQ 105

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA control of the gene has been replaced by a segment of a foreign DNA control of this segment of a foreign by the control of this aggregative finbriae (SEPI/TAP) mucleation depended assembly system of strains of Salmonella Eschericha coli and control of strains of finbriae comprising recombinant of Enterobacteriacae for the production of finbriae comprising recombination of a recombination of a recombinant gene into the chromosome of the homologous species, (3) directing recombination of a recombinant gene control of a recombinant gene into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a recombinant page.

Comprising separating an amino acid polymer comprising a recombinant page comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the control of the animal in conjunction which a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant AgfA protein which is useful consistent the hererologous antigens are presented in high numbers (up to system the hererologous antigens are presented in high numbers (up to system the hererologous antigens are presented in high numbers (up to vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response in anymore. The present sequence is given in the exemplification of the present invention invention in the exemple of the present invention.
                                                                                                                                                                                                                                           Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                        Kay WW,
                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 137; 139pp; English.
                                                                                                        Collison SK,
                                                 (UYVI-) UNIV VICTORIA
                                                                                                        Doran JL,
                                                                                                                                                                                   N-PSDB; AAC64626
05-APR-1999;
                                                                                                        White AP,
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Seguence 151 AA;

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61 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHA-------- 103
                                                                                                                            09
                                                                                                                                                                                                              98
                                                                                    1 MKLLKVAAFBAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                            1 MKLLKVAAFFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                          61 SDARK---------YDQLVTRVVTHEMAHAGQGADNSTIELTQNGFR
                                              Gaps
                                                                                                                                                                                                                                                      104 -----DQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                            99 NNATIDÓWNÁKNSDITVGQYGGNNAÁLVNQTÁSDSSVMVRQVGFGNNATÁNQY 151
                                              44;
Score 619; DB 3; Length 151;
Pred. No. 2e-52;
0; Mismatches 0; Indels
  79.8%;
                                            Conservative
                      Local Similarity
                                            Matches 129;
      Query Match
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Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen.
                                                                                                      AqfA::PT3#7 amino acid sequence SEQ ID NO:24.
                         AAB36352 standard; protein; 151 AA.
                                                                           (first entry)
                                                                            26-FEB-2001
                                                   AAB36352;
           AAB36352
ID AAB
RESULT 8
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RESULT

120

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The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbries (SEPI)/TAP) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enteropacteriacae for the production of fimbriae comprising recombinant of Enteropacteriacae for the production of fimbriae comprising recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of the chromosome of the homologous species, replacing the native copy of that gene, and (4) eliciting an immune response in an animal, copy of that gene, and (4) eliciting an immune response in an animal, copy of that gene, and (4) eliciting an immune response in an animal, copy of that gene or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence the animal in conjunction which a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which the carrier fimbrial submit protein possesses both the immunogens, which may be important for allecting an immune response in an animal in conjuncting in the carrier fimbrial submit proteins are usually strong immunogens, which may be important for directing an immune response in expensive to purify in large amount. The present sequence is given in the exemplification of the present invention received the present invention received the present invention received the present invention received to purify in large amount. The present sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----NYDQLVTRVVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEMAHADQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---NQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 609; DB 3; Length 151;
Pred. No. 1.9e-51;
0; Mismatches 0; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDARKSETTITQSGYGNGADVGQGAD------
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X
                                                                                                                                                                                                                                                                                                                                          Kay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                        Collison SK,
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llarity 73.6%;
Conservative C
                                                                                                                                                                                                  05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 138; 139pp;
                 Salmonella enteritidis.
Escherichia coli.
Synthetic.
                                                                                                                                                                                                                                                                                            (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                        Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-672631/65.
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Matches 128; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAC64628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 151 AA;
                                                                                                          WO200060102-A2
                                                                                                                                                                                                                                              05-APR-1999;
                                                                                                                                                      12-OCT-2000
                                                                                                                                                                                                                                                                                                                                          White AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA casequence which encodes a foreign epicope or antigen. Also described are: (1) use of thin aggregative fimbries (SEPI7/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and casembly system of strains of Salmonella, Escherichia coli and casembly system of strains of Salmonella, Escherichia coli and directing recombination of fimbriase comprising recombination of a recombination of a recombination of a recombinant gene into the chromosome of the homologous species, (3) directing recombination of a recombinant gene copy of that gene, and (4) eliciting an immune response in an animal. Comprising separating an amino acid polymer comprising a recombinant pactor or sequence or sequences grown on a Salmonella, E. coli or comprising separating an amino acid polymer comprising a replacement segment or sequence or sequences grown on a Salmonella, E. coli or comprising case bost cell, from the host cell and introducing the protein to the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrial in for directing an immunogens, which may be important for directing an immunogens, which may be important for directing an immune response in an animal in respect the inserted epitope, and hybrid fimbriae are easy and intention in a signification in the carrier the inserted epitope, and hybrid fimbriae are easy and intention in the carrier of inserted epitope, and hybrid fimbriae are easy and additional in the carrier of inserted epitope, and hybrid fimbriae are easy and intention in the carrier financial subunit proteins are usually strong incoments to manify, in larva and hybrid fimbriae are easy and additional and an animal manimal maniform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                       Salmonella, agfA, chromosomal gene replacement, fimbrin, epitope, vaccine, immune response, immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.8%; Score 604; DB 3; Length 151;
80.8%; Pred. No. 5.9e-51;
Live 6; Mismatches 23; Indels
                                                                                                                                                                        AgfA::PT3#1 amino acid sequence SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 135; 139pp; English.
                         AAB36346 standard; protein; 151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-APR-2000; 2000WO-CA000356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0127888P
                                                                                                                            (first entry)
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Best Local Similarity 80.8
Matches 122; Conservative
                                                                                                                                                                                                                                                                                             Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           White AP, Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-672631/65
                                                                                                                                                                                                                                                                                                                         Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAC64622
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                                                                                                                                                                                                                                                                                                                                                                                          WO200060102-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-APR-1999;
                                                                                                                         26-FEB-2001
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                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                           AAB36346;
AAB36346
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA segment of thin aggregative finbriae (SER17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the homologous species; replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the coll sequence the arrival in an animal. In a fimbrial presentation a useful for the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for the the hybrid finbrian protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit protein sequence is given in against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in
120
                                 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNÅTIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
61 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                    Salmonella, agfA, chromosomal gene replacement, fimbrin, epitope, vaccine, immune response, immunogen.
                                                                                                                                                                                                                                                                                                                               AgfA::PT3#2 amino acid sequence SEQ ID NO:14.
                                                                          NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                   |||||||
|NAALVNYDQLVTRVVTHEMAHANNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kay WW;
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                                                                                                                                                                                                             AAB36347 standard; protein; 151
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                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella enteritidis.
Escherichia coli.
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N-PSDB; AAC64623.
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26-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative finbriae (SBF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and harterobacteriaceae for the production of finbriae comprising recombinant AgfA, CsgA and AgfA-homologue finbrin subunits, respectively; (2) directing recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a relative comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG 120
                                                                                                                                                                            61 SDARKSETTITOSGYGNGADVGQGADNSTIELTONGFRNNATIDOWNAKNSDITVGOYDO 120
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                                                                                                  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSCPDSTLSIYQYGSANAALALQ
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                           Salmonella, agfA, chromosomal gene replacement, fimbrin, epitope,
                                                                          ..
                                                Length 151,
                                                                         Indels
                                                 Score 602; DB 3;
Pred. No. 9.3e-51;
                                                                                                                                                                                                                                                                                                                                                                    AgfA::PT3#8 amino acid sequence SEQ ID NO:26.
                                                                                                                                                                                                     121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
 of the present invention
                                                                                                                                                                                                                            121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
                                                                          5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 138; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                           vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Collison SK,
                                                                                                                                                                                                                                                                                          AAB36353 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-APR-2000; 2000WO-CA000356.
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                                                 77.6%;
81.5%;
                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                              Similarity 81.5
                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYVI-) UNIV VICTORIA
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 the exemplification
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Synthetic.
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                          Sequence 151 AA;
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                                                                          Matches 123;
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                                                    Query Match
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologue antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 601; DB 3;
Pred. No. 1.2e-50;
1; Mismatches 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine; immune response; immunogen.
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81.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 151 AA;
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N-PSDB; AAC64624.

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casembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and anterobacteriaceae for the production of fimbria comprising recombinant CC AgrA, cSgA and AgrA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising recombinant AgrA protein containing a replacement segment or segments of foreign amino acid polymer comprising a recombinant AgrA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequence strong man as a man a salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequence of recombinant AgrA protein which is useful for useful for the expression of recombinant AgrA protein which is useful for useful for the expression of recombinant AgrA protein mumbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the rearrier fimbrial subunit protein possesses both the vaccine, the carrier fimbrial subunit protein are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and immunogens, which may be important for present sequence is given in the exemplification of the present invention
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Pred. No. 1.5e-50;
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81.5%;
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Matches 123, Conservative
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Synthetic.
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are:

(I) use of thin aggregative finbriae (SEP1/7AF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Encoded the species of the production of finbriae comprising recombinant of directing recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of copy of that gene; and (4) eliciting an immune response in an animal. Copy of that gene; and (4) eliciting an immune response in an animal or protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a salmonella, E. coli or acid sequence or sequences grown on a salmonella, E. coli or acid sequence or sequences grown on a salmonella, E. coli or acid sequence or sequences grown on a salmonella, E. coli or acid sequence or sequences grown on the host cell, from the host cell and introducing the protein which is useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to solo, 000 copies/cell), the hybrid finbrin protein possesses both the immunogens which may be importent for an efficient liver in amunogens, which may be importent for an event acanally strong immunogens, which may be importent for an event acanally in the provent of against th
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                                           Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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Pred. No. 2.4e-47;
5; Mismatches 24; Indels
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                                                                                                                                              Disclosure; Page 136; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB36343 standard; protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.1%;
80.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200060102-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
AAB36343
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Herwald H;

Wikstroem M,

Olsen A,

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The invention relates to an isolated peptide capable of binding a mammal selected from sequences shown in ABRA2642, ABRA2648-49. The peptide or antibody is useful for tracting a baselectial infection in a human or animal or in the manufacture of a medicament for the prophylactic treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigalla infection. The peptide that is immobilized on a solid support is also useful as a reagent for determining the ability of a plasma protein to bind to bacteria. The present sequence represents an E. coli
                                                                                                                                                                                                                                                                                                                                                                           New isolated peptide capable of binding a mammalian plasma protein, useful in the manufacture of a medicament for the prevention and/or treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infections.
Plasma protein; immune response; antibacterial; vaccine; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 41-42; 42pp; English.
                                                                                                                                                                30-JAN-2003; 2003WO-EP000943
                                                                                                                                                                                                       31-JAN-2002; 2002GB-00002275
                                                                                                                                                                                                                                             (HANS-) HANSA MEDICAL RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                        WPI; 2003-646136/61.
N-PSDB; ACF36153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                          Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 151 AA;
                                                                                 WO2003064446-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 kDa protein
                                                                                                                          07-AUG-2003
                                                                                                                                                                                                                                                                                    Bjoerck L,
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                                                                                                                                                                                                                                                                                                                                       The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative finbriae (SEPA)/TAP) nucleation depended assembly system of strains of Salmonella Escherichia coli and Enteropacteriacae for the production of fimbriae comprising recombinant of Enteropagous species; (3) directing recombination of a recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or useful for the expression of recombinant AgfA protein which is useful for useful for the carrier finding an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to sequence, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response in expensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                        Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 521; DB 3;
; Pred. No. 7.5e-43;
17; Mismatches 29
                                                                                                                            Kay WW;
                                                                                                                                                                                                                                                                                                           English
                                                                                                                            Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.18;
        05-APR-2000; 2000WO-CA000356.
                                                                                                                                                                                                                                                                                                           Disclosure; Page 135; 139pp;
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                                                                                   (UYVI-) UNIV VICTORIA
                                                                                                                            White AP, Doran JL,
                                                                                                                                                                    2000-672631/65.
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SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG 120
               NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                        GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
  61
                                                       121
                            g
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E. coli CsgA subunit 15 kDa protein

04-DEC-2003

XEXEXEX

ABR82651;

ABR82651 standard; protein; 151 AA

RESULT 15 ABR8265

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2, 2004, 14:48:27
  Search completed: August
                        Job time : 45.9 secs
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61 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG 120 

151

121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 121 GNGAAVDOTASNSSVNVTQVGFGNNATAHOY

9 9

Gaps

·: 0

; Score 516; DB 7; Length 151; ; Pred. No. 2.3e-42; 17; Mismatches 30; Indels

66.5%;

1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 1 MKLLKVEAIAAIVFSGSALAGVVPQYGGGGHGGGGNNSGPNSELNIYQYGGGNSALAD

(010/sn) HUD/8 860/ 5/4/

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MXLLXVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALO
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Sequence 24...
Sequence 30710, A.
Sequence 2668, A.
Sequence 2668, A.
Sequence 199, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 59, Appl Sequence 57, Appl Sequence 37, Appl Sequence 42, Appl Sequence 337, App Sequence 180, App Sequence 180, App Sequence 180, App Sequence 7849, App Sequence 24717, A Sequence 24717, A Sequence 2658, A Sequence 2658,
                                                                          August 2, 2004, 14:40:48; Search time 12 Seconds (without alignments) 649.627 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 131,
Sequence 131,
Sequence 204,
Sequence 5434,
Sequence 42, A
                                                                                                                               US-09-543-407-22
776
1 MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
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Sequence
Sequence
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(GGDZ_6/ptodata/2/iaa/5A_COMB.pep:*

(GGDZ_6/ptodata/2/iaa/5B_COMB.pep:*

(GGDZ_6/ptodata/2/iaa/6A_COMB.pep:*

(GGDZ_6/ptodata/2/iaa/6A_COMB.pep:*

(GGDZ_6/ptodata/2/iaa/PGTUS.COMB.pep:*

(GGDZ_6/ptodata/2/iaa/PCTUS.COMB.pep:*

(GGDZ_6/ptodata/2/iaa/PCTUS.COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-233-788A-57

US-08-233-788A-57

US-08-234-417A-5

US-09-356-417A-5

US-09-58-419-337

US-09-58-419-337

US-09-59-419-180

US-09-59-419-180

US-09-489-039A-7849

US-09-252-991A-20717

US-09-252-991A-30710

US-09-252-991A-30710

US-09-252-991A-30710

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	78 10.1 878 4 US-09-540-236-3401 77.5 10.0 1216 4 US-09-134-000C-5130 77.5 10.0 437 2 US-09-136-519.32 77.5 10.0 673 3 US-09-196-387-8 77.5 10.0 673 4 US-09-196-387-8 77.5 10.0 941 4 US-09-316-447A-9 77.5 10.0 949 3 US-09-36-447A-9 77.5 10.0 949 3 US-09-36-87-10 77.5 10.0 1327 4 US-09-196-387-2 77.5 10.0 1327 4 US-09-196-387-2 77.5 10.0 1327 4 US-09-196-387-2 77.5 10.0 1327 4 US-09-196-387-2 77.5 10.0 1327 4 US-09-196-387-2 77.5 10.0 1327 4 US-09-196-387-2 77.5 10.0 1327 4 US-09-595-684B-39 77.5 10.0 1327 4 US-09-595-684B-39 77.5 10.0 1327 4 US-09-595-684B-39 77.5 10.0 1327 4 US-09-595-684B-39 77.5 10.0 1327 4 US-09-595-684B-39 77.7 9.9 26 4 US-09-595-684B-39 77.9 9.9 1339 4 US-09-336-447A-13	ALIGNMENTS	98-23 - 988A-59 sequence 59, Application US/08233788A sequence 59, Application US/08233788A sequence 59, Application US/08233788A setent No. 5635617 GENERAL INFORMATION: APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Gollinson, Karen S. APPLICANT: Gollinson, Karen S. APPLICANT: Gollinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Saddle S. CORRESPONDENCE ADREES: ADDRESSEE: Sed and Berry STRET: Washington COMPUTRY: U.S.A. ZIP: 98104-7092 COMPUTRY: U.S.A. ZIP: 98104-7092 COMPUTRY: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/233,788A FILING DATE: 26-ARR-1994 FILING DATE: 26-ARR-1994 FILING DATE: 26-ARR-1994 FILING DATE: 26-ARR-1994 FILING DATE: 26-ARR-1994 FILIERAX: 3723836 SEEDANBERY INFORMATION FOR SEQ ID NO: 59: SEQUENCE CHARACTERISTICS: LENGTH: 151 amino acid TYPE: amino acid TYPE: amino acid TYPE: mino acid TYPE: proctein	latch	Qy 1 MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ

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US-08-864-038A-3
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                                                                                                                                   61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Doran, James L.
APPLICANT: Ray, William W.
APPLICANT: Colimbon, Karen S.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TITLE OF INVENTION: OF SALMONELA
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.0%; Score 497; DB 1; Length 120; 87.5%; Pred. No. 1.2e-41; ive 2; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: King Joshus
REGISTRATION NUMBER: 35,570
REFREENCE/DOCKET NUMBER: 920043.403C2
TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 57, Application US/08233788A
Patent No. 5635617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 amino acids
amino acid
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Best Local Similarity 87.5
Matches 98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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Sequence 3, Application US/08864038A Patent No. 6001592 GENERAL INFORMATION:

RESULT 3 US-08-864-038A-3

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APPLICANT: KUNIO NAKASHIMA et al.

TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR

TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID

TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING

TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY

TITLE OF INVENTION: TO SAID POLYPEPTIDE

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --GGGAGALA---- 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             461 -----AALAAAGAGGGLGGGGGGG-----ALAAALAAAGAGGGFGGLGGLGGLGGGG 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 LLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGCNSSGPDSTLSIYQYGSANAALALQSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.2%; Score 94.5; DB 3; Length 738; 27.6%; Pred. No. 0.48; tive 14; Mismatches 58; Indels 41
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage COMPUTER: IBM Compatible OPERATING SYSTEM: Microsoft Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    419 LLKSSASASASASASASAG----GGGGGGNGGGNGGGG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 NAALVNQTASDSS--------10WVRQVGFGNNATA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: from 1 to 738
IDENTIFICATION METHOD: E (by experiment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/864,038A
FILING DATE: May 28, 1997
FRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 8-184459
FILING DATE: 15-7uly-1996
ATTORNEY/AGENT INFORMATION:
NAME: C. Bruce Hamburg
REGISTATION NUMBER: P-5610
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pinctada fucata
CELL TYPE: mantle epithelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-336-447A-5
; Sequence 5, Application US/09336447A
; Patent No. 6310190
; GENERAL INFORMATION:
; APPLICANT: HANSEN ERIC J.
; APPLICANT: ABEL, CHRISTOPH
; APPLICANT: COPE, LESLIE D.
; APPLICANT: MACIVER, ISOBEL
                                                                                                                                                                                                                                E: 812-5 Hirano
Isshinden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212)953-7733
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                        oraTE: Mie-prefecture
COUNTR: JAPAN
ZIP: 514-01
MpHTMF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein ORIGINAL SOURCE: ORGANISM: Pinctada fu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 14-
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                                                                                                                                                                                                                                                               STREET: Isshind
CITY: Tsu-city
STATE: Mie-pref
                                                                                                                                                                                                                                  ADDRESSEE:
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58 ALOSDARKSETTIT----OSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDIT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 GLYTDKNLSITNITGIIEIANNKATDVGGGA-----YVKGTLTCENSHRLQFLKNSSDKQ 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 ALQSDARKSETTIT---QSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDIT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               258 GLYTDKNLSITNITGIIEIANNKATDVGGGA-----YVKGTLTCENSHRLQFLKNSSDKQ 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKVAAFAAIVVSGSALAGVVPQWGGGGN--HNGGGNSSGPDS----TLSIYQYGSANAAL 57
  11. ALQSDAKGKLDSVATDYGAAIDGFIGDVSGLANGNGATGDFAGSNSQMAQVGDGDNS 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 LKVAAFAAIVVSGSALAGVVPQWGGGGN--HNGGGNSSGPDS----TLSIYQYGSANAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206 LKAQASAG---NADAWASSSPQSGSGATTVSDSGDSSSGSDSDTSETVPVTAKGG----
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                                                                                                                   US-09-620-412C-337
Sequence 337, Application US/09620412C
Sequence 337, Application US/09620412C
Sequence 337, Application US/09620412C
SENERAL INFORMATION:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: COMPOSITIONS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C7
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FEALESQ for Windows Version 3.0/4.0
SEQ ID NO 37
LENGTH: 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 337, Application US/09598419
Patent No. 656886
GENERAL INPORMATION:
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.46966
CURRENT APPLICATION NUMBER: US/09/598,415
CURRENT FILING DATE: 2000-06-20
NUMBER OF:SEQ ID NOS: 357
SOFTWARE: FEASLSEQ for Windows Version 3.0/4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 585;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.1%; Score 86.5; DE
llarity 31.6%; Pred. No. 2.2;
Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.1%; Score 86.5; Di
31.6%; Pred. No. 2.2;
tive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 VGQ-YGGNNAALVNQT 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           313 GGGIYGEDNITLSNLT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 31.6%
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
hes 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-620-412C-337
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US-09-598-419-337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: RUDERT, FRITZ
APPLICANT: GE, LIMING
APPLICANT: GE, LIMING
APPLICANT: ILAG, VIC
TITLE OF INVENTION: NOVEL METHOD AND PHAGE FOR THE IDENTIFICATION OF
TITLE OF INVENTION: NOVELED SEQUENCES ENCODING MEMBERS OF A MULTIMERIC
TITLE OF INVENTION: NOVELED COMPLEX
FILE REFERENCE: MORPHO/9;
CURRENT APPLICATION NUMBER: US/09/495,880A
CURRENT FILING DATE: 1998-08-03
PRIOR APPLICATION NUMBER: PCT/EP98/04836
PRIOR APPLICATION NUMBER: PCT/EP98/04836
PRIOR FILING DATE: 1997-08-01
NUMBER OF SEQ ID NOS: 50
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: ompA-FLAG-peptide3-
OTHER INFORMATION: gene IIIs encoded by phage vector fpep3_1B-IR3Seq (circular)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 GGGDYNEAKGNYSTVGGGSSNTAKGEKSTIGGGDIN------DANGTYSTIGGGYISRA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 -GNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYG---GNNAALV----N 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 IGDSSTIGGG--YYNQATGEKSTVAGGRNNÓATGNNSTVAGGSYNQATGNNSTVAGGSHN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48 YOYGSANAALALOSDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                          75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------VVPQWGGGGNH-NGGGNSSGPDSTLSI 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 KTAIAIAVALAGFATVAQADYKDVDCIVYHAHYLVAKCGGGGSEFNAGGGSGG----- 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKNSDI-----TVGQYG-----GNNAALVNQTA-----SDSSVMVRQVGFGNNA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                     28 GGGNHN-----GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGY---
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: 18PA1 AND USPA2 ANTIGENS OF MORAXELLA CATARHALIS
FILE REFERENCE: AMCY.024
CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47;
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                                                                                                                                                                                                                                                                                                                                             DB 4; Length 892;
                                                                                                                                                                                                                                                                                                                                                                                          57;
                                                                                                                                                                                                                                                                                                                                             11.2%; Score 87; DB 4
26.8%; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                          15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 OTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 OATGEGSF---AAGVENKANAN 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 KVAAFAAIVVSGSALAG------
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US-09-955-880A-42
Sequence 42, Application US/09495880A
Patent No. 6667150
                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43; Conservative
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Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMAL
US-09-495-880A-42
                                                                                                                                                                                                                                                                                                                                                                                          38;
                                                                                                                                                                                                                                                                              ; ORGANISM: MOJ
US-09-336-447A-5
                                                                                                                                                                                                                       892
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Sequence 7849, Application US/09489039A

Sequence 7849, Application US/09489039A

GENERAL INFORMATION:
APPLICANT GALY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747.
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7849
FERMAN FOR SEQ ID NOS: 14342
  440 GLYTDKNLSITNITGIIEIANNKAIDVGGGA----YVKGTLTCENSHRLQFLKNSSDKQ 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 ALQSDARKSETTIT---QSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDIT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | :| | | | | : | | | 440 GLYTDKNLSITNITGIIEIANNKATDVGGGA-----YVKGTLITCENSHRLQFLKNSSDKQ 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259 GGLDRNGANANGQTDTFGIYAFDTLTLTERIEINGGLRLDNYHTKYDSATACGGSGRGAI 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 VGQGADNYDQLVTRVVTHEMAHADQWNA-----KNSDITVGQYGGNNAALVNQTASDS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         388 LKAQASAG----NADAWASSSPQSGSGATTVSDSGDSSSGSDSDTSETVPVTAKGG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 LKVAAFPAIVVSGSALAGVVPQWGGGGN--HNGGGNSSGPDS----TLSIYQYGSANAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23; Gaps
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                                                                                                                                                                                                           US-09-598-419-180

; Sequence 180, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skediky, Yasir A.W.
; APPLICANT: Skediky, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DARGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.1%; Score 86.5; DB 4; Length 1752; 31.6%; Pred. No. 9; ive 12; Mismatches 58; Indels 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 589;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 GGNHNGGGNSSGPDSTLSIYQYGS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klebsiella pneumoniae
                                                     115 VGQ-YGGNNAALVNOT 129
                                                                                                           495 GGGIYGEDNITLSNLT 510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 31.6%
Matches 43; Conservative
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US-09-598-419-180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 180
LENGTH: 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Bratia, Ajay
APPLICANT: Bratia, Ajay
APPLICANT: Skeik, Yasir
APPLICANT: Skeik, Yasir
APPLICANT: Ring, Steve
APPLICANT: Maisonneuve, Jeff
TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TILLE OF INVENTION: DAGGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C5
CURRENT APPLICATION NUMBER: US/09/556,877
CURRENT FILING DATE: 2005-04-19
NUMBER OF SEQ ID NOS: 305
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 180, Application US/09620412C

Sequence 180, Application US/09620412C

Patent No. 6448234

GENERAL INFORMATION:

APPLICANT: Steven P. Fling

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND

TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

CURRENT APPLICATION NUMBER: US/09/620,412C

CURRENT FILING DATE: 2000-07-20

NUMBER OF SEQ ID NOS: 363

SOFTWARE: FastSEQ for Windows Version 3.0/4.0

SEQ ID NO 180

LENTH: 1752
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31.6%; Pred. No. 9;
iive 12; Mismatches 58; Indels
                                                                                                                                                        Sequence 180, Application US/09556877 Patent No. 6432916
313 GGGIYGEDNITLSNLT 328
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Best Local Similarity 31.6%
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Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Chlamydia
US-09-556-877-180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Chlamydia
US-09-620-412C-180
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US-09-620-412C-180
                                                                                                           SULT 8
-09-556-877-180
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Sequence 2668, Application US/0925291A;
Sequence 2658, Application US/0925291A;
Sequence 2658, Application US/0925291A;
Patent No. 6551795;
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS;
PRIOR FILING DATE: 1999-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26658
LENGTH: 1034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --DVGQGADNYDQLVT-----RVVTHEMAHADQWN- 107
                                     357 AARAPMPAITEPGRSGTGAPDPRRTAGTGEEQGELVVKDFAHPAYRLVTGQEIEGDSWNG 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 VSGSALAGVVPQWGGGGNHNG-----GGNSSGPDSTLSIYQYGS-ANAALALQSDAR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 -QWNAKNSDITVGQYG--GM------NA-LVNQTASDSSVMVRQVGF 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.8
                                                                                                                 ------AKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.3%; Score 80; DB 4; Length 1034; ilarity 26.7%; Pred. No. 20; Conservative 19; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 26.7%; Pred. No. 15;
Matches 31; Conservative 10; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT , ORGANISM: Pseudomonas aeruginosa US-09-252-991A-26658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30710
    62 DARKSETTITOSG-YGNGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
ses 47; Conserv
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US-09-252-991A-26658
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US-00-252-991A-24717
US-00-252-991A-24717
Sequence 24777, Application US/09252991A
Sequence 24777, Application US/09252991A
Sequence 24777, Application US/09252991A
Sequence 24777, Application US/09252991A
Sequence 24777, Application US/0925291A
TITLE OF INVENTION: ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION UNMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24717
                                                                                                                                                                                                                       Sequence 4764, Application US/09328352
Sequence 4764, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BADMANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 ALALQSDARKSETTI-----TQSGYG-----NGADVGQGADNYDQLVTRVVTHEM 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 AGNGIA-----SGNGEHNYGIGNGNGDDVDITAPITGVINISGNSFTLIGNSSSSSVNT 353
           319 ACPPGQSTGSPVTTVDTAKSGNLVNWKAGALYRLJEQGNVYV-----NYALSQQPPGGS 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 VAAFAAIVVSG-SALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANA---ALALQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --- SANA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       354 APTITSNIVNDNDTIDNGNSGGTGSGSGNGSGDGLLNGAASGNGEHNYG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 25.6%; Pred. No. 7;
Matches 43; Conservative 20; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 AHADOWNAKNSDIT-----VGQYGGNNAALVNQTASDS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 SGSALAGVVPQWGGGGNHNGG-GNSSGPDSTLSIYQYG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
10.6%; Score 82; DB 4;
Best Local Similarity 24.1%; Pred. No. 12;
Matches 38; Conservative 15; Mismatches 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Acinetobacter baumannii
US-09-328-352-4764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24717
                                                                                                                             373 SFALAASGSGNSANRTDF 390
                                                                                  134 SVMVRQVGFGNNATANQY 151
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65KSETTITOSGYGNGADVGQGADNYDQLVTRV 95	807 LGNLKASGSVTDQGGADLGGLVGNNSQSAIETAEATGKVSGGSNSRVGCLIGHNLGG 863	96 -VTHEMAHADQWNAKUSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNA 146	864 SVAHAISRGDVSGGFNS-LVGGLVGHNGGELVNVDASGRVSAAASASVGGLVGGNA 918	Search completed: August 2, 2004, 14:58:35 Job time : 13 secs
δλ	QD	δλ	qq	Search Job tir

us-09-543-407-22.rapb

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version 5.1.6
- 2004 Compugen Ltd.
 GenCore (c) 1993
            Copyright
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OM protein - protein search, using sw model

2, 2004, 14:54:48; Search time 36.8 Seconds (without alignments) 1287.123 Million cell updates/sec August Run on:

US-09-543-407-22 776 1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

Total number of hits satisfying chosen parameters:

1291235 segs, 313682936 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

Published Applications AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_TMW\_PUBL\_pep:\*
3: /cgn2\_6/ptodata/2/pubpaa/PCT\_TMW\_PUBL\_pep:\*
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
5: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
7: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
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10: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
11: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
11: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
12: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*
13: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
14: /cgn2\_6/ptodata/2/pubpaa/US108\_PUBCOMB.pep:\*
15: /cgn2\_6/ptodata/2/pubpaa/US108\_PUBCOMB.pep:\*
16: /cgn2\_6/ptodata/2/pubpaa/US108\_PUBCOMB.pep:\*
17: /cgn2\_6/ptodata/2/pubpaa/US108\_PUBCOMB.pep:\*
18: /cgn2\_6/ptodata/2/pubpaa/US108\_PUBCOMB.pep:\*
18: /cgn2\_6/ptodata/2/pubpaa/US108\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Sequence 4, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 20638, A	Sequence 146, App	Sequence 147343,	Sequence 56041, A	Sequence 275468,	Sequence 57763, A	Sequence 1130, Ap	Sequence 1130, Ap	Sequence 445, App	Sequence 594, App	Sequence 45. Appl
	ID	US-09-741-873B-4	US-09-741-873B-4	US-09-741-873B-2	US-09-741-873B-2	US-10-369-493-20638	US-09-793-306-146	US-10-437-963-147343	US-10-425-114-56041	US-10-424-599-275468	US-10-425-114-57763	US-09-880-748-1130	US-10-293-418-1130	US-09-841-132-445	9 US-09-841-132-594	IIS-10-467-534-45
	DB .	12	12	12	12	15	9	16	12	12	13	10	12	9	0	4
	Query Match Length DB	151	151	131	131	445	597	271	369	486	507	251	251	1751	1751	1751
ф	Query	66.8	8.99	56.7	56.7	12.2	12.2	12.1	12.0	12.0	12.0	11.9	11.9	11.7	11.7	7 11
	Score	518	518	440	440	95	O U	94	93	93	93	92.5	92.5	91	91	-6
	Result No.		7	ന	4	Ŋ	ø	7	80	on	10	11	12	13	14	יי

equence 112	equence 1122,	14850	equence 1477	7750	equence 15887	Sequence 162284,	20397	2061	equence 188971,	equence 5, 1	equence 105	'n	equence 337,	ò	406	3962,	77	22263,		1, App	8	70.	68952	quence 61520,	quence 2098,	guence 2098,	e 1153,	equence 115	e 998, A
US-09-880-748-112	US-10-293-418-1122	US-10-437-963-14850	US-10-437-963-1477	US-10-425-114-6775	US-10-437-963-15887	S-10-437-	US-10-424-599-2039	US-10-369-493-2061	US-10-437-963-1889	US-09-952-267-	US-10-437-963-1	US-10-634-862-4	9-841-132	9-841-132-18	US-10-437-963-1406	US-10-425-114-	US-10-282-122A-6779	US-10-437-963-1222	US-10-647-057	US-09-820-843A-2	US-10-437-963-18641	US-10-437-963-1707	US-10-437-963-16895	US-10-425-114-6152	US-09-880-748-209	US-10-293-418-209	US-09-880-748-115	8-	US-10-408-765A-99
51	51 1	93 1	45 1	97 1	03 1	54 1	04 1	86 1	89 1	92 1	91 1	38 1	85	52	448 1	35 1	10 1	70 1	80 1	54 1	00	89 1	76 1	42 1	53 1	53 1	55 1	255 1	48 1
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## ALIGNMENTS

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66.8%; Score 518; DB 12; Length 151;
Best Local Similarity 68.9%; Pred. No. 1.2e-44;
Matches 104; Conservative 18; Mismatches 29; Indels C
                                                                                                                                                                             TYPE: PRT
ORGANISM: Escherichia coli
                                                                                                                                                                                          US-09-741-873B-4
                                                                                                                                                                SEQ ID NO 4
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60

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3 10:54:39 2004

Tue Aug

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## PFPLICANT: Olsen, Arne
TILLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REPREBRENCE: 012899-064
CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT PILING DATE: 2003-04-04
FRIOR APPLICATION NUMBER: US 8801723-1
FRIOR PRIDE ADDICATION NUMBER: US 8801723-1
FRIOR PRIDE TILLING DATE: 1998-05-06
FRIOR FILING DATE: 1997-11-26
FRIOR PRIDE TILLING DATE: 1997-11-26
FRIOR PRIDE TILLING DATE: 1991-11-06
FRIOR FILING DATE: 1991-11-06
FRIOR FILING DATE: 1991-11-06
FRIOR FILING DATE: 1991-11-06
FRIOR FILING DATE: 1994-01-28
FRIOR FILING DATE: 1994-01-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 VGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GVVPQYGGGGNHGGGGNNSGPNSELNTYQYGGGNSALALQTDARNSDLTITQHGGGNGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
56.7%; Score 440; DB 12;
Best Local Similarity 65.6%; Pred. No. 8.3e-37;
Matches 86; Conservative 17; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 12;
PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR FILING DATE: 1990-05-04
PRIOR FILING DATE: 1991-11-06
PRIOR PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR PLING DATE: 1991-11-06
PRIOR PLING DATE: 1992-11-03
PRIOR FILING DATE: 1992-11-03
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-0-28
PRIOR FILING DATE: 1994-0-28
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 10
SSOFWARE: PALENTIN VEYSION 3.0
LENGTH: 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09741873B
Publication No. US20040096965A9
GENERAL INFORMATION:
APPLICANT: Normark, Staffan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.7%;
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US-09-741-873B-2
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ORGANISM: Escherichia coli
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JOURGALL INFORTHAION:

APPLICANT: Olsen, Arne

APPLICANT: Olsen, Arne

TITLE OF INVENTANION: Fibronectin Binding Protein As Well As Its Preparation

FILE REFERENCE: 01289-084

CURRENT APPLICATION NUMBER: US/09/741,873B

CURRENT FILING DATE: 2003-04-04

PRIOR FILING DATE: 1998-05-06

PRIOR FILING DATE: 1998-05-04

PRIOR FILING DATE: 1998-05-04

PRIOR FILING DATE: 1999-05-04

PRIOR FILING DATE: 1991-11-06

PRIOR FILING DATE: 1991-11-06

PRIOR FILING DATE: 1991-11-03

PRIOR FILING DATE: 1991-11-03

PRIOR PAPLICATION NUMBER: US 07/789,437

PRIOR FILING DATE: 1994-01-08

PRIOR FILING DATE: 1994-01-08

PRIOR FILING DATE: 1994-01-08

NUMBER OF SEQ ID NOS: 10

CONTRACT NOS: 10
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Publication No. US20020081722A1
GENERAL INFORMATION:
GENERAL INFORMATION:
Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084
CURRENT APPLICATION UNMER: US/09/741,873B
CURRENT FILING DATE: 2003-04-04
                                                                                                                                               :||| |: |||| | |||||||||||:||
TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG 120
                                                                                                           61 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKLLKVAAIAAIVFSGSAVAGVVPQYGGGGHGGGGNNSGPNSELNIYQYGGGNSALALQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 151;
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66.8%; Score 518; DB 12;
Best Local Similarity 68.9%; Pred. No. 1.2e-44;
Matches 104; Conservative 18; Mismatches 29;
                                                                                                                                                                                                                                             121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                        121 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09741873B Publication No. US20040096965A9 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli
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US-09-741-873B-2
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APPLICANT: Li, Fing Tries of Mucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21 (53221) B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 147343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     358 FGNSGNNNIGFFNSG-NNNVGFFNSGNNN------FGFGNAGDINTGF 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 DNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNN 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGA 85
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                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence:mTTC#3-His US-09-793-306-146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                12.2%; Score 95; DB 9; Length 597; 27.4%; Pred. No. 0.59; ive 14; Mismatches 50; Indels
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US-10-437-963-147343
             CURRENT APPLICATION NUMBER: US/09/793,306
CURRENT APPLICATION NUMBER: US/09/793,306
CURRENT FILING DATE: 2001-02-26
PRIOR FILING DATE: 2000-02-25
PRIOR FILING DATE: 2000-02-25
PRIOR FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 164
SOFTWARE: Patentin Ver: 2.1
SENGTH: 597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yinua
APPLICANT: Cao, Yorgwei
APPLICANT: Wu, Wei
APPLICANT: Bu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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Best Local S:
Matches 37,
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Sequence 20638, Application US/10369493

Publication No. US2030233675A1

GENERAL INFORMATION:

APPLICANT: Gac, Yongwei

APPLICANT: Slater, Steven C.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

CURRENT APPLICANTION NUMBER: US/10/369,493

CURRENT APPLICANTION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 20638

FROM IN OUR SEQ ID NOS: 47374
                                                                                                                                                                             81 VGCGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQV 140
                                                                                                                                                                                                     61 VGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGGGNGAAVDQTASNSSVNVTQV 120
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APPLICANT: Ovendale, Pamela
APPLICANT: Jen, Shyian
APPLICANT: Lodes, Minael
APPLICANT: Lodes, Minael
APPLICANT: Cotixa Orional
TITLE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
                                                                                                          1 GVVPQYGGGGNHGGGGNNSGPNSELNTYQYGGGNSALALQTDARNSDLTITQHGGGNGAD
                                                                             21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
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                             28; Indels
     Pred. No. 8.3e-37;
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LOCATION: (1)..(445)
OTHER INFORMATION: unsure at all Xaa locations
                          17; Mismatches
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Patent No. US20020098200Al
GENERAL INFORMATION:
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APPLICANT: Skeiky, Yasir
APPLICANT: Ovendale, Pamela
APPLICANT: Jen, Shyian
  65.6%;
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Best Local Similarity 24.6
Matches 35; Conservative
Best Local Similarity 65.6
Matches 86; Conservative
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US-09-793-306-146
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Sequence 57763 Application US/10425114

Sequence 57763 Application US/10425114

Sequence 57763 Application US/10425114

Sequence 57763 Application US/10403488A1

Sequence 57763 Application No. USZ004003488A1

APPLICANT: Liu, Jingdong

APPLICANT: Acovalic, David K.

APPLICANT: Acovalic, David K.

APPLICANT: Acovalic, David K.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

WUMBER OF SEQ ID NOS: 73128

SEQ ID NO 57763

LEMATH: 507
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                                                                       14 VSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQS
                                                                                                                                                                                                                         74 GYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNAALVNQTASDS
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20; Gaps
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PPS23
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR PLING DATE: 2000-06-15
PRIOR PLING DATE: 2000-06-15
PRIOR PLING DATE: 2000-10-17
PRIOR PLING DATE: 2001-01-17
PRIOR PLING DATE: 2001-03-16
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   Indels
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US-10-425-114-57763
   63;
   Mismatches
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   18;
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US-09-880-748-1130
   36;
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   Matches
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                                                                                                                                                                                                                                                                    Sequence 56041, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION

APPLICANT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Promyen E

APPLICANT: Tabaska, Jack E

APPLICANT: Papartion: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPRENDENCE: 38-21(5313)

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 56041

LENGTH: 369
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Caro Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 275468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 GYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNAALVNQTASDS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 VSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.0%; Score 93; DB 12; Length 369; larity 26.3%; Pred. No. 0.51; Conservative 18; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 93; DB 12; Length 486;
Pred. No. 0.72;
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US-10-424-599-275468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:

OTHER INFORMATION: Clone ID: 701205720_FLI.pep
US-10-425-114-56041
                                                                           :: |: | : | : | : | 113 AARKVKYV-YANDLNPTAVEY 132
                                   SSVMVRQVGFGN--NATANQY
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26.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Glycine max
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Best Local Similarity
Matches 36; Conserv
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Best Local Similarity
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US-10-424-599-275468
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LENGTH: 1751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 ALAGVVPQWG------GGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSE- 67
                                                                                                                                                                                                                                                                                                                                                                                                                                         68 TITITQSGYGNGADVGQGADN-YDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNAAL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 ALAGVVPQWG------GGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSE-
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US-10-293-418-1130

Sequence 1130, Application US/10293418

Publication No. US20030223996A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: FF5292

CURRENT PELICATION NUMBER: US/10/293,418

CURRENT PELING DATE: 2002-11-27

PRIOR PELING DATE: 2001-11-27

PRIOR FILING DATE: 2001-11-27

PRIOR FILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-06-15

PRIOR PELING DATE: 2001-06-15

PRIOR PELING DATE: 2001-06-15

PRIOR PELING DATE: 2001-06-15

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-06-16

PRIOR FILING DATE: 2000-06-16

PRIOR FILING DATE: 2000-06-16

PRIOR FILING DATE: 2000-06-16

PRIOR SEQ ID NOS: 3247

"WHER OF SEQ ID NOS: 3247

"WHER OF SEQ ID NOS: 3247

"WHER OF PET DATE: 2000-06-16
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                                                                                                                                                                                                                                                                  Length 251;
                                                                                                                                                                                                                                                                                                          51; Indels
                                                                                                                                                                                                                                                              ch 11.9%; Score 92.5; DB 10; Similarity 27.7%; Pred. No. 0.36; 33; Conservative 14; Mismatches 51;
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
                                                                                     NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1130
LENGTH: 251
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ORGANISM: Homo sapiens
US-10-293-418-1130
                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-09-880-748-1130
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Best Local Similarity
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Best Local Similarity
Matches 33; Conserv
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US-10-293-418-1130
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RESULT 13 US-09-841-132-445

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    394 NADAWASSSPOSGSGATTVSNSCDSSSGSDSDTSETVPATAKGG-GLYTDKNLSITNITG 452
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Sequence 445, Application US/09841132
Patent No.: US20020061848A1
GENERAL INFORMATION:
APPLICANT Bhatia. Ajay
APPLICANT Skeiky, Yasir A.W.
APPLICANT Probst, Peter
ITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C8
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE FEASEQ for Windows Version 3.0/4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 594, Application US/09841132
; Ratent No. US20020061848A1
; CRNERAL INFORMATION:
APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 21012.1 469C8
; CURRENT RITING DATE: 2001-04-23
; CURRENT RITING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: PastSEQ for Windows Version 3.0/4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 33.1%; Pred. No. 5.7;
Matches 40; Conservative 10; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Chlamydia trachomatis serovar D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: C. Trachomatis D serovar
US-09-841-132-594
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72 -- QSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQ-YGGNNAALVNQ 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 11.7%; Score 91; DB 16; Length 1751; Best Local Similarity 33.1%; Pred. No. 5.7; Matches 40; Conservative 10; Mismatches 59; Indels 13
RESULT 15
US-10-467-534-45
Sequence 45, Application US/10467534
Sequence 45, Application US/10467534
Sequence 45, Application US/10467534
Sequence 45, Application Vo. US20040131625A1
GENERAL INFORMATION:
APPLICANT: Bethet, Francois-Xavier Jacques
APPLICANT: Bethet, Francois-Xavier Jacques
APPLICANT: Poolman, Jan
APPLICANT: Poolman, Jan
APPLICANT: Poolman, Variant, Vincent Georges Christian Louis
ITILE OF INVENTION: Vaccine Composition
FILE REFERENCE: B45261
GURRENT FELIANG DATE: 2003-08-08
PRIOR APPLICATION NUMBER: US/10/467,534
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: GB 0103169.9
PRIOR PRILING DATE: 2001-02-08
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 45
LENGTH: 1751
TYPE: PRI
CUS-10-467-534-45
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Search completed: August 2, 2004, 15:36:12 Job time : 37.8 secs

Sequence 57, Ai Sequence 30, A Sequence 20, A Sequence 24, A

Sequence Sequence Sequence Sequence

Perfect score:

Sequence:

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Run on:

Scoring table:

Minimum DB Maximum DB

Database :

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3 10:54:39 2004
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APPLICANT: White, Agron P.
APPLICANT: White, Agron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE: OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: Requence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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US-10-437-963-147343
US-09-739-449-8854
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ORGANISM: Artificial Sequence
      \begin{array}{c} 0.00\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\ 0.01\\
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                                                                                                                                                                                                                                                                                                                                  US-09-543-407-22
776
1 MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151
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| Cgn2_6/ptodata/2/paa/USO6_COMB.pep:*
| Cgn2_6/ptodata/2/paa/USO8_COMB.pep:*
| Cgn2_6/ptodata/2/paa/USO9_COMB.pep:*
| Cgn2_6/ptodata
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                                        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext
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Match Length DB
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Score

No.

Result

Sequence 20216, A Sequence 24, Appl Sequence 20638, A Sequence 20638, A Sequence 146, App Sequence 147343,

Sequence 8854, Ap

Sequence 5833, Ap Sequence 5833, Ap Sequence 21, Appl Sequence 688, App

Sequence 21, Appl Sequence 688, App Sequence 25488, A Sequence 25488, A Sequence 25607, A

Sequence 11, Appl Sequence 14, Appl Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 5834, Ap Sequence 5834, Ap Sequence 5834, Ap Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 35, Appli Sequence 35, Appli Sequence 35, Appli Sequence 35, Appli Sequence 35, Appli Sequence 35, Appli Sequence 35, Appli Sequence 35, Appli Sequence 35, Appli Sequence 35, Appli Sequence 35, Appli Sequence 35, Appli Sequence 35, Appli Sequence 35, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli Sequence 37, Appli

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Indels

Length 151;

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61 SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDOWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                              87.9%; Score 682; DB 19;
90.7%; Pred. No. 1.5e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                              2; Mismatches
  CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 151
                                                                                                                                                 ) ORGANISM: Salmonella enteritidis
US-09-543-407-5
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TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 amino acids
                                                                                                                                                                                                                                                                              Matches 137; Conservative
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                                                                                                                                                                                                                                                      Similarity
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US-08-233-642A-57
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Best Local
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                                                                                                                                                                                                                                                      SDARKSETTITQSGYCNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                      9
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                                                                                                                                                    1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Cay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REPERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
SOFTWARE: FASTSEQ for Windows Version 4.0
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SEQUENCE A Application US/09543407

GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: AAVINIAN W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGGUS PEPTIDE SEQUENCES
FILE REPERENCE: 920043-406
CURRENT APPLICATION NUMBER: US/09/543,407
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                                                  Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 19; Length 151;
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                                                                                                    Indels
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                                                  Query Match 100.0%; Score 776; DB 19; Best Local Similarity 100.0%; Pred. No. 1.2e-74; Matches 151; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 91.8%; Score 712; DB 19;
Best Local Similarity 91.1%; Pred. No. 9.1e-68;
Matches 144; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                        121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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US-09-543-407-22
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US-09-543-407-28
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LENGTH: 151
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JOS-USA: APPLICATION US/08233642A

GENERAL INFORMATION:

APPLICANT: RAY, William W.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Raren

APPLICANT: Collinson, S. Raren

APPLICANT: Collinson, S. Raren

APPLICANT: Collinson, S. Raren

APPLICANT: Collinson, S. Raren

APPLICANT: Collinson, S. Raren

ITILE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-

TITLE OF INVENTION: MAETHODS AND COMPOSITIONS FOR SALMONELLA-

TITLE OF INVENTION: MAETHODS AND CONPOSITIONS FOR SALMONELLA-

CORRESPONDENCES: Sed and Berry

STREE: Washington

COUNTRY: Osattle

STATE: Washington

COUNTRY: US.A.

IIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: PLODBY Misk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

COMPUTER: APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLICANTON MAEN APPLIC
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Pred. No. 5.2e-64;
2; Mismatches 13; Indels
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CURRENT APPLICATION DAYS.

APPLICATION DAYS.

FILING DATE: 26-APR-1994

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: King, Joshua

REGISTRATION NUMBER: 920043.403C3

TELEPRACE/DOCKET NUMBER: 920043.403C3

TELEPRACE/DOCKET NUMBER: 920043.403C3

TELEPRACE (206) 682-6031

TELEPRACE (206) 682-6031
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Best Local Similarity 90.1%;
Matches 136; Conservative
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61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHA-- 118
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                                                                                               SDARKSETTITOSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG 120
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Sequence 20, Application US/09543407

SEQUENCE 20, Aaron P.

APPLICANT: White, Aaron P.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

TITLE OF INVENTION: BRCTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

FILE REFERENCE: 920043.406

CUTRENT APPLICATION NUMBER: US/09/543,407

CUTRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 20

SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                  Sequence 30, Application US/09543407

Sequence 30, Application US/09543407

SEQUENCE 310, Application US/09543407

APPLICANT: White, Aaron P.

APPLICANT: White, Aaron P.

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

FILE REFERENCE: 92043.406

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT APPLICATION NUMBER: US/09/543,407

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKLLKVAAFPAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                     61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQMNAKNSDITVGQYGG
MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                           1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 657; DB 19; Length 151;
Pred. No. 7.4e-62;
0; Mismatches 0; Indels 30
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                                                                                                                                                                                                                                                  121 NNPALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                       121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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Best Local Similarity 81.9%;
Matches 136; Conservative (
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ORGANISM: Artificial Sequence
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US-09-543-407-20
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US-09-543-407-30
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US-09-543-407-30
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61 SDARKSETTITQSGYGNGADVGGGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                           61 SDARK------YDQLVTRVVTHEMAHAGQGADNSTIELTQNGFR 98
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CRGANISM: Artificial Sequence FRATURE: ORGANISM: Actificial Sequence COTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-20
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                                                                                                                                                                              Length 151;
                                                                                                                                                                                                                             0; Indels
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Rest Local Similarity 73.6%; Pred. No. 1.1e-56;
Matches 128; Conservative 0; Mismatches 0;
                                                                                                                                                                              Ouery Match
Best Local Similarity 74.6%; Pred. No. 8.9e-58;
Matches 129; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT White, Aaron P.
APPLICANT Doran, James L.
APPLICANT Collinson, S. Karen
APPLICANT CALLINGON, S. Karen
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEN
TITLE OF INVENTION: BRESENTATION OF HETEROLG
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 151
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US-08-243-407-12
Sequence 12, Application US/09543407
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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DB 19; Length 151;

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121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
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US-09-543-407-26
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GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Oran, James L.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

ITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

ITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

ITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

ITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

ITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

ITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

ITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

ITLE OF INVENTION OF HETEROLOGOUS PEPTIDE SEQUENCES

CURRENT APPLICANT

CURRENT APPLICANT

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 14

LENGTH: 151
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APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Recombinant Salmonella enteritidis 35 afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 77.8%; Score 604; DB 19; Length 151; Best Local Similarity 80.8%; Pred. No. 3.6e-56; Matches 122; Conservative 6; Mismatches 23; Indels
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                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 123; Conserv
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US-09-543-407-14
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61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                              APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 151
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APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REPREBRUCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DAIR: 2000-04-05
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 151
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Best Local Similarity 81.5%; Pred. No. 7.7e-56;
Matches 123; Conservative 4; Mismatches 24;
121 NNAALVNOTASDSSVMVRQVGFGNNATANOY 151
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                                                                                                                                                                                         Sequence 26, Application US/09543407 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
FEATURE:
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; OTHER INFORM
US-09-543-407-16
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US-08-978-878-4
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                                                                               1 MKLLKVAAFFAAIVVSGSALAGVVPQWGGGGNHNCGCNSSGPDYDQLVTRVVTHEMAHALQ 60
                                                   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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US-09-543-407-16
US-09-543-407-16
Sequence 16, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Obran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: CAILINGON, S. Karen
TITLE OF INVENTION: BACTERIAL FINBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 92043-406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
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                 Gaps
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APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
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                   Indels
Pred. No. 9.8e-56;
; Mismatches 23;
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Pred. No. 2.8e-55;
2; Mismatches 12;
                                                                                                                                                                                                NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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; ORGANISM: Salmonella enteritidis
US-09-543-407-31
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Best Local Similarity 81.5%;
Matches 123; Conservative
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Best Local Similarity 89.3%;
Matches 117; Conservative
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LENGTH: 151
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GENERAL INFORMATION:
APPLICANT: NORMARK, Staffan
APPLICANT: OLSEN, Arne
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS ITS PREPARATION
FILE REFERENCE: 01289-081
CURRENT APPLICATION NUMBER: US/08/978,878
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION WHERE: SE 8801723-1
EARLIER APPLICATION UNMER: SE 8801723-1
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                                                                                                                                                                                          Gaps
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GENERAL INFORMATION:
APPLICANT MALE, Aaron P.
APPLICANT Doran James L.
APPLICANT Collinson, S. Karen
APPLICANT KAY, William W.
TITLE OF INVENTION: PRESENTAL FIMERIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ION NOS: 59
SOFTWARE: FRASESQ for Mindows Version 4.0
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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69.5%; Pred. No. 3e-47;
tive 17; Mismatches 29;
                                                                                                                                    Score 567; DB 19;
Pred. No. 3.4e-52;
5; Mismatches 24;
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Best Local Similarity 80.8%;
Matches 122; Conservative
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Matches 105, Conserv
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66.8%; Score 518; DB 13; Length 151;

Best Local Similarity 68.9%; Pred. No. 6.3e-47;

Matches 104; Conservative 18; Mismatches 29; Indels (
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EARLIER APPLICATION NUMBER: US 07/347,189
EARLIER FILING DATE: 1989-05-04
EARLIER FILING DATE: 1989-05-04
EARLIER APPLICATION NUMBER: US 07/789,437
EARLIER APPLICATION NUMBER: US 07/970,846
EARLIER APPLICATION NUMBER: US 08/187,865
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-10-05
EARLIER FILING DATE: 1994-10-05
EARLIER FILING DATE: 1995-06-28
NUMBER OF SEQ.ID NOS: 10
SOFTWARE: PATENTIN UVET: 2.0
SSOFTWARE: PATENTIN UVET: 2.0
                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT; ORGANISM: Escherichia coli
US-08-978-878-4
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Search completed: August 2, 2004, 15:26:45 Job time : 168.9 secs

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Sequence 2, Appli
Sequence 7906, App
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Sequence 180, App
Sequence 309662,
Sequence 84, Appl
Sequence 304391,
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1. /cgn2_6/ptodata/2/paa/Neq.NEW_COMB.pep:*

2. /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3. /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

3. /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5. /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

5. /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

7. /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

7. /cgn2_6/ptodata/2/paa/US00_NEW_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-741-873C-2
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US-09-248-796A-17306
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US-10-872-115-309662
US-10-872-115-30991
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US-10-425-115-304391
US-10-425-115-304391
US-10-425-115-304391
US-09-248-7997
US-09-248-7997
US-0-565-632-7997
US-0-561-351-11388
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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equence 2420, equence 2422,	equence 301334, equence 38, App	514, 515,	Seguence 16659, A Seguence 9, Appli	equence	equence 511	equence 2782	37, A	Sequence 285216,	equence 285214	Я			Sequence 11, Appl	Sequence 45603, A
US-10-501-282-2420 US-10-501-282-2422	US-10-425-115-301334 PCT-US04-10229-38	US-10-170-205E-35514 US-10-170-205E-35515	US-10-170-205E-16659 PCT-US04-09388-9	PCT-US03-24982A-317	US-10-854-439-511	US-10-425-115-278239	PCT-US04-11210-37	US-10-425-115-285216	US-10-425-115-285214	US-10-489-425-18	US-60-565-632-7905	US-60-579-062-7905	US-10-778-804-11	US-10-767-701-45603
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                                      APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084
CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1999-11-26
PRIOR FILING DATE: 1999-11-06
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN OF SEQ ID NOS: 11
SOFTWARE: PATENTIN OF SEQ ID NOS: 11
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US-10-479-638-21

SQUENCE 21, Application US/10479638

GENERAL INFORMATION:

APPLICANT: Don A. Roth

APPLICANT: The University of Wyoming

TITLE OF INVENTION: Expression of Spider Silk Proteins in Higher Plants

TITLE OF INVENTION: Expression of Spider Silk Proteins in Higher Plants

TITLE OF INVENTION: Expression of Spider Silk Proteins in Higher Plants

CURRENT FILING DATE: 2003-102-03

PRIOR APPLICATION NUMBER: US/10/479,638

CURRENT FILING DATE: 2002-06-06

PRIOR APPLICATION NUMBER: 60/296,184

PRIOR FILING DATE: 2001-06-06

PRIOR PLING DATE: 2001-06-06

NUMBER OF SEQ ID NOS: 54

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 21

LENGTH: 520

TYPE: RAT

ORGANISM: Argiope trifasciata

US-10-479-638-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.7%; Score 440; DB 5; Length 131;
65.6%; Pred. No. 1.4e-30;
live 17; Mismatches 28; Indels
Sequence 2, Application US/09741873C GENERAL INFORMATION:
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Best Local Similarity 65.6*
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Escherichia coli
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Length 520;

DB 6;

12.6%; Score 97.5;

Query Match

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APPLICANT: Zhang, Bei
TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
TITLE OF INVENTION: Compositions Thereof
FILE REFERENCE: 38-21(53403)B COURENT APPLICATION WINBER: US/60/565,632
CURRENT FILING DATE: 2004-04-27
NUMBER OF SEQ ID NOS: 15449
SOFTWARE: Patentin version 3.2
LENGTH: 841
                                                                                                                                                                                         74 GYGNGADVG-----QGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNAALVN 127
                                                                                                                                                                                                                                              ---AVNRVSSNIGAVAS 448
                                                                                                                                  347 AGAGAAAAASAGAGAGGYGYGYAGGSS----ISYGATSSSATSSSTASSSRSGIVTSG 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 GQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSET-TITQS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 GNHNGGG--NSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSG-----YGNGADV 81
                             25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc_feature
LOCATION: (810)..(810)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 11.9%; Score 92; DB 7; Length 841; Best Local Similarity 28.3%; Pred. No. 8.9; Matches 36; Conservative 16; Mismatches 59; Indels
                             62; Indels
Best Local Similarity 22.9%; Fred. No. 1.7; Matches 33; Conservative 24; Mismatches
                                                                                                                                                                                                                                              403 GYGAGAAAGAGAAAAGAGSYSGSISKLSSAE--
                                                                                                                                                                                                                                                                                                     128 QTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                        449 GGASALPGVISNIFSGVSSSAGSY 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Monsanto Technology, LLC APPLICANT: Baum, James A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Baum, James A
APPLICANT: Rovalic, David K
APPLICANT: Larosa, Thomas J
APPLICANT: Lu, Maclong
APPLICANT: Munyikwa, Tichifa R. I.
APPLICANT: Roberts, James K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baum, James A
Kovalic, David K.
Larosa, Thomas J.
Lu, Maolong
Munyikwa, Tichifa R. I
Roberts, James K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Diabrotica virgifera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 FGNNATA 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lu, Maolc
APPLICANT: Munyikwa,
APPLICANT: Roberts,
APPLICANT: Wu, Wei
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394 NADAWASSSPOSGSGATIVSNSGDSSSGSDSPISETVPATAKGG-GLYIDKNLSIINIIG 452
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                                                                                                                                   APPLICANT Skeiky, Vasir A.W.
APPLICANT Skeiky, Vasir A.W.
APPLICANT Skeiky, Vasir A.W.
APPLICANT Skeiky, Vasir A.W.
APPLICANT Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall Shall 
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GENERAL INFORMATION:
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llarity 33.1%; Pred. No. 25;
Conservative 10; Mismatches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Chlamydia trachomatis serovar D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 594, Application US/10872155
GENERAL INFORMATION:
                                                               ; Sequence 445, Application US/10872155
; GENERAL INFORMATION:
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                             US-10-872-155-445
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APPLICANT: Zhang, Bei
TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
TITLE OF INVENTION: Compositions thereof
FILE REFERENCE: 38-21 (53403) C
CURRENT APPLICATION NUMBER: US/60/579,062
CURRENT FILING DATE: 2004-06-11
NUMBER OF SEQ ID NOS: 41445
SOFTWARE: Patentin version 3.2
SEQ ID NO 7906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          657 GNENGSAAENTGNADSQNDAGQ-GSANAA-----NADNNANTDAQNGADQGNENGSAAEI 710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 GNHNGGG--NSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSG-----YGNGADV 81
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NAME/KEY: misc feature

LOCATION: (810)..(910)

OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-60-579-062-7906
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GENERAL INFORMATION:
APPLICANT: Caradi, Guido
APPLICANT: Ratti, Giuido
TITLE OF INVENTION: Immunisation Against Chlamydia Trachomatis
FILE REPERENCE: 002441.00085
CURRENT FILING DATE: 2004-06-10
PRIOR APPLICATION NUMBER: PCT/IB02/05761
PRIOR APPLICATION NUMBER: PCT/IB02/05761
PRIOR FILING DATE: 2002-12-12
NUMBER OF SEQ ID NOS: 262
NUMBER OF SEQ ID NOS: 262
SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.9%; Score 92; DB 7; Length 841; llarity 28.3%; Pred. No. 8.9; Conservative 16; Mismatches 59; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Diabrotica virgifera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 33.1<sup>3</sup>
Matches 40; Conservative
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Best Local Similarity
Matches 36; Conserv
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LENGTH: 1751
TYPE: PRT
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US-10-498-327-115
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RESULT 10
19.09-248-796A-17306
Sequence 17306, Application US/09248796A
Sequence 17306, Application US/09248796A
Sequence 17306, Application US/09248796A
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-13
FRIOR APPLICATION NUMBER: US 60/074,725
FRIOR APPLICATION NUMBER: US 60/074,725
FRIOR APPLICATION NUMBER: US 60/096,409
FRIOR SEQ ID NOS: 28208
SEQ ID NO 17306
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US-10-425-115-254240

Sequence 254240, Application US/10425115

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Royalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: APPLICANT: Application Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 254240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         368 SSGSTGGGNCAGVNVYPNWTARDWSGGAYNHANAGDQMVYQNSLYRANWYTNSVPGSDAS 427
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                                                                                                                                                                                                                                               12 IVVSGSALAGVVPQWG---GGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSET 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89
                                                                                                                                                                                                                                                                                       30 GNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNYD
                                                                                                                                                                            28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.5%; Score 89.5; DB 5; Length 388; 22.1%; Pred. No. 6;
                                                                                                      Length 1010;
                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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   OTHER INFORMATION: Cellulose or protein binding domain
                                                                                                                                                                            26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
11.5%; Score 89.5; DB 5; 1
Best Local Similarity 22.1%; Pred. No. 6;
Matches 33; Conservative 17; Mismatches 44;
                                                                                               Query Match
11.6%; Score 90; DB 1;
Best Local Similarity 22.4%; Pred. No. 16;
Matches 32; Conservative 27; Mismatches 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           428 WTSLGACGGNGSTTSSSSSSSS 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CRGANISM: Candida albicans
US-09-248-796A-17306
                  FCT-US04-21492-402
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APPLICANT: Steer, Brian
APPLICANT: Steer, Brian
APPLICANT: Callen, Walter
APPLICANT: Healey, Shaun
APPLICANT: Healey, Shaun
APPLICANT: Healey, Shaun
APPLICANT: Pulliam, Derrick
TITLE OF INVENTION: GLUCANASES, NUCLEIC ACIDS ENCODING THEM AND METHODS FOR MAKING AN FILE REFERENCE: 56462005540
CURRENT APPLICATION NUMBER: PCT/US04/21492
CURRENT APPLICATION NUMBER: 604484,725
PRIOR FILING DATE: 2003-07-02
PRIOR FILING DATE: 2003-07-02
NUMBER OF SEQ ID NOS: 518
SOFTWARE: Patent In version 3.1
SEQ ID NO 402
LENTER FOR THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 --QSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQ-YGGNNAALVNQ 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 SGSALAGVVPQWGGGGN--HNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTIT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.7%; Score 91; DB 6; Length 1751; 33.1%; Pred. No. 25; tive 10; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               family 5)
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LOCATION: (39)...(300)
OTHER INFORMATION: Cellulase (glycosyl hydrolase
                         PRIOR FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 09/410,568
PRIOR FILING DATE: 1999-10-01
PRIOR PILING DATE: 1999-10-01
PRIOR PILING DATE: 1999-04-08
PRIOR FILING DATE: 1999-04-08
PRIOR FILING DATE: 1999-04-08
PRIOR FILING DATE: 1999-12-08
NUMBER: 0F SEQ ID NOS: 599
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 594
TYPE: PRI
TYPE: PRI
CORGANISM: C. Trachomatis D serovar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (610)...(959)
OTHER INFORMATION: Glycosyl hydrolases family 6
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INFORMATION: Carbohydrate binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 402, Application PC/TUS0421492 GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: 09/426,571
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: C. Trachomatis D serovar US-10-872-155-594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 33.1%
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (493)...(521)
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LOCATION: (1)...(30)
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NAME/KEY: DOMAIN
LOCATION: (393)...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: DOMAIN
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NAME/KEY: DOMAIN
LOCATION: (493)..
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; Pred. No. 26;
15; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200 QATGEGSF---AAGVENKANAN 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 5; Application US/10872769
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                                                                              ), ORGANISM; Moraxella catarrhalis
US-10-872-768-5
                                                                                                                                                                                                                                                                                                     11.2%;
1 Similarity 26.8%;
38; Conservative 1
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: MC
US-10-872-769-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28
                                                                                                                                                                                        SEQ ID NO 5
                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                             LENGTH:
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                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 IGDSSTIGGG--YYNQATGEKSTVAGGRNNQATGNNSTVAGGSYNQATGNNSTVAGGSHN 199
                                                                                                                                                                                                                                                                                                                              63 --PYGAHASAGGGGAGGGASQN--GGSGYGSGSGSGSGSGSTYSQ-----GGYYSGYG 110
                                                                                                                                                                                                                                                                                       47 IYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQW 106
                                                                                                                                                                                                                                                5 KLISLGLLVLIGIGLANAVRVARYSSADGTGTGEGQGGGYVNGGGSGSGSGGGGDSS-- 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-09-952-267B-5
; Sequence 5, Application US/09952267B
; Sequence 5, Application US/09952267B
; GENERAL INPORMATION:
APPLICANT: ABBI, CHRISTOPH
; APPLICANT: APEL, CHRISTOPH
; APPLICANT: COPE, LEGLIE D.
APPLICANT: FISSE, MICHAEL J.
APPLICANT: FISSE, MICHAEL J.
APPLICANT: FISSE, MICHAEL J.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REPRESENCE: AMCY:02-4
FILING DATE: 2001-09-12
CURRENT FILING DATE: 199-06-21
NUMBER OF SEQ ID NOS: 98
; SOFFWARE: PATCHIN VOF: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 GGGNHN-----GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGY---
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32;
                                                                                                                                                                      62; Indels 39;
                                                                                                                                                                                                                                                                                                                                                                                         DB 6; Length 193;
                                                                                                                                                                                                                                                                                                                                                                   107 NAKNSDITVGQYGGNNA-ALVNQTASDSSVMVRQVGFGNNAT-ANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.2%; Score 87; DB 5; Length 892; 26.8%; Pred. No. 26; tive 15; Mismatches 57; Indels
                                                                           OTHER INFORMATION: Clone ID: MRT4577_163446C.1.per
                                                                                                                               Query Match
11.4%; Score 88.5; DB
Best Local Similarity 26.3%; Pred. No. 3.3;
Matches 44; Conservative 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 QTASDSSVMVRQVGFGNNATAN 149
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GENERAL INFORMATION:
APPLICANT: HANSEN, ERIC J.
APPLICANT: ABEL GRISTOPH
APPLICANT: COPE, LESLIE D.
APPLICANT: MACIVER, ISOBEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                                               5 KVAAFAAIVVSGSALAGVV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 26.8
Matches 38; Conservative
                                       ORGANISM: Zea mays
                                                                                  ; OTHER INFORMATION
US-10-425-115-254240
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US-10-872-768-5
LENGTH: 193
TYPE: PRT
                                                       FEATURE:
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APPLICANT HANSEN, LESLIE D.
APPLICANT COPE, LESLIE D.
APPLICANT FISTE J.
APPLICANT FISTE MICHAEL J.
APPLICANT FISTE, MICHAEL J.
APPLICANT FISTE, MICHAEL J.
APPLICANT FISTE, MICHAEL J.
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APPLICANT FISTE, MICHAEL J.
APPLICANT FISTE, MICHAEL J.
APPLICANT FISTE ANCY:024
CURRENT FILING DATE: 2004-06-21
RICH APPLICATION NUMBER: US/09/336,447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 GGGNHN-----GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGY---
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APPLICANT: FISKE, MICHAEL J.

APPLICANT: FREDENBURG, ROSS A.

TILLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
CURRENT APPLICATION WINBER: US/10/872,768
CURRENT FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US/09/336,447
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PATENTIN VOS: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGNHN------GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGY-
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11.2%; Score 87; DB 6; Length 892;
Best Local Similarity 26.8%; Pred. No. 26;
Matches 38; Conservative 15; Mismatches 57; Indels
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RESULT 15

US-10-422-115-333419

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US-10-422-115-333419

US-10-422-115-333419

US-10-422-115-333419

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US-10-423-115-333419

US-10-423-1
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Search completed: August 2, 2004, 15:29:54 Job time : 18.8 secs

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August 2, 2004, 14:39:53; Search time 9.4 Seconds (without alignments) 1545.204 Million cell updates/sec
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776
1 MKLLKVAAFAAIVVSGSALA........DSSVMVRQVGFGNNATANQY 151
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000 PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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30	31	) KI	3.4	3	36	37	38	68	40	41	42	43	44	45

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A42049 A44951 P10021 S10021 S00275 C70830 C70830 C70830 F16356 F16675 F16675 F16958 F16958 F16958 F1998 F198	magfA precursor - Salmonella e monella enteritidis - 1996 #sequence revision 31-Dec (2039; PG6015; A44898 molla enteritidis agfBAC operor mber: JC639; MUID:96146512; PN (2039; MUID:96146512; PN (2039; MUID:96146512; PN (2039; MUID:96146512; PN (2039; MUID:96146512; PN (2039; MUID:96146512; PN (2039; MUID:96146512; PN (2039; MUID:96146512; PN (2015)	
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	n agfA pre 11.96   Rae 12.8.   PC6 12.9.   PC6 12.9.   PC6 13.9.	
	protein protei	
2	PESULT CONTROL OF CONT	

CSGA

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A,Description: major component of wild-type curli; interaction between CsgA and CsgB tri
A,Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli that
and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-151/Product: curlin #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               curlin major subunit CsgA [imported] - Escherichia coli (strain O157:H7, substrain RIMD
A,Title: The RpoS sigma factor relieves H-NS-mediated transcriptional repression of A,Reference number: S31202; MUID:93211294; PMID:8459772
A,Accession: S31202
A,Accession: BAA
A,Molecule type: DNA
A,Residues: 1-6,'V', 8-151 < OLS1>
A,Cross-references: EMBL:L04979
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Cidecies del Colo Hasquence Carlo Harbary, K.; Ishii, K.; Yokoyama, K.; Han, gasawara, N.; Yasunagawa, H.; Muha, Res. 8, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and shitches number: A99629; MUID:21156231; PMID:11258796
A;Accession: D90806
A;Accession: Dposidinary
A;Molecule type: DMA
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A; Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs1420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 QSDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A)Residues: 1.133, RQRDSGWLW' <01.83>
A)Cross-references: EMBL.L04979; NID:9290424; PIDN:AAA23616.1; PID:9290425
A)Experimental source: strain K-12, substrain W3110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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69.5%; Pred. No. 4.6e-37;
iive 17; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151
                                                                                                                                                                                                                                                               A,Molecule type: protein
A,Residues: 21-42;44-50 < OLS2>
R;Olsen, A.N.; Arnqvist, A.M.
submitted to the EMBL Data Library, October 1992
A,Reference number: $34559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Matches 105; Conserv
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A, Map position: 23.15
C, Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
                                                                                                                                                                                                                                        A; Accession: S34560
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S34559
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Matches
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NyAlternate names: csgA protein; major curlin protein
C;Specias: Escherichia coli
C;Date: 12-Feb-1998 #secquence revision 20-Feb-1998 #text_change 01-Mar-2002
C;Accession: S70788; G64846; $\tilde{S}1202; S34560; S34559
R;Hammar, M.; Arnqqist, A.; Blan, Z.; Olsen, A.; Normark, S.
Mol. Microbiol. 18, 661-670, 1995
A;Title: Expression of two csg operons is required for production of fibronectin- and CA
A;Recence number: S70788
A;Accession: S70788
A;Accession: S70788
A;Status: nucleic acid sequence not shown; translation not shown
A;Residues: 1-15: 4HAM
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Cippecies: Salmonella enterica subsp. enterica serovar Typhi
A;Note: Lihis species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: A10635
R;Parkhill, J; Dougan, G; James, K.D; Thomson, N.R.; Pickard, D; Wain, J; Churcher, th, T; Connerton, P; Cronin, A; Davis, P; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; O'daora, P.
Nature 413. 484-852, 2001
A;Authors: Parry, C; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUD:21534947; PMID:11677608
A;Accession: A10635
A;Status: prefilminary
A;Molecule type: DNA
A;Residues: 1-151 cPAR>
A;Cross-references: GB:AL513382; PIDN:CAD08268.1; PID:g16502315; GSPDB:GN00176
C;Genetics:
A;Gene: STY1181
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A; Residues: 1-151 cBLAT>
A; Cross-references: GB.AE000205; GB:U00096; NID:g1787265; PIDN:AAC74126.1; PID:g1787279; A; Experimental source: strain K-12, substrain MG1655
R;Olsen, A.; Arnqvist, A.; Hammar, M.; Sukupolvi, S.; Normark, S.
Mol. Microbiol. 7, 523-536, 1993
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Pred. No. 1.2e-50;
2; Mismatches 12; Indels
       NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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90.7%;
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Best Local Similarity 90.7
Matches 137; Conservative
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A,Cross-references: EMBL:X06462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 33.6%; Pred. No. 0.39;
Matches 37; Conservative 11; Mismatches 32; Indels 3
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ilarity 27.0%; Pred. No. 0.49;
Conservative 20; Mismatches 52;
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Best Local Similarity
Matches 40; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein csgA [imported] - Escherichia coli (strain O157:H7, substrain EDL93 C; Species: Escherichia coli (Species: Escherichia coli (Species: Escherichia coli (Species: Escherichia coli (Species: Escherichia coli (Space: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C; Accession: H85665
R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotheck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A; Reference number: A65480; MUID:21074935; PMID:11206551
A; Accession: H85665
A; Scatus: preliminary
A; Molecule type: DNA
A; Residues: 1-152 <STO-A;
Cross-references: GB:AE005174; NID:g12514574; PIDN:AAG55788.1; GSPDB:GN00145; UWGP:216
A; Experimental source: strain 0157:H7, substrain EDL933
C; Genetics:
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A; Residues: 1164-1174;1179-1198;1233-1252;1285-1293;1297-1309;1316-1326;1331-1341;1343-1
A; Cross-references: EMBL:L03110
R; Martindale, D.W.; Taylor, F.M.
Nucleic Acids Res. 16, 2189-2201, 1988
A; Title: Multiple introns in a conjugation-specific gene from Tetrahymena thermophila.
A; Reference number: S03650; WUID:88189811; PMID:3357771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               β
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                  QSDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYG 119
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C;Species: Tetrahymena thermophila
C;Species: Tetrahymena thermophila
C;Bate: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 07-Dec-1999
C;Accession: S42136; S42135; S30550
R;Taylor, F.M.; Martindale, D.W.
submitted to the EMBL Data Library, October 1992
A;Reference number: S42136
A;Reference number: S42136
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A; Residues: 1-1748 <TAY>
A; Cross-roces: EMBL:L03710; NID:g161751; PID:g161752
R; Taylor, F.M.; Martindale, D.W.
Nucleic Acids Res. 21, 4610-4614, 1993
A; Title: Retroviral-type zinc fingers and glycine-rich reg
A; Reference number: S42135; MUID:94051569; PMID:8233798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 499.5; DB 2;
; Pred. No. 3e-35;
18; Mismatches 30;
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A;Residues: 236-250,'I',252-255,'N',257-773 <MAR>
                                                                                                                                                                                                        GGGAAAVDQTASNSTVNVTQVGFGNNATAHQY
                                                                                                                                                 GNNAALVNQTASDSSVMVRQVGFGNNATANQY
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Best Local Similarity 67.8
Matches 103; Conservative
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Richards, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, E.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Naturer, 33.537-544, 1998
A, Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A, Rittle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A, Recession: E70946
A, Recession: E70946
A, Residues: preliminary, nucleic acid sequence not shown; translation not shown
A, Molecule type: DNA
A, Residues: 1-590 <COL>
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bacces: T5-Cot-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T21956
R;Lennard, N.
submitted to the EMBL Data Library, June 1996
A;Accession: T21966
A;Accession: T21966
A;Accession: T21996
A;Accession: T21996
A;Accession: T21996
A;Accession: T21996
A;Accession: T21960
A;Accession: T21960
A;Accession: T21970
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                                                                                                                                                                                                                                                                                                                                        probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 15-Sep-2003
C;Accession: E70946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.1%; Score 94; DB 2
25.8%; Pred. No. 1.4;
cive 19; Mismatches
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A; Introns: 12/1; 57/3; 124/2; 163/1; 330/3
                                                                459
Best Local Similarity 27.4%
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 25.87
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 ATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            445 GTLN 448
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A,Gene: CESP:F38B7.3
A,Map position: 5
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Accession: 17-Jul.1998 #sequence_revision 17-Jul-1998 #text_change 15-Sep-2003
C;Accession: E70663
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:962997; PMID:9634230
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Mochaule type: DMA
A;Residues: 1-615 cCol-
A;Cross-references: GB:283860; GB:All23456; NID:g3261681; PIDN:CAB06165.1; PID:e290763;
A;Gene: PPE
A;Gene: PPE
                                                                                                                                                                                                             hypothetical protein Y38E10A.g - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Dacesion: T26667
R;Wallis, J.
Submitted to the EMBL Data Library, September 1999
A;Reference number: Z20252
A;Accession: T26667
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-586 < WIL>
A;Residues: 1-586 < WIL>
A;Residues: 1-586 < WIL>
A;Residues: clone Y38E10A.g
A;Residues: 1-586 < WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 QSDARKSETTITQSGYGNGAD----VGQGADNYDQLVTRVVT-----HEMAHADQWNAKN 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---YGSSANEVKSVGFGAQQYGGSVFAKPSGTGGGYVSAGSSARKSGE 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---TG 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GGGNSSGPDSTLSIYQYGSANAALAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 12.6%; Score 98; DB 2; Length 615; Best Local Similarity 22.5%; Pred. No. 1; Matches 31; Conservative 16; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
13.1%; Score 102; DB 2; Length 580
Best Local Similarity 28.8%; Pred. No. 0.44;
Matches 47; Conservative 14; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          540 SGAGGGGKAGGAKNSASYGSSANEVKSVGFG----AQQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 LKVAAFAAIVVSGSALAGVVPQWGGGGNHN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSSVMVRQVGFGNNATAN 149
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ice incleation protein - Xanthomonas campestris
C;Species: Xanthomonas campestris
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 26-Aug-1999
C;Accession: 811672
R;Zhao, J; Orser, C.S.
Mol Gen. Genet. 23, 163-166, 1990
A;Title: Conserved repetition in the ice nucleation gene inax from Xanthomonas campestr
A;Reference number: $11672; MUID:91080859; PMID:2259339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-645 <COL>
A;Cross-references: GB:AL021958; GB:AL123456; NID:g3261536; PIDN:CAA17522.1; PID:e12532
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D.; Goruc.,
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Ual-1998 #sequence_revision 17-Jul-1998 #text_change 15-Sep-2003
C;Accession: F70825
B;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go
B;Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamiln, N.; Holr
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      296 Prpgngnverghegenenfegenten------Aniglanvedenvefensesynfer 345
                                                                                  ALALQSDARKSETTITQSGYGNGADVGQ-GADNYDQLVTRVVTHEMAHADQWNAKNSDIT 114
A;Status: preliminary, nucleic acid sequence not shown, translation not shown A;Molecule type: DNA
A;Residues: 1-645 <COL>
                                                                                                                                       --NGNRNVAG 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGNGNVGIGPSSFNVGSGNIGNANVGGGNSG-DNNFGFGNFGNANIGIGNAGPNMSSPAV
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-1567 <ZHA>
A,Cross-references: EMBL:X22970; NID:g48531; PIDN:CAA37140.1; PID:g48532
C,Superfamily: ice nucleation protein
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                                                                                                                                                                                                  VGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQ 150
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                                                                                                                                          ----HOYGRHNLSAVGÓEGHDNÝGSTTQ-
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12.0%; Score 93.5; DB 2;
Best Local Similarity 24.5%; Pred. No. 2.6;
Matches 39; Conservative 17; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.0%; Score 93.5; DB
llarity 28.2%; Pred. No. 6.9;
Conservative 21; Mismatches
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Best Local S:
Matches 42
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Rywood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, I Rywood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, I rapp. G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A,Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Recession: AD3143
A,Status: preliminary
A,Accession: AD3143
A,Status: preliminary
A,Residues: 1-145 KUR>
A,Experimental Source: Strain C58 (Dupont)
A,Experimental Source: Strain C58 (Dupont)
A,Genetics:
A,Map position: linear chromosome
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C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Accession: H9844
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2321-2328, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                        conserved hypothetical protein Atu4768 [imported] - Agrobacterium tumefaciens (strain C5
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-145 < KUR>
A, Cross-references: GB: AE007870; PIDN: AAK88682.1; PID: g15158413; GSPDB: GNC0170
           341
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        SD---NDTTVTNNYYNYGDNDNNGGNNHSS-SSNAITDAPGNAGDQSQQQSD-----
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12.0%; Score 93.5; DB 2;
Best Local Similarity 21.8%; Pred. No. 0.48;
Matches 34; Conservative 25; Mismatches 64;
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A,Gene: AGR L 228
A,Map position: linear chromosome
                                                              NNAALVNQTASD 132
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2, 2004, 14:36:12 ; Search time 5.3 Seconds (without alignments) 1483.508 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-543-407-22 776 1 MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 141681 segs, 52070155 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt 42:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	i Ø	Ð	Ψ	×	chi	pantoea		chlamydi	Q8z7m3 salmonella	salmonel	P20469 pantoea ana	Q10707 mycobacteri	P23223 leishmania	P15706 leishmania	P08148 leishmania				Q47502 escherichia	P51521 drosophila			E	Φ	ъ		Q04893 saccharomyc		mycob	Q05925 homo sapien	P75411 mycoplasma	P13709 drosophila	P25074 oryza sativ
SUMMAKIES	ID	SALT	CSGA_ECOLI	CSGA_ECO57		CSGB_ECOLI	ICEN_PANAN	ICEN_ERWHE	PMPB_CHLTR	CSGB_SALTI	CSGB_SALTY	ICEA_PANAN	YK98_MYCTU	GP63_LEIDO	GP63_LEICH	GP63_LEIMA	GP63_LEIME	VG38_BPT2	X442_MYCTU	CEAK ECOLI	OVO DROME	ICEN_PSEFL	N189_SCHPO	PO33_MOUSE	YBIL_ECOLI	BUN2 DROME	PO33_RAT	YM96_YEAST	PO33 HUMAN	YF48_MYCTU	HME1_HUMAN		ᆵ	GRP1_ORYSA
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Q9zfh0 azotobacter	033479 pseudomonas	Q07202 medicago sa	O05156 staphylococ	P18899 saccharomyc	Q10540 mycobacteri	Q50630 mycobacteri	P91698 drosophila	P51989 xenopus lae	O30611 pseudomonas	P49687 saccharomyc	Q50367 mycoplasma
ALE6 AZOVI	ICEV_PSESX	CORA_MEDSA	ALE1 STACP	DR48 YEAST	Y878 MYCTU	YP91 MYCTU	PER DROPV	RO21 XENLA	ICEK_PSESX	N145 YEAST	P35_MYCPE
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80.5	80.5	80	80	80	80	80	79:5	78.5	78,5	78:5	78
34	32	36	37	38	ტ ტ	40	41	42	43	44	45

## ALIGNMENTS

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SEQUENCE FROM N.A.

SPECIES=S. 19ph; STRAIN=CT18;

MEDLINE=21534947; PubMed=11677608;

MEDLINE=21534947; PubMed=11677608;

MEDLINE=21534947; PubMed=11677608;

MEDLINE=21534947; PubMed=11677608;

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MEDLINE=21534947; PubMed=11677608;

MEDLINE=21534947; PubMed=11677608;

MEDLINE=21534947; PubMed=1167, Medlen M.T.G., Sebaihia M., Medlen M.T.G., Connerton P.,

MACTORIN A., Davies R., Medlen T., Mollen N., Farrar J.,

MEDLE M., Medlen M., Medlen M., Medlen M., Jagels K.,

Medlen M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,

Medlen M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,

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SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534949; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Mguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=S.typhimurium, STRAIN=SR-11;
MBDLINE=98117058; PubMed=9457880;
Romling U., Bian Z., Hammar M., Sterralta W.D., Normark S.;
"Curli fibers are highly conserved between Salmonella typhimurium and Escherichia coli which respect to operon structure and regulation.";
J. Bacteriol, 180:722-731(1998).
                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
NCBI_TaxID=602, 601, 592;
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SPECIES=S.typhi; STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
                                                                                                                          01-02T-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Major curlin subunit precursor (Fimbrin 58F17)
CSGA OR AGFA OR STM1144 OR STY1181 OR T1776.
Salmonella typhimurium,
Salmonella typhi, and
salmonella enteritidis.
                                                                    151 AA
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                                                                    STANDARD;
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriol. 173:4773-4781(1991).
- FUNCTION: CURLIN IS THE STRUCTURE SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
'Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
                                                                                                                                                                                                                                                                                                                                                                     SPECIES=S.enteritidis; STRAIN=27655-3B; MEDLINE=21310586; PubMed=1677357; Collinson S.K., Emecdy L., Mueller K.-M., Trust T.J., Kay W.W.; "Putification and characterization of thin, aggregative fimbriae from Salmonella enteritidis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                               SPECIES=S.enterritidis; STRAIN=27655-3B; MEDLINE=94013373; PubMed=8104955; Doran J.L. Collinson S.K., Burian J. Sarlos G., Todd E.C.D., Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., Kay W.W.; Munro C.K. as a sanser p.A., Peterkin P.I., Kay W.W.; The Structural gene for thin, aggregative fimbriae. "; J. Clin. Microbiol. 31:2263-2273(1993).
                                                                                SPECIES-S.enteritidis; STRAIN-27655-3B; MEDLINE-56146521; PubMed-8550497; Collinson S.K., Clouchier S.C., Doran J.L., Banser P.A., Kay W.W. Salmonella enteritidis agfBAC operon encoding thin, aggregative
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SVMVRQVGFGNNATANQY -> DSYTQVAS
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90.7%; Pred. No. 2.2e-50;
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PIR; JC6039; JC6039.
StyGene; SG10608; csgA.
Fimbria; Signal; Complete proteome.
SIGNAL
                                 Bacteriol. 185:2330-2337(2003)
                                                                                                                                                                    Bacteriol. 178:662-667(1996).
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EMBL, AAE008749; AAL20074.1; -.
EMBL, AL627269; CAD08266.1; -.
EMBL, AE016840; AA069399.1; -.
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RAY MEDINE-91310586; bubMed=1677357;

RAY Collinson S.K., Emoedy L., Trust T.J., Kay W.W.;

RT "Purification and characterization of thin, aggregative fimbriae from RT "Purification and characterization of thin, aggregative fimbriae from RT "Purification and characterization of thin, aggregative fimbriae from RT "Salmonelia enteritidis.";

RL "Salmonelia enteritidis.";

RL "Salmonelia enteritidis.";

RL "Salmonelia enteritidis.";

CC "IEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN.

CC FIBRONECTIN.
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STAIN=K12;
STAIN=K12;
STAIN=K12;
STAIN=K12;
STAIN=S-07661202; PubMed=8905232;
SSTAIN=S-07661202; PubMed=T., Fujita K., Hayashi K., Honjo A.,
Shimua T., Alba H., Baba T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masauda S., Miki T., Mizohuchi K.,
Sampei G., Seki Y., Tagami H., Takemoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuthi T.,
"A 718-kb DNA sequence of the Escherichia coli K-12 genome
Corresponding to the 12.7-28.0 min region on the linkage map.";
DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE 56414489; PubMed=8817489; MEDLINE 56414489; PubMed=8817489; Memmar M., Arngvist A., Bian Z., Olsen A., Normark S.; "Expression of two csg operons is required for production of fibronectin- and congo red-binding curli polymers in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=K12 / W3110;
MEDELINE=92311294; PubMed=8459772;
MEDELINE STRAINS
THE PLOSS A: Arnqvist A. relieves H-NS-mediated transcriptional repression of csgA, the subunit gene of fibronectin-binding curli in
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SEQUENCE FROM N.A.
MEDIJUE=97426617; PubMed=9278503;
Blattner F.R., Flunkett G. III, Bloch C.A., Perna N.T., Burland V. Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.,
                                                                                                                                                                                                                                                                                      Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
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MEDLINE=93023873; PubMed=1357528;
Arnqvist A., Olsen A., Pfeifer J., Russell D.G., Normark S.;
"The Cri protein activates cryptic genes for curli formation and fibronectin binding in Bscherichia coli HBI01.";
MOI. Microbiol. 6:2443-2452(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997)
                                                                     01-DEC-1992 (Rel. 24, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
151 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bscherichia coli.";
Mol. Microbiol. 7:523-536(1993)
                                                                                                                                                                              Major curlin subunit precursor
STANDARD;
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STRAIN=K12 / MC4100;
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SEQUENCE OF 21-40.
                                                                                                                                                                                                                                                           Escherichia coli
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01-OCT-1996
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P28307
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                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                61 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG 120
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MEDLINE=21218556; Pubmed=11319125;

Whileh GA., Keen J.E., Elder R.O.;

"Mutacions in the csgb promocer associated with variations in curli

expression in certain strains of Escherichia coli 0157:H7.";

Appl. Environ. Microbiol. 67:2367-2370(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21074935, PubMed=11206551, Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J. Kirkpatrick H.A., Posfai G., Hackett J., Kilnk S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K., Apodaca J., Ananthaxaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Major curlin subunit precursor.
CSGA OR 21676 OR ECS1420.
Escherichia coll 0157:HT.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                               tch 67.1%; Score 521; DB 1; Length 151; al Similarity 69.5%; Pred. No. 6e-37; 105; Conservative 17; Mismatches 29; Indels
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7 7 A -> E (IN REF. 1).

151 AA; 15049 MW; C003470D208D395F CRC64;
-!- SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY
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STRAIN=0157:H7 / EDL933 / ATCC 700927;
                                                                                                                  EMBL; L04979; AAA23616.1; -.
EMBL; X90754; CAA62282.1; -.
EMBL; AE00205; AAC4126.1; -.
EMBL; D90741; BAA5832.1; -.
EMBL; S70789; S70788.
ECGGNe; EG11489; CSGA.
Fimbria; Signal; Complete proteome.
SIGNAL
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Q93U24;
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"Conserved repetition in the ice nucleation gene inaX from Xanthomonas campestris pv. translucens.";
Mol. Gen. Genet. 223:163-166(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151
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01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNNAALVNQTASDSSVMVRQVGFGNNATANQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91080859; PubMed=2259339;
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Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ice nucleation protein.
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us-09-543-407-22.rsp

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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                  -----DQLVTRVVTHEMAHAD-----QWNAKUSDITVGQYG----GNNAALV 126
                                                                                                                                                                                                                                                                                                                                                                                                                       491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGAD---NY--
                                                                                                                                                                                                                                                                                                                                                                                                              GSTGTAGADSTL-IAGYGSTQTA-----GGESSLT-AGYGSTQTARQGSDITAGYGS
                                                                                                                                                                                                                                                                                                                                   Gaps
-!- FUNCTION: Ice nucleation proteins enable bacteria to nucleate crystallization in supercooled water.
-!- SUBCELLIULAR LOCATION: Outer membrane (By similarity).
-!- DOMAIN: CONTAINS 153 IMPERFOT REPEATS OF THE CONSENSUS OCTAPERINE A-G-Y-G-S-T-L-T; FUNTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE PERIODICITY IS SUPERINFOSED.
-!- MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
-!- SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROW N.A.
STRAIN-RIA / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                  45;
                                                                                                                                                                                                                                                                                                            12.0%; Score 93.5; DB 1; Length 1567; 28.2%; Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                  InterPro; IPR000258; Ice_nucleatn.
Pfam; PF00818; Ice_nucleation; 81.
PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE_NUCLEATION; 57.
Ice_nucleation; Repeat; Outer membrane.
SEQUENCE 1567 AA; 152548 MW; C8B451D959ECAD63 CRC64;
                                                                                                                                                                                                                                                                                                                                  21; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1995 (Rel. 31, Created)
01-07-1996 (Rel. 34, Last sequence update)
01-07-1996 (Rel. 34, Last sequence update)
Minor curlin subunit precursor.
CSGB OR B1041 OR 21675 OR ECS1419.
Escherichia coli, and
Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                               ----NQTASDSSVMVRQVGFGNNATANQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                             492 AGYGSTQTAGSESSLT--AGYGSTQTAQQ 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 83334;
                                                                                                                                                                                                           EMBL; X52970; CAA37140.1; -. HSSP; P06620; 11NA.
                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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Matches 42; Conserv
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Armqvist A., Olsen A., Normark S.;
"Sigma S-dependent growth-phase induction of the csgBA promoter in
"Sigma S-dependent growth-phase induction of the absence
of the nucleoid-associated protein H-NS.";
Mol. Microbiol. 13:1021-1032(1994).
-! FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE
COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH
TEMPERATURES BELOW 37 DESREES CELSIUS. CURLI CAN BIND TO
FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=0157:H7 / RIMD 0509952;
MEDLINB=21156231; PubMed=11258796;
MEDLINB=21156231; PubMed=11258796;
Mayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.; Scherichia coli
"Complete genome sequence of enterchemorrhagic Escherichia coli
"Complete genome comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                    Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mortomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21074935, PubMed=11206551;
MEDLINE=21074935, PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.,
"Genome sequence of entrohaemorrhagic Escherichia coli O157:H7.",
Nature 409:529-533(2001).
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Amau B., Shoa Y., Shoa Y., "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y. Yano M., Horiuchi T., "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."; DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURLIN MONOMERS.
SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97061202; PubMed=8905232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=K12;
MEDLINE=95157246; PubMed=7854117;
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EMBL; AE005315; AAG55787.1; -.
EMBL; AP002584; BAB34842.1; -.
PIR, C90806, C90806.
PIR, G85665;
PIR, S70787; S70787.
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46;
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                                                                                                                                38 SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVT 97
                                                                                                                                                        AAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biosci. Biotechnol. Biochem. 58:762-764(1994).

-! FUNCTION: Ice mucleation proceins enable bacteria to nucleate crystallization in supercooled water.

-! SUBCELLULAR LOCATION: Outer membrane.

-! SUBCELLULAR IDCATION: Outer membrane.

-! DAMAIN: CONTAINS THRERERET REPEATS OF A CONSENSUS OCTAPEPTIDE A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.

-! MISCELLANBOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE NUCLEATION PROTEIN DISELAYS A SYMMETRY RELATED TO THAT OF ICE.

-! SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRANDAMEDINE-STRANDE STRANDE NG OF AN ICE nucleation active gene of Erwinia
                                                                                                                                                                                     151
                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae; Pantoea.
                                                                                                                                                                                                           77 SNRAKIDÓTGBYNL-AYIDÓAGSANDÁSISÓGAYGNTAMILÓKGSGNKANITGY
                                                                                                                                                                                   98 HEMAHADOWNAKNSDITVGOYGGNNAALVNQTASDSSVMVRQVGFGNNATANOY
                                                                                                        2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.8%; Score 91.5; DB 1; Length 1034; 26.3%; Pred. No. 3.7; ive 20; Mismatches 54; Indels 55
                                                                           11.9%; Score 92.5; DB 1; Length 151; 28.1%; Pred. No. 0.36; ive 15; Mismatches 62; Indels E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1034 AA; 103378 MW; FA222523D333EADD CRC64;
                                                  B18D266B964014B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OCTAPEPTIDE PERIODICITY
                        POTENTIAL.
MINOR CURLIN SUBUNIT.
                                                                                                                                                                                                                                                                                                        (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                               1034 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP, P06620; IINA.
InterPro; IPR00258; Ice nucleatn.
Pfan, PP00818; Ice nucleation; 51.
PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE_NUCLEATION; 34.
                                                                                                                                                                                                                                                                                                                                                                            Pantoea ananas (Erwinia uredovora).
           Signal; Complete proteome 1 21 POTENT
                                                 151 AA; 15882 MW;
                                                                                                                                                                                                                                                                                                                                                 nucleation protein inaU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D14992; BAA03636.1; -.
                                                                                                        32; Conservative
                                                                                                                                                                                                                                                                              STANDARD;
EG12621; csgB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JC2143; JC2143.
                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=553;
                                                                                                                                                                                                                                                                                                        01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                    16-OCT-2001
                                                                                                                                                                                                                                                                              PANAN
EcoGene; Fimbria; SIGNAL
                                                  SEQUENCE
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                                                                            Query Match
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Matches
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10;

Gaps

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Conservative

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Best Loc Matches

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                                                                                                                                                                                  -----GEESSQMAGYGSTQTGMKGSDLTAGYGSTGTAGDDSSLIAGYGSTQTAGEDS 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -:- FUNCTION: Ice nucleation proteins enable bacteria to nucleate crystallization in supercooled water.
-: SUBCELLULAR LOCATION: Outer membrane.
-:- DOMAIN: CONTAINS 126 IMPERED REPEATS OF A CONSENSUS OCTAPEPTIDE A-G-Y-G-S-T-X-T; FUNTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE PREDIOTICITY IS SUPERINPOSED.
-:- MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE NUCLEARION PROTEIN DISBLAYS A SYMMETRY RELATED TO THAT OF ICE.
-:- SIMILARITY: Belongs to the bacterial ice nucleation protein
                                          ALQSDARKSETTITQSGYGN-----GADVGQG-----ADNYDQLVTRVVTHEMAHAD-
--GPDSTLSIYQYGSANAAL
                                                                                                                                                                                                                                                -----QWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQ 150
                                                                                                                                                                                                                                                                                     271 SLTAGYGSTQTAQKGSDLTAG-YGSTGTA----GADSSLI---AGYGSTQTAGE 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Erwinia herbicola.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Warren G.J., Corotto L.V.;

"The consensus sequence of ice nucleation proteins from Erwinia herbicola, Pseudomonas fluorescens and Pseudomonas syringae.";
Gene 85:239-242(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OCTAPEPTIDE PERIODICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 IVVSGSALAGVVPQW--GGGGNHNGGGNSS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.8%; Score 91.5; 26.3%; Pred. No. 4.
IVVSGSALAGVVPQW--GGGGNHNGGGNSS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000258; Ice_nucleatn.
Pfam; PF00818; Ice_nucleation; 65.
PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE NUCLEATION; 45.
Ice_nucleation; Repeat; Outer_membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence
16-OCT-2001 (Rel. 40, Last annotatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=M1;
MEDLINE=90152370; Pubmed=2515997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, M26382, AAA24823.1; -.
PIR, JQ0188, JQ0188.
HSSP; P06620; 1INA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enterobacteriaceae; Pantoea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ce nucleation protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1217
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-use European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 -- OSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQ-YGGNNAALVNQ 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GEESSQMAGYGSTQTGMKGSDLTAGYGSTGTAGDDSSLIAGYGSTQTAGEDS 270
---ADNYDQLVTRVVTHEMAHAD- 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGSALAGVVPQWGGGGN--HNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTIT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable outer membrane protein pmpB precursor (Polymorphic membrane
                                                            271 SLTAGYGSTQTAQKGSDLTAG-YGSTGTA----GADSSLI---AGYGSTQTAGE 316
                                                                                                                                                                                                                                                                                               MEDDINE=99000899; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN PMPB.
                                                                                                                                                                                                                                                                                                                                               "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to the PMP outer membrane protein family.
                                              ----OWNAKUSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQ
                                                                                                                                                                                                                                                                                                                                                            Chlamydia trachomatis.";
Science 282:754-759(1998).
-!- SUBCELLULAR LOCATION: Cell wall surface (elementary bodies)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                             Chlamydia trachomatis.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGRPAMs; TIGRO1376; POMP repeat; 18.
Outer membrane; Signal; Multigene family; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 91; DB 1; Length 1754;
; Pred. No. 7.3;
10; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
PROBABLE OUTER MEMBRANE PRO
W; 969CF8D85D36185D CRC64;
  --GADVGQG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE001314; AAC68010.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHCI-2DPAGE, 084418; ...
Interarpo, IPR003368; Chlamydia PMP.
Pfam, PF02415; Chlamydia PMP; 4.
TIGRFAMS; TIGR01376; POWE. repeat; 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 1754 PROF
1754 AA; 183317 MW;
 ALQSDARKSETTITQSGYGN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.7%;
33.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 33.1
Matches 40; Conservative
                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=D/UW-3/Cx;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 T 129
                                                 105 ----
                                                                                                                                                                                                                                                                                                                                                                                                (Potential
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                                                                                                                                                                                                      protein B).
PMPB OR CT413.
                                                                                                                                                                                                                                                                                                                                      Davis R.W.;
                                                                                                                                  CHLTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                 PMPB CHI
084418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E----MAHADQWNAKNSDIT-VGQXGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                     Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Bashama D., Barooks K., Chillingworth T., Connerton P., Cronin A., Davisa P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
Whitehead S., Barrell B.G.;
Whitehead S., Barrell B.G.;
Manue sequence of a multiple drug resistant Salmonella enterica servar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng M., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Bacteriol. 185:2330-2337 (2003).

-i. FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19; Gaps
                                                                                                                                                                                     Bacteria, Prôteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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16254 MW; 161C54326E573495 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.7%; Score 90.5; D 28.8%; Pred. No. 0.53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fimbria, Signal, Complete proteome.
SIGNAL 1 21 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21534947; PubMed=11677608;
                                                                                            Minor curlin subunit precursor.
CSGB OR STY1180 OR T1777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AL627269; CAD08267.1; -. EMBL; AE016840; AAO69400.1; -.
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151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURLIN MONOMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 34; Conserv
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                 Salmonella typhi
                                                                                                                                                                                                                                                              NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CSGB_SALTY
ID _CSGB_SALTY
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RESULT 9 CSGB\_SALTI

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNYDQLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Abe K., Watabe S., Emorary Y., Watanabe M., Arai S.;
"An ice nucleation active gene of Erwinia ananas. Sequence similar to those of Pseudomonas species and regions required for ice nucleation activity."

FEBS Lett. 258:297-300(1989).

-! FUNCTION: Ice nucleation proteins enable bacteria to nucleate. STRSCELDLAR LOCATION: Outer membrane (By similarity).

-! STRSCELDLAR LOCATION: Outer membrane (By similarity).

-! STRSCELDLAR A. A.G. Y. G. S. T. Y. T. FURTHER ON A 16-RESIDUE AND A RECIONAL 48-RESIDUE PRRIODICITY IS SUPERIMPOSED.

-! SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1322;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   933 GSTSTAGPDSSL-IAGYGSTQTA------GYNSILTAGYG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.5%; Score 89.5; DE 26.8%; Pred. No. 7.1; iive 18; Mismatches
                                                                                                                                                                                                                                                                                                                                  1322 AA
                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ice nucleation; Repeat; Outer membrane.
DOMAIN 162 1281 OCTAPEPTID
SEQUENCE 1322 AA; 131094 MW; 89BOEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00818; Ice nucleation; 69.
PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE NUCLEATION; 49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pantoea ananas (Erwinia uredovora)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR, S07053; S07053.
HSSP; P06620; IINA.
InterPro; IPR000258; Ice nucleatn.
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                                                                                                                                                                                                                                                                                            | CEA PANAN | SIALL- | CEA PANAN | SIALL- | CO4659; | C104659; | C1-FEB-1991 | (Rel. 17, Last seque | C1-FEB-1991 | (Rel. 40, Last anno | C1-FEB-1991 | (Rel. 40, Last anno | C1-FEB-1991 | (Rel. 40, Last anno | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1-FEB-1991 | C1
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|SQSAYGNSAAIIQKGSGN-
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Matches 34; Conservative
                                                                                                   129 TASDSSVMVRQ 139
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                                                                                                                                                                    140 KOSHMAIRVTO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=553;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 IIQSGYGNGADVGQ-GADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGGNNAALVNQ 128
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                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=S.typhimurium; STRAIN=SR-11;
MEDLINE=98117058; PubMed=9457880;
Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;
"Curli fibers are highly conserved between Salmonella typhimurium and Escherichia coli with respect to operon structure and regulation.";
J Bacteriol. 180:722-731(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIESS. Lyphimurium, STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=2134944; PubMed=11677609;
MEDLINE=2134944; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H. Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fimbriae.";
J. Bacteriol. 178:662-667(1996).

-1- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI AR COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIRRORETIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF CURLIN MONOMERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ryan E., Sun H., Florea L., Miller W., Stoneking T., Mhan M.,
Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                 Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SPECIES-S.enteritidis; STRAIN=27655-3B;
MEDLINE=96146512; PubMed=8550497;
Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W.W.
"Salmonella enteritidis agfBAC operon encoding thin, aggregative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39;
                                     01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Minor curlin subunit precursor (Pimbrin SEF17 minor subunit).
CSGB OR AGFB OR STM1143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 151;
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MINOR CURLIN SUBUNIT.
; COFC5430E6DD361D CRC64;
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EMBL; AB008749; AAL20073.1; -.
EMBL; U43280; AAC43598.1; -.
PIR; JC6040; JC6040.
SryGene; SG10609; csgB.
Fimbria; Signal; Complete protecome.
SIGNAL
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                                                                                                                                                                                                       Salmonella typhimurium, and Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=602, 592;
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                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Local Sima
36;
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Best Local S:
Matches 36,
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EMBL; M60048; AAA29244.1; -. HSSP; P08148; 1LML.
                                                                                               28.2%;
                                                    Query Match
Best Local Similarity 28.2'
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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NCBI_TaxID=5661;
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ID GP63_LEI
AC P23223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES—W. tuberculosis, STRAIN=H37Rv;
MEDLINE=98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eiglmeier K., Gas, Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
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-!- CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 59. Ref.1 sequence has been checked by authors in Ref.1 and they report that no errors have been found.
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MEDLINE 22206494; PubMed=12218036,
Fleischmann R.D., Alland D., Elsen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Elsen J.A., Carpenter L., White O.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishal W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SPECIES=M.Dovis; STRAIN=AF2122/97;
SPECIES=M.Dovis; STRAIN=AF2122/97;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.",
Proc. Natl. Acad. Sci. US. A. 100:7877-7882(2003).
-! SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS
                                                                                                                                                                                                                                                                 Mycobacterium bovis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                        01-0CT-1996 (Rel. 34, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Hypothetical glycine-rich protein Rv2098c/MT2159/Mb2125c.
RV2098C OR MT2159 OR MTCX49.38C OR MB2125C.
                                                                                                                                                                                                                                                                                                                  Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCBI_TaxID=1773, 1765;
   491 AA
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   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteriol. 184:5479-5490(2002).
                                                                                                                                                                                                                                     Mycobacterium tuberculosis, and
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InterPro, IPR000084; PE_region.
Pfam, PF00934; PE, 1.
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   STANDARD;
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YK98 MYCTU
                                   010707
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                                                                                                                                                                                                                                                                                                                                                                     264
                                                                                                                                                                                                                                                                                                       20 AGVVPQWGGGGN-----HNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSG 74
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LEISHMANOLYSIN.
REMOVED IN MATURE FORM (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euglenozoa, Kinetoplastida, Trypanosomatidae, Leishmania.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (RC 3.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YGNGGAAGSGGNGGD-AGTGVSSDGFAGLGGSGGRGGDAGLIGVGGGGGN 313
                                                                                                                                                                                                                                               26;
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InterPro; IPR06025; Pept M Zn BS.
InterPro; IPR0157; Peptidase MS.
Pfan; PF01457; Peptidase MS.
PRINTS; PR00782; LSHMANOLYSIN.
PROSITE; PS00142; ZINC PROTEASE; 1.
PROSITE; PS0142; ZINC PROTEASE; 1.
PROSITE; PS0141; Cell adhesion; GP1-anchor; Lipoprotein.
Signal. 1 39 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                   75 YGNGADVGOGADNYDQLVTRVVTHEMAHADQWNAKNSD---ITVGQYGGN
                                                                                                                                                                                 DB 1; Length 491;
                                                                                                                                                                                                                                                                                                                                                                  AGLIGHGGAGGNGGDGGHGGSGKAGGSGGSGGFGQFGGAGGLL---
ProDom; PD001223; PE_region; 1.

Hypothetical protein; Complete proteome.

CONFLICT 312 312 G -> GG (IN REF. 1).

CONFLICT 1312 312 MW; 12C8630C59CA0C13 CRC64;
                                                                                                                                                                                                                                               45;
                                                                                                                                                                          Score 87; DB 1;
Pred. No. 3.8;
8; Mismatches
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EMBL; M28527; AAA29235.1;
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J. Biol. Chem. 267:1888-1895(1992).

-!- FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.

-!- GATALYIC ACTIVITY: Preference for hydrophobic residues at Pl and Pl' and basic residues at P2 and P3'. A model nonapeptide is cleaved at _Ala-Tyr-|-Leu-Lys-Lys-.

-!- COFACTON: Binds 1 zinc ion per subunit (By similarity).

-!- SUBCELLULAR LOCATION: Attrached to the membrane by a GPI-anchor.

-!- SIMILARITY: Belongs to peptidase family M8.
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=92112918; PubMed=1370484;
Ramamoorthy R., Donelson J.E., Paetz K.E., Maybodi M., Roberts S.C.,
Ramamoorthy R., Donelson J.E., Paetz E.E., Maybodi M., Roberts S.C.,
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=44271;
                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
ZINC (CATALYTIC) (BY SIMILARITY).

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CALCHAC. (COTENTIAL).
GPI-anchor amidated asparagine (By GPI-anchor amidated asparagine (By
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                                                                                                                                                                                             Mismatches
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                                                                                                                                        similarity)
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                                                                                                                                                                                            Conservative
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                                          373
4443
412
477
498
                                                                                                                                                   590 AA;
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Best Local Similarity
    endopeptidase)
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GP63_LEICH
ID GP63_LEICH
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Matches
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ACTIVATION PEPTIDE.
LEISHMANDLYSIN.
REMOVED IN MATURE FORM (BY SIMILARITY).
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Eukaryota, Buglenozoa, Kinetoplastida, Trypanosomatidae, Leishmania.
NCBI_TaxID=5664;
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WEDLINES-$1009116; PubMed=2145267;
Schneider P., Ferguson M.A.J., McConville M.J., Mehlert A.,
Homans S.W., Bordier C.;
Structure of the glycosyl-phosphatidylinositol membrane anchor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P08148; P15906;
01-AUG-1988 (Rel. 08, Created)
01-APR-1990 (Rel. 14, Last aquence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
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MEDLINE-88154764; PubMed-3346625;
Button L.L., McMaster W.R.;
"Molecular cloning of the major surface antigen of leishmania.";
J. Exp. Med. 167:724-729(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. . .) (POTENTIAL) GPI-anchor amidated asparagine (By
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                                                                                                                                                                       FIGHT.

PROSITE; PRO1982; LESHMANOLYSIN.

PROSITE; PS00142; ZINC_PROTEASE; 1.

Hydrolase; Metalloprotease; Glyroprotein; Metal-binding; Zinc; Zymogen; Signal; Cell adhesion; GPI-anchor; Lipoprotein.

1 39 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 87; DB 1; Length 599; Pred. No. 4.8;
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                                                                              InterPro, IPR006025, Pept M Zn BS.
InterPro, IPR001577, Peptidase_M8.
Pfam, PF01457, Peptidase_M8, 1.
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J. Exp. Med. 171:589-589(1990)
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Best Local Similarity 89.5
Matches 17; Conservative
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HSSP; P08148; 1LML.
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MEROPS; M08.001;
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 **RAY CRYSTALLOGRAPHY (1.86 ANGSTROMS).

**REAL CRYSTALLOGRAPHY (1.86 ANGSTROMS).

**REDINB=98416698; PubMed=9739094;

**Schlagenbard E., Berges R., Metcalf P.;

**Schlagenbard E., Berges R., Metcalf P.;

**The crystal structure of the Leishmania major surface proteinase

**REAL STRUCTURE of the Leishmania major surface proteinase

**REAL STRUCTURE AND TRUCTURE TO THE PREFERENCE for hydrophobic residues at P1 and

**PLYTURICATIVITY: Preference for hydrophobic residues at P1 and

**PLY and basic residues at P2 and P3'. A model nonapeptide is

**Cleaved at -Ala-Tyr-|-Leu-Lys-Lys-.

**COFACTOR: Binds 1 zinc ion per subunit.

**COFACTOR: Binds 1 zinc ion per subunit.

**COFACTOR: Binds 1 zinc ion per subunit.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R InterPro; JPR006025; Pept M Zn BS.
R InterPro; JPR001677; Peptidase_M8.
R Pfam: PF01467; Peptidase_M8.
R Pfam: PF01467; Peptidase_M8.
R PS0142; SR00782; LSHMANOLYSIN.
R PROSTITE; PS00142; ZINC_PROTEASE; I.
R PROSTITE; PS00142; ZINC_PROTEASE; I.
R STWGGEN; Signal; Cell adhesion; GPI-anchor; 3D-structure; Lipoprotein.
T SIGNAL 1 39 adhesion; GPI-anchor; 3D-structure; Lipoprotein.
T CHAIN 101 577 LEISHMANOLYSIN.
T PROPEP 602 REMOVED IN MATURE FORM.
T ACT_SITE 264 264 ZINC (CATALYTIC).
T METAL 268 ZINC (CATALYTIC).
T METAL 334 334 ZINC (CATALYTIC).
                                    X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
MEDULNE-95406217; PubMed=7675788;
Schlagenhauf E., Erges R., Metcalf P.;
Crystallization and preliminary X-ray diffraction studies of leishmanolysin, the major surface metalloproteinase from Leishmania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
GPI-anchor amidated asparagine.
 the Leishmania major promastigote surface protease.";
J. Biol. Chem. 265:16955-16964(1990).
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PIR, PL0221, PL0221.
PDB, 1LML; 17-SEP-97.
MEROPS, M08.001; -.
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## ALIGNMENTS

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PRT; 152 AA. Created) Last sequence update) Last annotation update)	Gammaproteobacteria; Enterobacteriales; nella.	332; Gordon J.I., Bian Z., Pfeifer J.D.,	Normark S.J., knen M., "Expression of "Expression of thin, aggregative fimbriae promotes interaction of Salmonella typhimurium SR-11 with mouse small intestinal epithelial cells.";	997). 9DA7DADC2364B006 CRC64;	Score 673; DB 2; Length 152; Pred. No. 3.7e-47; 3; Mismatches 13; Indels 0; Gaps	MKLLKVAAFAAIVVSGSALAGVVPOWGGGGNHNOGGNSSGPDSTLSIYQYGSANAALALQ 6 	SDARKSETTITOSGYGNGADVGQGADNYDQLVTRVVTHEMAHDDQWNARNSDITVGQYGG 1 
PRELIMINARY; 1998 (TYEMBLRE1. 05, 1998 (TYEMBLRE1. 05, 2001 (TYEMBLRE1. 19,	yphimurium. oteobacteria; iaceae; Salmor	1] MEDLINE-98053981; PubMed-9393832; Sukupolvi §.S., Lorentz R.G., Gordon J.I.,	Normark S.J., Rhen M.; "Expression of thin, aggregati Salmonella typhimurium SR-11 v Cells.";	Infect Immun. 65:5320-5325(1997) BEMBL; AJOO0514; CAA04151.1; NON TER 152 SEQÜENCE 152 AA; 15401 MW; 9D	86.7%; Similarity 89.4%; 5; Conservative 3	1 MKLLKVAAFAAIVVSGSALAC 	61 SDARKSETTITQSGYGNGADV
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MEDLINE-22388234; PubMed=12471157;
Melch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Melch R.A., Burkles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
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Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
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Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Enterobacter.
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Zogaj X., Bokranz W., Nimtz M., Romling U.;
Zogaj X., Bokranz W., Nimtz M., Romling U.;
Production of Cellulose and Curli Fimbriae by Members of the Family
Enterobacteriaces Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 72:4151-4158 (2003).
EMBL; AJ515700, CAD56672.1;
SEQUENCE 150 AA; 15016 MW; 1D7141B8D6973DC6 CRC64;
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"Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 72:4151-4158 (2003).
EMBL; AJSIS701; CADS66751; -.
SEQUENCE 149 AA; 15260 MW; 946DD52017F648FD CRC64;
                                                                                                                                                                                                                                                    Bacteria; Profeobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
NCBI_TaxID=213763;
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                 NNAAL VNOTASDSSVMVRQVGFGNNAPANQY 151
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149
                                                                                                                                                Created)
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                                                                                                                                                25,
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                                                                                                         PRELIMINARY;
                                                                                                                                          01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                      Citrobacter sp. Fec2.
                                                                                                                                                                                                  Curlin-csgA protein.
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Curlin-csgA protein.
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01-OCT-2003
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Q7X240; Q7X240

RESULT 3 Q7X240

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SEQUENCE FROM N.A.

TRANSPOSON-Insertion sequence 181;

MEDLINE-99314153; PubMed-1036375;

La Ragione R.M., Collighan N.J., Woodward M.J.;

La Ragione R.M., Collighan coli O78:K80 isolates associated with

"Non-curliation of Escherichia coli O78:K80 isolates associated with

"ISI inserti on in csgB and reduced persistence in poultry infection.";

PEMS Microbiol. Lett. 175:247-253(1999).

EMBL; AJ131756; CAB45380.1; -.

29
                                   Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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EMBL; AE015532; AAN53942.1; -.
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                                                                                                                                                                                                                                                                                                                                                                               15.7%;
ilarity 89.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 28.3
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shewanella oneidensis."
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                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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SEQUENCE 139 AA;
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                            Escherichia coli
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01-MAR-2003
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                                                                                                                                                                                                                                                                                                                  61 SDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG 120
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Enterobacteriaceae, Salmonella.
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Cox J.M., Eglezos S., Woolcock J.B.;
"Virulence of Salmonella enteritidis in chickens correlates with
colony morphology and expression of SEF17 fimbriae.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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"Production of Cellulose and Curli Fimbriae by Members of the Enterobacteriaceae Isolated from the Human Gastrointestinal Tr. Infect. Immun. 72:4151-4158 (2003).
EMBL, AJ515702; CAD56678.1; - SEQUENCE 150 AA; 15112 MW; 5D8BB2D872DF15F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 305.5; DB 2; Length 76; Pred. No. 1e-17; 4; Mismatches 6; Indels 49
                                                                                                                                        Length
                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SEF17 fimbrin (Fragment).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Curlin subunit monomer (Fragment).
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                                                                                                                                      54.3%; Score 421.5; DB 258.9%; Pred. No. 9.2e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                   120 LNGALVDQTASNSTVNVTQIGFGNHATAHQY 150
                                                                                                                                                                                                                                                                                                                                                                                                           121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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54.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella enteritidis.
                                                                                                                                        Query Match
Best Local Similarity
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Q983J5;
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Q54069;
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Matches
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Q54069
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Q983JS
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                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
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                                                       Score 122; DB 2; Length 29;
Pred. No. 0.0025;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.8%; Score 115; DB 16; Length 13
28.3%; Pred. No. 0.061;
.ive 19; Mismatches 33; Indels
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29 AA; 2789 MW; E290DFC07ABBB243 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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TIGR; S00865;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 ISNNATILĢFGATNTATILĢIGS-----LLTVNTAVIGQGGITATASNIALT-GQVG
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                                                                                                                                                                                                                                                                                                                                 STRAIN-USDA 110;
MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genomic sequence of nitrogen-fixing symbiotic bacterium addyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
EMBL; AP005954; BAC50564.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shewanella oneidensis.
Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 130; Score 110; DB 16; Length 130; Local Similarity 25.8%; Pred. No. 0.14; les 39; Conservative 28; Mismatches 56; Indels 2
                                                                                                                                                                                                                 Bacteria, Protecbacteria, Alphaprotecbacteria, Rhizobiales,
Bradyrhizobiaceae, Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12699 MW; ACFB2D66A48D260F CRC64;
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                                                                                                Last sequence update)
Last annotation update)
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                                                                         Created)
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EMBL; AE015532; AAN53941.1; -.
                           PRT;
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STRAIN=MR-1;
MEDLINE=22297686; PubMed=12368813;
                                             Q89J14;
01-UUN-2003 (TrEMBLrel. 2-
01-UUN-2003 (TrEMBLrel. 2-
01-UUN-2003 (TrEMBLrel. 2-
Bll5299 protein.
                                                                                                                                                                                             Bradyrhizobium japonicum.
                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 AA;
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                                                                                                                                                                                                                                                               NCBI_TaxID=375;
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Matches
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Q8EIH4
Q89J14
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                                                                                                                                                                                        405
                                                                                                                                                                                                                                ----N 107
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                                                                                                                                                78
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                                                                                                                                                  --LALQSDARKSETTITQSGYGNG
                                                                                                                                                                             Tetrahymena thermophila.
Bukaryota, Alveolata, Ciliophora, Oligohymenophorea, Hymenostomatida,
Tetrahymenina, Tetrahymena.
NCBI_TaxID=5911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 QWGGGGNHNGG---GNSSGPDSTLSIYQYGSANAALALQSDARKSETTIT----QSGYGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1640 QFGGGGNSNGGQSWGTSSGSDWN-------CQSNVQESTITSSGGWGSSGSGN
                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-88189811; PubMed=3357771;
Martindale D.W., Taylor F.W.;
"Multiple introns in a conjugation-specific gene from Tetrahymena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1686 OTGGGWGSNDNQQQ-----ONENTGGGGWGSSNSNQTNNESSWGSNNQA 1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q94821; P92146; P92145; P92144; P92143; P92141; Q94820; O1-FBB-1997 (TYEMBLrel. 02, Created)
01.FEB-1997 (TYEMBLrel. 02, Last sequence update)
01.OCT-2003 (TYEMBLrel. 25, Last sequence update)
                                                                                                        49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 GADVGQGA-DNYDQLVTRVVTHEMAHADQWNAKNSDITVGQ--YGGNNAA 124
                                                                DB 16; Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.0%; Score 109; DB 5; Length 1748; 33.6%; Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                             GDNNSLMITQTGNDNLVLGSQAGNNNSISVTQSGDMVATVVQY 502
                                                                                                                                                                                                                                79 ADVG------QGADNYDQLVTRVVTHEMAHADQW----
                                                                                                                                                                                                                                                                                                                     108 AKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                        Indels
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I -> N (IN REF. 1).
WW; OB03F210104008A3 CRC64;
Hypothetical protein, Complete proteome.
SEQUENCE 502 AA; 52441 MW; D08CA23D6C46B62D CRC64;
                                                                                                        50;
                                                              14.1%; Score 109.5; Di 23.8%; Pred. No. 0.79;
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InterPro; IPR001878; Znf CCHC.
Pfam; PF00098; zf-CCHC; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1748 AA
                                                                                                      26; Mismatches
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                                                                                                                                                  29 GGNHNGGGNSSGPDSTLSIYQYGSANAA-
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SMART; SM00343; ZNF CZHC; 7.
PROSITE; PSS0158; ZF CCHC; 7.
CONFLICT 251 251 M --
SEQUENCE 1748 AA; 199624 MW;
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                                                       Query Match
Best Local Similarity 23.8%
Matches 39, Conservative
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Best Local Similarity 33.69
Matches 37; Conservative
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MEDLINE=21681879; PubMed=11823852;
MEDLINE 21681879; PubMed = 11823852;
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01-MAR-2002 (TrEMBLrel. 20,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 -LALQSDARKSETTITQSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                750 GLTLTTQGSHAAGIVAQS-VGGGGGTGGTASSYSAGI-------GFTASVAV 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=1021,

MEDLINE=21396508; PubMed=11481431;

A Finan T.M., Weddener S., Wong K., Buhrmester J., Chain P.,

A Finan T.M., Weddener S., Wong K., Buhrmester J., Chain P.,

A Orthoelter Wed, Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,

Golding B., Puehler A.;

The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-

Tixing endosymbion tionnizobium mellioti.";

The proc. Natl. Acad. Sci. U.S.A. 98:9889-9894 (2001).

R EMBL, AL603645; CAC49389.1; -.

R GO; GO:0004601; F:peroxidase activity; IEA.

R GO; GO:0006501; F:peroxidase activity; IEA.

R GO; GO:0006501; F:peroxidase activity; IEA.

R GO; GO:0006501; F:peroxidase activity; IEA.

R InterPro; IPRO05546; Autotransporter.

R InterPro; IPRO052173; PfkB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

14.0%; Score 109; DB 16; Length 2174;
Best Local Similarity 27.0%; Pred. No. 5.1;
Matches 40; Conservative 20; Mismatches 52; Indels 36;
                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
Hyporhetical glycine-rich protein SMb21548.
RB0989 OR SMB21548.
RRizobium mellicti (Sinorhizobium mellioti).
Plasmid pSymB (megaplasmid 2).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEGNITE; PS01797; Autotransporter; 1.
PROSITE; PS00435; PEROXIDASE 1; 1.
PROSITE; PS00583; PFKB_XINASES 1; 2.
PROSITE; PS00583; PFKB_XINASES 1; 2.
Plasmid; Hypochetical protein; Complete proteome.
SEQUENCE 2174 AA; 203314 WW; 008EB68297B44182 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Probable hemagglutinin-related protein.
RSC0887 OR RSO6116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 3501 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                794 GGTGGNGGAGGEVSVSLTDSAIRTGQGG 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burkholderiaceae; Ralstonia.
NCBI_TaxID=305;
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                                                                                                                         PRELIMINARY;
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                                                                  RESULT 12
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Azlanchart. S. Attiguenave F., Gouzy J., Mangenot S., Ariath M., Genin S., Attiguenave F., Gouzy J., Mangenot S., Ariath M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurim W., Schiex T., Squier P., Thebault P., Malen M., Wincker P., Levy M., Meisenbach J., Boucher C.A.; "Genome:Sequence of the plant pathogen Ralstonia solanacearum."; T. "Genome:Sequence of the plant pathogen Ralstonia solanacearum."; Ruture 415:497-502(2002).

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Ruture 4
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"Genome Sequence of the plant pathogen Ralstonia solanacearum.";

Nature 415:497-502(2002).

EMBL, AL646079; CAD17691.1; -.

GO; GO:0004821; F:endcleic acid binding; IEA.
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Burkholderiaceae, Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 SGSALAGVVPQWGGGGNHNGGG-NSSGPDSTLSIYQYGSANAA----
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InterPro: IPR008619; Fil haemagg.
InterPro: IPR008638; Haemagg.act.
Pfam; PP05594; Fil haemagg; 20.
Pfam; PP05860; Haemagg_act; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 LALQSDARKSETTITQSGYGNGADVG----QGADNYDQLVTRVVTHEMA--HADQWNAKN 110
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                                                                                                                                                                                                                                               Gaps
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MEDLINE=98053981; PubMed=9393832;
Sukupolvi S.S., Lorentz R.G., Gordon J.I., Bian Z., Pfeifer J.D.,
Normark S.J., Rhen M.;
"Expression of thin, aggregative fimbriae promotes interaction of
Salmonella typhimurium SR-11 with mouse small intestinal epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella typhimurium.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriacee, Salmonella.
NCBI_TaxID=602;
                                                                                                                                                    Query Match
13.7%; Score 106.5; DB 16; Length 3552;
Best Local Similarity 29.5%; Pred. No. 15;
Matches 43; Conservative 19; Mismatches 45; Indels 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
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13.7%; Score 106; DB 2; Length 179;
Best Local Similarity 32.3%; Pred. No. 0.44;
Matches 41; Conservative 17; Mismatches 55; Indels
PROSITE; PS01070; NUCLEASE_NON_SPEC; 1.
Plasmid; Complete proteome.
SEQUENCE 3552 AA; 352934 MW; C5432AABE2CCF59C CRC64;
                                                                                                                                                                                                                                                                                                                      15 SGSALAGVVPQWGGGGNHNGGG-NSSGPDSTLSIYQYGSANAA---
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Infect. Immun. 65:5320-5325(1997).
EMBL; AJ000514; CAA04150.1; -.
SEQUENCE 179 AA; 19318 MW; A2BCCB648B3C0B0B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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# SUMMARIES

	no	AgfA::PT3	AgfA::PT3	AgfA::PT3	AgfA sequ	Salmonell	Salmonell	Ag£A::PT3	AgfA::PT3	AgfA::PT3	AgfA::PT3	AgfA::PT3	AgfA::PT3	AgfA::PT3	Escherich	E. coli C	AgfA sequ	Salmonell		FNB curli	Salmonell	Salmonell	Salmonell	Salmonell	Salmonell	Salmonell
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SUMMAKIES	QH	AAB36352	AAB36347	AAB36355	AAR74625	AAB36341	AAW23570	AAB36346	AAB36353	AAB36351	AAB36349	AAB36350	AAB36354	AAB36348	AAB36343	ABR82651	AAR62761	AAW23569	AAR52664	AAR52663	AAB36316	AAB36318	AAB36321	AAB36326	363	AAB36325
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## ALIGNMENTS

RESULT 1

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1000	the state of the s	AGTA. CSGA and AGTA-homologue ilmbrin subunits, respectively, (2)	Agfa. CsaA and Agfa-homologue fimbrin subunits, respectively; (2)	N-PSDB; AAC46628. N-PSDB; AAC46628. Recombinant agfA gene having a segment replaced by a foreign DNA swhich encodes foreign epitope or antigen, expresses recombinant Agprotein useful for eliciting immune response in animal.  Disclosure, Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign DN sequence which encodes a foreign epitope or antigen. Also describe (1) use of thin aggregative finbriae (SEP17/TAF) nucleation depend assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of finbriae comprising recompands.
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05-APR-1999; 99US-012788BP.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of this aggregative fimbriae (SEF17/TAF) nucleation dependance which necodes a foreign epitope or antigen. Also describe use of thin aggregative fimbriae (SEF17/TAF) nucleation dependance which aggregative fimbriae (SEF17/TAF) respectively recombinant aggregative fimbriae (SEF17/TAF) respectively; (ESCA and AcfA. CscA and AcfA-homologue fimbria, respectively; (2)	UTVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672611/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign cannot be continued by the encodes a foreign epitope or antigen. Also describe (I) use of thin aggregative fimbriae (SERI7/TAF) nucleation depends assembly system of Strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombination.	05-APR-1999; 99US-012788BP.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign sequence which encodes a foreign epitope or antigen. Also described in use of thin aggregative fimbriae (SEF17/TAF) nucleation dependence the present of strains of Salmonella. Escherichia coli and Enrencharteriaceae for the production of fimbriae comprising recompressions.	UTVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esquence which encodes a foreign epitope or antigen. Also describe use of thin aggregative fimbriae (SEF17/TAF) nucleation depend assembly system of strains of Salmonells, inhibitory coli and	05-APR-1999; 99US-01278BBP. (UTVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
UTVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign E segment of thin aggregative fimbriae (SERIT/TAR) nucleation depends assembly system of strains of Salmonella, Escherichia coli and Enterpobacteriaceae for the production of filmbriae comprising recombined coad and Acfa-homologue filmbria subunits, respectively: (2) Acfa. Coad and Acfa-homologue filmbriae insubunits, respectively: (2)	(UTVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene neodes a foreign epitope or antigen. Also describe segment of the gene of think aggregative fimbriae (SEF17/TAF) nucleation depends sembly system of Stains of Salmonella, Escherichia coli and Enerobacteriaceae for the production of fimbriae congrising recomplication.	05-APR-1999; 99US-0127888P.  (UYVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (1) where segment of the gene has been replaced by a segment of a foreign sequence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salmonella: Escherichia coll and Enrichance of Strains of Salmonella: Escherichia coll and Enrichance and Enrichance of the production of finbrise comprising recompressions.	UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esquence which encodes a foreign epitope or antigen. Also describ assembly system of strains of Salmonells, inheritant of the series of this agreement of strains of Salmonells, inheritant of the series of the series of the series of the series of the series of the series of the series of the series of the series of the series of salmonells.	05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
05-APR-1999; 99US-0127888P.  (UYVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign E segment of the gene has been replaced by a segment of a foreign E segment of thin aggregative fimbriae (SERI)/TAR) nucleation depering thin aggregative fimbriae (SERI)/TAR) nucleation depering assembly system of strains of Sahmonella, Escherichia coli and affa. CscA and AcfA. CscA and AcfA. CscA and AcfA. CscA and AcfA. CscA box locusing recontactively; (2)	05-APR-1999; 99US-0127888P.  (UTVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esement of the gene as foreign epitope or antigen. Also describe in a dependent as sembly system of Stains of Salmonella, Escherichia coli and assembly system of Stains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of finbriae congrising reconstraints.	05-APR-1999; 99US-0127888P.  (UYVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign sequence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salmonella: Bscharichia coll and sasembly system of strains of Salmonella: Bscharichia coll and Enterphaceae for the production of finbriae comprising recompanishing r	05-APR-1999; 99US-0127888P.  (UYVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign E segment of the gene has been replaced by a segment of a foreign Esquence which encodes a foreign epitope or antigen. Also describ use of thin aggregative fimbriae (SERI)/TARF) nucleation depering assembly system of strains of Samonella, interiorian and	05-APR-1999, 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of thin aggregative fimbriae (SERI)/TARF) nucleation dependance which encodes a foreign epitope or antigen. Also describ (1) use of thin aggregative fimbriae (SERI)/TARF) nucleation dependance which accompanies of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and AffA. CscA and AcfA. CscA end AcfA. CscA controlled the production of fimbriae comprising reco	05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-P8DB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (1) where segment of the gene has been replaced by a segment of a foreign E segment of the gene has been replaced by a segment of a foreign contains and assembly system of Strains of Salmonella, Escherichia coli and assembly system of Strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae congrising reconstraints.	05-APR-1999; 99US-0127888P.  (UTVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign E sequence which encodes a foreign epitope or antigen. Also described in use of thin aggregative fimbriae (SEFI)/TAR) nucleation dependence which encodes a foreign epitope or antigen. Also described by use of thin aggregative fimbriae (SEFI)/TAR) nucleation dependence which encodes a foreign epitope or antigen. Also described by system of strains of Salmonella, Escherichia coli and Encoharteria case for the production of fimbriae comprising reconstraints.	05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC6462B.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of this aggregative fimbriae (SERI)/TARF) nucleation depering assembly system of strains of Salmonells, interestinia recombinant assembly system of strains of Salmonells, interestinia coli and	05-APR-1999; 99US-0127888B. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
UCYVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI, 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of thin aggregative fimbriae (SERI/YTAR) nucleation depends sembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and AffA. CscA and AgfA. CscA and AgfA. CscA and AgfA. CscA and AgfA. Momologue fimbrin subunits, respectively? (2)	05-APR-1999; 99US-0127888P.  (UYVI-) UNIV VICTORIA.  White Ab, Doran JL, Collison SK, Kay WW;  WPI, 2000-672631/65.  N-PBDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign E segment of the gene has been replaced by a segment of a foreign contain and assembly system of Strains of Salmonella, Escherichia coli and assembly system of Strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae congrising reconstraints.	05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esequence which encodes a foreign epitope or antigen. Also described to use of thin aggregative fimbriae (SEFI)/TAR) nucleation dependence which encodes a foreign epitope or antigen. Also described by use of thin aggregative fimbriae (SEFI)/TAR) nucleation dependence which encodes a foreign epitope or antigen. Also described assembly system of strains of Salmonella, Escherichia coli and Encondence and Encodes a foreign epitope or antigen comprising recomprising UCYVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI, 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the gene has dereign epitope or antigen. Also describe use of thin aggregative fimbriae (SERI)/TAR) nucleation depering assembly system of strains of Salmonella, interiorian and	05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,	
05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White Ab, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-P8DB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign E segment of the gene has been replaced by a segment of a foreign (I) use of thin aggregative fimbriae (SEFI)/TAPF) nucleation depends sembly system of strains of Salmonella, Escherichia coli and aster. CacA and AcfA. CacA end AcfA. CacA and AcfA.	(UTVI-) UNIV VICTORIA.  (White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign E segment of the gene has been replaced by a segment of a foreign segment of the gene has been replaced by a segment of a foreign epitope or antigen. Also describe (I) uses of thin aggregative fimbriae (SERIJ/TAF) nucleation depends sembly system of Stains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae congrising reconstricti	(UTVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-67264528.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprocess foreign epitope or antigen, expresses recombinant Aprocess in useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esequence which encodes a foreign epitope or antigen. Also describe in use of thin aggregative fimbriae (SEFI)/TAF) nucleation dependence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salmonella, Escherichia coli and Enrarchance encomprising recomprising recompresents.	(UYVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the neodes a foreign epitope or antigen. Also describe use of thin aggregative fimbriae (SEF17/TAF) nucleation dependassembly system of strains of Salmonella.	05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-P8DB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esement of the neodes a foreign epitope or antigen. Also describe use thin aggregative fimbriae (SEF17/TAF) nucleation dependance which neodes a foreign epitope or antigen. Also describe assembly system of strains of Salmonella, Escherichia coli and Enterpobacteriaceae for the production of fimbriae comprising recomb age. CasA and AcfA-homologue fimbria subunits, respectively; (2)	05-APR-1999; 99US-012788BP.  (UYVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign segment of the gene has been replaced by a segment of a foreign casement which encodes a foreign epitope or antigen. Also describe (I) use of thin aggregative fimbriae (SER17/TAF) nucleation depends semmly system of Strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae congrising recombinations.	05-APR-1999; 99US-0127888P.  (UYVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esequence which encodes a foreign epitope or antigen. Also describe in use of thin aggregative fimbriae (SERIYTAR) nucleation dependence the strains of Salmonella, Escherichia coli and Enrencharteria case for the production of fimbriae comprising recomprising recompresses.	05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-P89BB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esement of the neodes a foreign epitope or antigen. Also describe use of thin aggregative fimbriae (SEFI7/TAF) nucleation depend assembly system of strains of Salmonells.	05-APR-1999; 99US-0127888P. (UTVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
05-APR-1999; 99US-0127888P.  (UYVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esquence which encodes a foreign epitope or antigen. Also describe use of thin aggregative fimbriae (SERI7/TAR) nucleation deperasembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and ApfA. CscA and AcfA-homologue fimbria, respectively; (2)	05-APR-1999; 99US-012788BP.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign response to antigen. Also describe segment of the gene assembly system of Strains of Salmonella, Escherichia coli and assembly system of Strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombination.	05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-P89BB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign sequence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salmonella, Escherichia coli and Enrarcharderia case for the nocduction of finbriae comprising reach antenchardere.	05-APR-1999; 99US-0127888P.  (UYVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esquence which encodes a foreign epitope or antigen. Also describe use of thin aggregative fimbriae (SERI7/TAR) nucleation depering assembly system of strains of Salmonella.	05-APR-1999; 99US-0127888BP. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
05-APR-2000; 2000MO-CA000356.  05-APR-1999; 99US-0127888P.  (UTVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the neodes a foreign epitope or antigen. Also describ (1) use of thin aggregative fimbriae (SERI)/TAR) nucleation deperance which neodes a foreign epitope or antigen. Also describ (1) use of thin aggregative fimbriae (SERI)/TAR) nucleation deperance which acceptance of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and Argh. CscA and AcfA. CscA and AcfA. CscA and AcfA. CscA substitutis, respectively; (2)	05-APR-2000; 2000MO-CA000356.  (UTVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign E segment of the gene foreign epitope or antigen. Also describe segment of the gene foreign epitope or antigen. Also describe segment of the gradient of fambriae (SEF17/TAF) nucleation dependacembly system of Stains of Salmonella, Escherichia coli and Encerobacteriaceae for the production of finbriae comprising reconstricting reconstributed.	05-APR-2000; 2000WO-CA000355.  05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign epitope or antigen. Also describe sequence which encodes a foreign epitope or antigen. Also describe a segment by system of strains of Salmonella, Escherichia coll and Enterphacteria case for the norduction of finbriae comprising recomprising recompaniants.	05-APR-2000; 2000MO-CA000356.  05-APR-1999; 99US-0127888P.  (UTVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esquence which encodes a foreign epitope or antigen. Also describ use of thin aggragative fimbriae (SERI) TARRY nucleation depering assembly system of strains of Samonella.	05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
05-APR-2000; 2000MO-CA0000356. 05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esquence which encodes a foreign epitope or antigen. Also describ (1) use of thin aggregative fimbriae (SERI)/TAR) nucleation deperasembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and ApfA. CscA and AcfA. CscA and AcfA. CscA and AcfA. ScaLubuilts, respectively; (2)	05-APR-2000; 2000MO-CA0000356. 05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (1) where segment of the gene has been replaced by a segment of a foreign Esement of the gene has been replaced by a segment of a foreign Esement of the gene foreign epitope or antigen. Also descrift (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depen assembly system of Strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising reconstricting	05-APR-2000; 2000MO-CA0000356. 05-APR-1999; 99US-0127888P. (UTVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign segment of the gene has been replaced by a segment of a foreign segmence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salmonella: Bscherichia coll and Enterphaceae for the norduction of finbriae comprising reacher and eace the comprising reacher characteristes.	05-APR-2000; 2000MO-CA0000356. 05-APR-1999; 99US-0127888P. (UYUI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the neodes a foreign epitope or antigen. Also describe use thin aggragative fimbriae (SERI) TARRY nucleation deperates a sesembly system of strains of Salmonella.	05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
05-APR-1900; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign E segment of the gene has been replaced by a segment of a foreign E segment of the neodes a foreign epitope or antigen. Also describ (1) use of thin aggregative fimbriae (SERI)/TAR) nucleation dependance which encodes a foreign epitope or antigen. Also describ (1) use of thin aggregative fimbriae (SERI)/TAR) nucleation dependance and AcfA-homologue fimbriae insubmitts, respectively; (2) AcfA. CscA and AcfA-homologue fimbrin submitts, respectively; (2)	05-APR-1000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-P8DB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (1) where segment of the gene has been replaced by a segment of a foreign E segment of the gene has been replaced by a segment of a foreign E segment of the gene foreign epitope or antigen. Also descrift (1) use of thin aggregative fimbriae (SETI/TAF) nucleation dependence which encodes a foreign epitope or antigen. Also descrift (1) use of thin aggregative fimbriae comprising recombinations of fimbriae contributions.	05-APR-1000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant protein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign E sequence which encodes a foreign epitope or antigen. Also described in use of thin aggregative fimbriae (SERI/TAR) nucleation dependence which encodes a foreign epitope or antigen. Also described by system of strains of Salmonella, Escherichia coll and Enrachatement encomprising recomprising recomprising recomprising recomprising recomprising recomprising recompressions.	05-APR-1900; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the gene has dereign epitope or antigen. Also describe used thin aggregative fimbriae (SERI) TARRY nucleation depering assembly system of strains of Salmonella.	05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UTVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign E segment of the neodes a foreign epitope or antigen. Also describ (1) use of thin aggregative fimbriae (SERI/YTAR) nucleation dependance which encodes a foreign epitope or antigen. Also describ (1) use of thin aggregative fimbriae (SERI/YTAR) nucleation dependance and AcfA-homologue fimbriae in subunits, respectively; (2) AcfA. CscA and AcfA-homologue fimbrin subunits, respectively; (2)	05-APR-2000; 2000WO-CA000356.  05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White Ab, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign E segment of the gene has been replaced by a segment of a foreign epitope or antigen. Also describe segment of the gene of strains of Salmbinae (SERI/TAF) nucleation dependence which encodes a foreign epitope or antigen. Also describe assembly system of Strains of Salmbinae comprising recomplexing recombinations.	05-APR-2000; 2000WO-CA000356.  05-APR-1999; 99US-0127888P.  (UTVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antiqen, expresses recombinant protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esequence which encodes a foreign epitope or antigen. Also describe thin aggregative fimbriae (SEFI)/TAR) nucleation dependence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salmonella, Escherichia coll and Enrachateria case for the production of fimbriae comprising recomprising recomprising recomprising recompressions.	05-APR-1000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UTVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign E segment of the anodes a foreign epitope or antigen. Also describe use of thin aggregative fimbriae (SERI)/TAR) nucleation deperate assembly system of strains of Samonella.	05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DWA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign E segment of thin aggregative fimbriae (SEFI7/TAF) nucleation dependance which encodes a foreign epitope or antigen. Also describe use of thin aggregative fimbriae (SEFI7/TAF) nucleation dependance which and strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and ApfA. CscA and AcfA-homologue fimbrin subunits, respectively; (2)	05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign segment of the gene has been replaced by a segment of a foreign epitope or antigen. Also describe cannot be segment of the gene of strains of Salmannella, Escherichia coll and assembly system of Strains of Salmannella, Escherichia coll and Enterobacteriaceae for the production of fimbriae comprising recomplication.	05-APR-1999; 99US-0127888P.  (UYVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esequence which encodes a foreign epitope or antigen. Also describe in use of thin aggregative fimbriae (SERIYTAR) nucleation dependence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salmonella, Escherichia coli and Enrachatement agreament of the production of fimbriae comprising recomprising recompressions.	05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esquence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salmonella, interior and assembly system of strains of Salmonella, interior and coli and	05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
05-APR-1999; 99US-0127888P.  (UTVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esquence which encodes a foreign epitope or antigen. Also describ(1) use of thin aggregative fimbriae (SEFI7/TAF) nucleation depenasembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and ApfA. CscA and AcfA-homologue fimbria subunits, respectively? (2)	05-APR-1999; 99US-012788BP.  (UTVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfa gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign cannot be contined a foreign epitope or antigen. Also describe in assembly system of strains of Salmonella, Escherichia coli and assembly system of Strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recomplication.	05-APR-1999; 99US-0127888P.  (UTVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign English assembly by the encodes a foreign epitope or antigen. Also describe in use of thin aggregative fimbriae (SERIYTAR) nucleation dependence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salmonella, Escherichia coli and Enrarchareae for the production of fimbriae comprising recomprising recompressing recompressing recompressing recompressing recompressing recompressing recompressing recompressing recompressing recompressing recompressing recompressing recompressing recompressions.	05-APR-1999; 99US-0127888P.  (UYVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfa gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfa gene (I) where segment of the gene has been replaced by a segment of a foreign Esquence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salmonella, incleation dependence which aggregative fimbriae (SERI7/TAR) nucleation dependence which aggregative fimbriae (SERI7/TAR) nucleation dependence which aggregative fimbriae (SERI7/TAR) nucleation dependence which aggregative fimbriae coli and assembly system of strains of Salmonella, interesticities and coli and	05-APR-1999; 99US-0127888P. (UTVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
05-APR-2000; 2000WO-CA000356.  05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of this agreement which encodes a foreign epitope or antigen. Also describ(1) use of thin aggregative fimbriae (SERIJ/TAR) nucleation depends assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and AgfA. CscA and AgfA. CscA encodesulvely; (2)	05-APR-2000; 2000WO-CA000356.  (UTVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign E segment of the gene has been replaced by a segment of a foreign E segment of the gene moodes a foreign epitope or antigen. Also describe the use of thin aggregative fimbriae (SEF17/TAF) nucleation depends sembly system of Stains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae congrising reconstraints.	05-APR-1999; 99US-0127888P.  (UYVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (1) where segment of the gene has been replaced by a segment of a foreign sequence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salnonella, Escharichia coll and Enrarchardere for the production of finbriae comprising red	05-APR-2000; 2000WO-CA000356.  05-APR-1999; 99US-0127888P.  (UTVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esquence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salmonella, interiorian and assembly system of strains of Salmonella, interiorian and assembly system of strains of Salmonella, interiorian and strains of Salmonella, interiorian and strains of Salmonella, interiorian and strains of Salmonella, interiorian and strains of Salmonella, interiorian and strains of Salmonella, interiorian	05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
05-APR-2000; 2000WO-CA0000356. 05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of thin aggregative fimbriae (SERI)/TAR) nucleation depends assembly system of strains of Sahmonella, Escherichia coli and assembly system of strains of Sahmonella, Escherichia coli and ApfA. CscA and AcfA. CscA and AcfA. CscA and AcfA. CscA subunits, respectively; (2)	05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UTVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esement of the gene has been replaced by a segment of a foreign Esement of the gene foreign epitope or antigen. Also describe segment of the gene foreign epitope or antigen. Also describe the segment of a foreign esembly system of Stains of Salmonella, Escherichia coli and assembly system of Stains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of finbriae congrising rec	05-APR-2000; 2000WO-CA0000356. 05-APR-1999; 99US-0127888P. (UTVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign sequence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salmonella: Benerichia coli and Enterphaceae for the production of finbriae comprising red	05-APR-2000; 2000WO-CA0000356. 05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esquence which encodes a foreign epitope or antigen. Also describe use thin aggregative fimbriae (SERI) TARRY nucleation depering assembly system of strains of Salmonella, Escherichia recombinations	05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
12-0C:1-2000. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the prodegative fimbriae (SERI)/TARF) nucleation depering use of thin aggregative fimbriae (SERI)/TARF) nucleation depering the computation of timbriae comprising recompandate assembly system of strains of Sahmonella, Escherichia coli and assembly system of strains of fimbriae comprising recompandation and AcfA. CscA and AcfA. CscA and AcfA. CscA and AcfA. CscA subunits, respectively; (2)	05-APR-1090; 2000WO-CA000356. 05-APR-1099; 99US-0127888P. (UTVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PBDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign E segment of the gene has been replaced by a segment of a foreign escence which encodes a foreign epitope or antigen. Also descrift (I) use of thin aggregative fimbriae (SERI7/TAF) nucleation dependence which acceptance finance of Salmonella, Escherichia coli and assembly system of Stains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of financial constitution.	12-0CT-20U0. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White Ab, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant protein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esequence which encodes a foreign epitope or antigen. Also described in use of thin aggregative fimbriae (SEFI)/TAF) nucleation dependence the comprising recomprehence assembly system of strains of Salmonella, Escherichia coll and Enrencharteria case to the norduction of fimbriae comprising recomprehence.	05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the gene has dereign epitope or antigen. Also describe used thin aggregative fimbriae (SERI) TARRY nucleation depering assembly system of strains of Salmonella, Escherichia coli and	12-0CT-2000. 05-APR-2000; 2000WO-CA0000356. 05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
12-OCT-2000. 05-APR-1999; 99US-0127888P. (UTVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign E segment of the gene has been replaced by a segment of a foreign E segment of the green direction epicope or antigen. Also describ (1) use of thin aggregative fimbriae (SEFI)/TARF) nucleation dependance which encodes a foreign epicope or antigen. Also describ (1) use of thin aggregative fimbriae (SEFI)/TARF) nucleation dependance and AcfA-Losa and AcfA-Losa for the production of fimbriae comprising recondant. CacA and AcfA-Losa and AcfA	12-OCT-2000. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White Ab, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA, which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign E segment of the gene has been replaced by a segment of a foreign epitope or antigen. Also describe segment of the gene for the production of Salmonella, Escherichia coli and assembly system of Strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae congrising reconstraints.	12-OCT-2000. 05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UTVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSBB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant protein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esequence which encodes a foreign epitope or antigen. Also describe in use of thin aggregative fimbriae (SEFI)/TAF) nucleation dependence which encodes a foreign epitale (SEFI)/TAF) nucleation dependence which system of strains of Salmonella! Escherichia coll and Enrechance and Enrechance of Almonella Escherichia coll and Enrechance and Enrechance of Almonella Escherichia coll and Enrechance and Enrechance of Almonella Escherichia coll and Enrechance and Enrechance of the Comprising recomparises	12-OCT-2000. 05-APR-1999; 99US-0127888P. (UTVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign E segment of the neodes a foreign epitope or antigen. Also describe used thin aggregative fimbriae (SERI/TARF) nucleation depering assembly system of strains of Salmonella, Escherichia recombinations	12-OCT-2000. 05-APR-2000, 2000WO-CA000356. 05-APR-1999, 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
12-OCT-2000. 05-APR-2000; 2000WO-CA0000356. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White Ab, Doran JL, Collison SK, Kay WW; WPJ; 2000-672631/65. N-PBDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprocein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the produce which encodes a foreign epitope or antigen. Also describ (1) use of thin aggregative fimbriae (SEFI)/TARF) nucleation dependance which encodes a foreign epitope or antigen. Also describ Strains of Strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and aster. CacA and AcfA. CacA challed the production of fimbriae comparising reco	12-OCT-2000. 05-APR-1999; 99US-0127888P. (UTVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign E segment of the gene has been replaced by a segment of a foreign epitope or antigen. Also describe in useful system of strains of Salmonella, Escherichia coli and assembly system of Strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae contribing.	12-OCT-2000. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSBB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antifen, expresses recombinant Aprocessing for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esequence which encodes a foreign epitope or antigen. Also describe in use of thin aggregative fimbriae (SEF17/TAF) nucleation dependence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salmonella! Escherichia coll and Enrencharteria case to the norduction of fimbriae comprising recomprehence.	12-OCT-2000. 05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White Ab, Doran JL, Collison SK, Kay WW; WPJ; 2000-672631/65. N-P8DB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign E segment of the neodes a foreign epitope or antigen. Also describe used thin aggregative fimbriae (SERI) TARY indication deperited assembly system of strains of Salmonella, Escherichia recombinations.	12-OCT-2000. 05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
12-OCT-2000. 05-APR-1999; 99US-0127888P.  (UTVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-P8DB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprocin useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esquence which encodes a foreign epitope or antigen. Also describe use thin aggregative fimbriae (SEF17/TAF) nucleation dependance which angergative fimbriae (SEF17/TAF) nucleation dependance which and strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and Enterpoacteriaecae for the production of fimbriae comprising recondance. CacA and AcfA-homologue fimbrin subunits, respectively; (2)	12-OCT-2000. 05-APR-1999; 99US-012788BP. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant protein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign E segment of the gene has been replaced by a segment of a foreign epitope or antigen. Also describe segment of the gene of strains of Salmonella, Escherichia coli and assembly system of Strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recomplication.	12-OCT-2000. 05-APR-1999; 99US-0127888P. (UTVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign sequence which encodes a foreign epitope or antigen. Also describe thin aggregative fimbriae (SEF17/TAF) nucleation dependence the probaction of stabing reduction of fimbriae comprising reduction assembly system of strains of Salmonella. Escherichia coli and	12-OCT-2000. 05-APR-1999; 99US-0127888P.  (UTVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esquence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salmonella, interior and assembly system of strains of Salmonella, interior coli and	12-OCT-2000. 05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UTVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
12-OCT-2000. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esquence which encodes a foreign epitope or antigen. Also describ use of thin aggregative fimbriae (SERIJ/TAR) nucleation depends sembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and ApfA. CscA and AcfA-homologue fimbrin subunits, respectively; (2)	12-OCT-2000. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant protein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign epitope or antigen. Also describe segment of the gene has been replaced by a segment of a foreign epitope or antigen. Also describe (I) use of thin aggregative fimbriae (SERI7/TAP) mucleation dependancemby system of Strains of Salmonella, Escherichia coli and assembly system of Strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising reco	12-OCT-2000. 05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PBDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Engenence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salmonella! Escherichia coll and Enrichatese for the production of finbriae comprising reachers assembly system of strains of Salmonella! Escherichia coll and	12-OCT-2000. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White Ab, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esquence which encodes a foreign epitope or antigen. Also describ assembly system of strains of Salmonella, interiorient and	12-OCT-2000. 05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
12-OCT-2000. 05-APR-2000; 2000WO-CA0000356. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of thin aggregative fimbriae (SERI)/TAR) nucleation deperations of thin aggregative fimbriae (SERI)/TAR) nucleation deperative contains of Sahmonella, Escherichia coli and assembly system of strains of Sahmonella, Escherichia coli and ApfA. CscA and AcfA. CscA and AcfA. homologue fimbrin subunits, respectively; (2)	12-OCT-2000. 05-APR-2000; 2000WO-CA0000356. 05-APR-1999; 99US-0127888P. (UTVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (1) where segment of the gene has been replaced by a segment of a foreign Esement of the gene has been replaced by a segment of a foreign esement of the gene funding epitope or antigen. Also descrift (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depen assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae constitution.	12-OCT-2000. 05-APR-1999; 99US-0127888P. (UTVI-) UNIV VICTORIA. White Ab, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign epitope or antigen. Also describe sequence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salmonella: Benevichia coli and assembly system of strains of Salmonella: Benevichia coli and Enrachatenese Apriances of the production of finbriae comprising recomprising recompaniance.	12-OCT-2000. 05-APR-2000; 2000WO-CA0000356. 05-APR-1999; 99US-0127888P. (UYUI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esquence which encodes a foreign epitope or antigen. Also describe use thin aggregative fimbriae (SERI) TARRY nucleation depering assembly system of strains of Samonella, interiories coli and	12-OCT-2000. 05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
12-OCT-2000. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the prodegative fimbriae (SERI)/TARF) nucleation deperasembly system of strains of Sahmonella, Escherichia coli and assembly system of strains of Sahmonella, Escherichia coli and ApfA. CscA and AcfA. CscA and AcfA. CscA and AcfA. CscA subunits, respectively; (2)	12-OCT-2000. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI, 2000-672631/65. N-PBDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign E segment of the gene has been replaced by a segment of a foreign epitope or antigen. Also descrift (I) use of thin aggregative fimbriae (SERI/TAFF) nucleation depenasembly system of strains of Salmonella, Escherichia coli and Enerobacteriaceae for the production of fimbriae congrising rec	12-OCT-2000. 05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign epitope or antigen. Also describes assembly system of strains of Salmonella: Becherichia coli and assembly system of strains of Salmonella: Becherichia coli and Enterphacteria case of the production of finbriae comprising recomprising recompaniance.	12-OCT-2000. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the gene has been foreign epitope or antigen. Also describ use of thin aggregative fimbriae (SERI)/TAR) nucleation depering assembly system of strains of Sammonella, interestinia recombinant assembly system of strains of Sammonella, interestinia	12-OCT-2000. 05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
12-OCT-2000. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the anodes a foreign epitope or antigen. Also describ (1) use of thin aggregative fimbriae (SEFI)/TAR) nucleation dependance which encodes a foreign epitope or antigen. Also describ (1) use of thin aggregative fimbriae (SEFI)/TAR) nucleation dependance which and off-the production of fimbriae comprising recondance. Agfa. CscA and AgfA-homologue fimbrin subunits, respectively; (2)	12-OCT-2000. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White Ab, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA, which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esement of the gene has been replaced by a segment of a foreign Esement of the gene has been replaced by a segment of a foreign cannot be segment of the gene (I) where segment of the gene for the gene of thinh aggregative fimbriae (SERI/TAF) nucleation dependence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae constitution, 10, 10, 10, 10, 10, 10, 10, 10, 10, 10	12-OCT-2000. 05-APR-1999; 99US-0127888P. (UTVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672641/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant protein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esequence which encodes a foreign epitope or antigen. Also describe thin aggregative fimbriae (SEFI)/TAR) nucleation dependence which encodes a foreign epitope or antigen. Also describe the assembly system of strains of Salmonella, Escherichia coll and Enrencharteriaceae for the orduration of fimbriae comprising recomprising recomparatements.	12-OCT-2000. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI, 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign (I) use of thin aggregative fimbriae (SERI)/TAR) nucleation depering assembly system of strains of Samonella, Escherichia and	12-OCT-2000. 05-APR-2000, 2000WO-CA000356. 05-APR-1999, 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
12-OCT-2000. 05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White Ab, Doran JL, Collison SK, Kay WW; WPJ; 2000-672631/65. N-PBDB; AAC64628. Recombinant adfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprocein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the gene of critical epitope or antigen. Also describ (1) use of thin aggregative fimbriae (SEFI)/TAR) nucleation dependance which encodes a foreign epitope or finbriae contained assembly system of strains of Salmonella, Escherichia coli and assembly system of the production of fimbriae comprising recondance. Agfa. CseA and Agfa-homologue fimbrian subunits, respectively: (2)	12-OCT-2000. 15-APR-1999, 99US-0127888P. (UTVI-) UNIV VICTORIA. White Ab, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign E segment of the gene has been replaced by a segment of a foreign epitope or antigen. Also describe segment of the gene of strains of Salmanella, Escherichia coli and assembly system of Strains of Salmanella, Escherichia coli and Enterobacteriaceae for the production of fimbriae contribing reconstraints.	12-OCT-2000.  15-APR-1999; 99US-0127888P.  (UYVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign E segment of the gene has been replaced by a segment of a foreign E sequence which encodes a foreign epitope or antigen. Also descrift (1) use of thin aggregative fimbriae (SEFI)/TAF) nucleation dependence when a sesembly system of strains of Salmonella, Escherichia coli and Enrachateria case for the norduction of fimbriae comprising recomprising recompressing recompressions.	12-OCT-2000. 05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White Ab, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-P8DB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign E segment of the neodes a foreign epitope or antigen. Also describe used thin aggregative fimbriae (SERI)/TAR) nucleation depering assembly system of strains of Samonella, Escherichia recoil and collished assembly system of strains of Samonella, Escherichia	MOZOUGSUIOZ-AZ. 12-OCT-2000. 05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UTVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
W02000650102-AZ.  12-OCT-2000. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esement of the gene has been replaced by a segment of a foreign Esement of thin aggregative fimbriae (SERI7/TAF) nucleation dependence which neodes a foreign epitope or antigen. Also describ (1) use of thin aggregative fimbriae (SERI7/TAF) nucleation dependence which and strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and ApfA. CscA and ApfA. CscA and ApfA. CscA and ApfA. Monologue fimbrin subunits, respectively? (2)	W0200060102-A2.  12-OCT-2000. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-6726611/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant protein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign segment of the gene has been replaced by a segment of a foreign epitope or antigen. Also describe segment of the gene of finh aggregative fimbriae (SER17/TAF) nucleation depends assembly system of Stains of Salmonella, Escherichia coli and assembly system of Stains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae contribing.	W02000650102-AZ.  12-OCT-2000.  05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign epitope or antigen. Also describe the ascendance which encodes a foreign epitope or antigen. Also describe the ascendance which encodes a foreign epitope or antigen. Also describe the ascendance of the encodes a foreign epitope or antigen. Also describe the ascendance of the encodes a foreign epitope or antigen. Also describe the ascendance of the encodes a foreign epitope or antigen. Also describe the ascendance of the encodes a foreign epitope or antigen. Also describe the ascendance of the encodes of the enc	W0200060102-AZ.  12-OCT-2000. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfa gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfa gene (I) where segment of the gene has been replaced by a segment of a foreign Esquence which ancodes a foreign epitope or antigen. Also describe use of thin aggregative fimbriae (SERI7/TAR) nucleation depend assembly system of strains of Salmonella.	WO2000661102-A2. 12-OCT-2000. 05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UTVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
W0200065102-A2.  12-OCT-2000.  05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esquence which encodes a foreign epitope or antigen. Also describ segment of this agraegative fimbriae (SERI)/TAR) nucleation deperates thin aggregative fimbriae (SERI)/TAR) nucleation deperates the production of fimbriae comprising recombined assembly system of strains of Salmonella, Escherichia coli and aggree casa and AcfA-homologue fimbriae is subunits, respectively; (2) AcfA. CscA and AcfA-homologue fimbrin subunits, respectively; (2)	W0200065102-A2.  12-OCT-2000.  05-APR-1999; 99US-0127888P.  (UTVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfa gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign cannot encodes a foreign epitope or antigen. Also describe segment of the gene has been replaced by a segment of a foreign epitope or antigen. Also describe segment of the gene of thinh aggregative fimbriae (SERI7/TAF) nucleation dependence which encodes a foreign epitope or antigen. Also describe assembly system of Strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae continent.	W0200065102-A2.  12-OCT-2000.  05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65.  N-P89B; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprocein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign sequence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salnonella, Escherichia coli and Enracharteria case for the production of finbriae comprising reach assembly system of strains of Salnonella, Escherichia coli and Enracharteria case for the production of finbriae comprising reach	W0200065102-A2.  12-OCT-2000.  05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esquence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salmonella.	WO200060102-A2. 12-OCT-2000. 05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
WO200060102-A2.  12-OCT-2000.  05-APR-1999; 99US-0127888P.  (UTVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esquence which encodes a foreign epitope or antigen. Also describ segment of thin aggregative fimbriae (SERI)/TAR) nucleation deperasembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and safe. CsaA and AsfA-homologue fimbriae isomprising reco	WO200060102-A2.  12-OCT-2000.  05-APR-1999; 99US-0127888P.  (UTVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (1) where segment of the gene has been replaced by a segment of a foreign Esement of the gene has been replaced by a segment of a foreign Esement of the gene in animal.  The present invention describes a recombinant agfA gene (1) where segment of the gene foreign epitope or antigen. Also describe segment of the gene foreign epitope or antigen. Also describe segment of the gene of fainting factoriances of fainting and assembly system of Stains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of finbriae comprising recomplished.	WO200060102-A2.  12-OCT-2000.  05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign epitope or antigen. Also describe sequence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salmonella, Escherichia coli and Enrarchardera for the orduration of fimbriae comprising reacher and eace the production of fimbriae comprising reachers.	WO200060102-A2.  12-OCT-2000.  05-APR-1999; 99US-0127888P.  (UTVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the neodes a foreign epitope or antigen. Also describ use of thin aggregative fimbriae (SERI) TYAR; nucleation depering assembly system of strains of Sammonella.	WO200060102-A2. 12-OCT-2000. 05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
WO200060102-A2.  12-OCT-2000.  05-APR-1999; 99US-0127888P.  (UYVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign E segment of the gene has been replaced by a segment of a foreign E segment of the gene has been replaced by a segment of a foreign E segment of the gene docated imprise phone or antigen. Also describ (1) use of thin aggregative fimbriae (SERI)/TAR) nucleation dependance which an of strains of Sahmonella, Escherichia coli and assembly system of strains of Sahmonella, Escherichia coli and ApfA. CscA and AcfA. CscA and AcfA. CscA and AcfA. CscA substitutive, respectively; (2)	WO200060102-A2.  12-OCT-2000. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Approtein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (1) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the gene foreign epitope or antigen. Also descrift (1) use of thin aggregative fimbriae (SETI/TAF) nucleation dependence which encodes a foreign epitope or antigen. Also descrift (1) use of thin aggregative fimbriae comprising reconstraince of the production of fimbriae constraint.	WO200060102-A2.  12-OCT-2000.  05-APR-2000; 2000WO-CA0000356.  05-APR-1999; 99US-0127888P.  (UTVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign epitope or antigen. Also describe sequence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Sahonella: Bscherichia coll and Enterphaceae for the norduction of fimbriae comprising reachers assembly system of strains of Sahonella: Bscherichia coll and Enterphacteria case for the norduction of fimbriae comprising reachers.	WO200060102-A2.  12-OCT-2000. 05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the gene has been foreign epitope or antigen. Also describ assembly system of strains of Salmonella.	WO200060102-A2. 12-OCT-2000. 05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
WOZ00060102-A2.  12-OCT-2000, 05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the produce which anodes a foreign epitope or antigen. Also describ (1) use of thin aggregative fimbriae (SERI)/TAR) nucleation dependance which acceptains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and AgfA. CscA and AgfA. CscA and AgfA. CscA and AgfA. CscA boxologue fimbrin subunits, respectively: (2)	WO200060102-A2.  12-OCT-2000, 05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65.  N-P8DB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (1) where segment of the gene has been replaced by a segment of a foreign E segment of the gene has been replaced by a segment of a foreign segment of the gene full magnetative fimbriae (SER17/TAF) nucleation dependence which encodes a foreign epitope or antigen. Also descrift (1) use of thin aggregative fimbriae comprising recombinating recombinations of fimbriae constitutions.	WO200060102-A2.  12-OCT-2000. 05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign segment of the describe sequence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Sahnonella. Becherichia coli and assembly system of strains of Sahnonella. Becherichia coli and Enterchareae for the norduction of finbriae comprising recomprehences.	WO200060102-A2.  12-OCT-2000, 05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the gene has been foreign epitope or antigen. Also describe assembly system of strains of Salmonella.	WO200060102-A2. 12-OCT-2000. 05-APR-1099; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
WOZ00060102-A2.  12-OCT-2000. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI, 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the gene fareign epitope or antigen. Also describ (1) use of thin aggregative fimbriae (SEFI)/TAR) nucleation dependance which encodes a foreign epitope or antigen. Also describ (1) use of thin aggregative fimbriae (SEFI)/TAR) nucleation dependance and AcfA-homologue fimbriae is fimbriae comprising reco	WOZOU060102-A2.  12-OCT-2000. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White Ab, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (1) where segment of the gene has been replaced by a segment of a foreign E segment of the gene has been replaced by a segment of a foreign computation describes a foreign epitope or antigen. Also descrift (1) use of thin aggregative fimbriae (SERI7/TAF) nucleation dependence which encodes a foreign epitope or antigen. Also descrift (1) use of thin aggregative fimbriae comprising recomputations of fimbriae comprising recombinations.	WO200060102-A2.  12-OCT-2000. 05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprocess In an animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esequence which encodes a foreign epitope or antigen. Also describe sequence which encodes a foreign epitope or antigen. Also describe in use of thin aggregative fimbriae (SEFI)/TAR) nucleation dependence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salmonella, Escherichia coll and Enracharteria ease for the norduction of fimbriae comprising recomprising recomprising recomprising recomprising recomparises.	WO200060102-A2.  12-OCT-2000. 05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprocein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the gene has been foreign epitope or antigen. Also describe used thin aggregative fimbriae (SERI)/TAR) nucleation dependance which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salmonella.	WO200060102-A2. 12-OCT-2000. 05-APR-2000, 2000WO-CA000356. 05-APR-1999, 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
WO200060102-A2.  12-OCT-2000. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the gene foreign epitope or antigen. Also describ (1) use of thin aggregative fimbriae (SEFI)/TAR) nucleation dependance which encodes a foreign epitope or antigen. Also describ (1) use of thin aggregative fimbriae (SEFI)/TAR) nucleation dependance and AcfA-homologue fimbriae insubmitts, respectively; (2) AcfA. CscA and AcfA-homologue fimbrin submitts, respectively; (2)	WO200060102-A2.  12-OCT-2000. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White Ab, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (1) where segment of the gene has been replaced by a segment of a foreign E segment of the gene has been replaced by a segment of a foreign epitope or antigen. Also describe segment of the gene of Stains of Stains of Stains of Stains of Stains of Stains of Stains of Stains contains assembly system of Stains of Stains contains and Enterobacteriaceae for the production of fimbriae comprising recontains.	WO200060102-A2.  12-OCT-2000.  05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprocessing immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esequence which encodes a foreign epitope or antigen. Also describe segment met agranged by a segment of a foreign Esequence which encodes a foreign epitope or antigen. Also describe thin aggregative fimbriae (SEFI)/TAF) nucleation dependence the strain of Strains of Salmonella, Escherichia coli and Enrachateria rease for the norduction of fimbriae comprising recomprising recompressing recompressing recompressing recompressing recompressing recompressing recompressing recompressing recompressing recompressing recompressing recompressing recompressing recompressing recompressions of the propagation of finibriae comprising recompressions and an expensive the present in the present in the present in the present invention of the present in the present invention of the present in the present in the present invention of the present in the present	WO200060102-A2.  12-OCT-2000. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the neodes a foreign epitope or antigen. Also describe use of thin aggregative fimbriae (SERI)/TAR) nucleation deperation assembly system of strains of Salmonella.	WO200060102-A2. 12-OCT-2000. 05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
WO200060102-A2.  12-OCT-2000. 05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White Ab, Doran JL, Collison SK, Kay WW; WPJ; 2000-672631/65. N-P8DB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DWA which encodes foreign epitope or antigen, expresses recombinant Approtein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the produce which encodes a foreign epitope or antigen. Also describ (1) use of thin aggregative fimbriae (SEFI)/TAR) nucleation dependance which encodes a foreign epitope or antigen. Also describ AgfA. CscA and AgfA-homologue fimbriae comprising reco	WO200060102-A2.  12-OCT-2000.  05-APR-1999, 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign E segment of the gene has been replaced by a segment of a foreign epitope or antigen. Also describe segment of the gene of Stains of Salmbriae Complising recomplacteriaceae for the production of fimbriae comprising recomplacteriaceae for the production of fimbriae comprising recomplacements.	WO200060102-A2.  12-OCT-2000.  05-APR-1999; 99US-0127888P.  (UYVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esequence which encodes a foreign epitope or antigen. Also describe thin aggregative fimbriae (SERIYTAR) nucleation dependence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salmonella, Escherichia coll and Enrachatement agreated the production of fimbriae comprising recomprising recomprising recomprising recompresses.	WO200060102-A2.  12-OCT-2000. 05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White Ab, Doran JL, Collison SK, Kay WW; WPJ; 2000-672631/65. N-P8DB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprocein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the neodes a foreign epitope or antigen. Also describe use which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salmonella.	WO200060102-A2. 12-OCT-2000. 05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
W0200060102-A2.  12-OCT-2000.  05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfa gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfa gene (I) where segment of the gene has been replaced by a segment of a foreign Esement of the gene has been replaced by a segment of a foreign esement of thin aggregative fimbriae (SERI7/TAF) nucleation dependance which neodes a foreign epitope or antigen. Also describ(1) use of thin aggregative fimbriae (SERI7/TAF) nucleation dependance which aggregative fimbriae (SERI7/TAF) respectively recombinant Apfa. CseA and Agfa-homologue fimbria subunits, respectively; (2)	W0200060102-A2.  12-OCT-2000.  05-APR-1999, 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign cannot encodes a foreign epitope or antigen. Also describe segment of the gene has been replaced by a segment of a foreign epitope or antigen. Also describe segment of the gene of fariance of Salmanonla, Escherichia coll and assembly system of Strains of Salmanonla, Escherichia coll and Enterobacteriaceae for the production of fimbriae comprising reconstricting to the production of fimbriae contribution.	W0200060102-A2.  12-OCT-2000.  05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprocessing protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign English of the gene has been replaced by a segment of a foreign Esequence which encodes a foreign epitope or antigen. Also describe the assembly system of strains of Salmonella, Escherichia coli and Enrachatement for the production of finbriae comprising recomprising recompressions.	W0200060102-A2.  12-OCT-2000. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfa gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfa gene (I) where segment of the gene has been replaced by a segment of a foreign Esquence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salmonella, Escherichia recombination dependence which aggregative fimbriae (SERI7/TAR) nucleation dependence which aggregative fimbriae (SERI7/TAR) nucleation dependence which aggregative fimbriae (SERI7/TAR) nucleation dependence which aggregative fimbriae (SERI7/TAR) nucleation dependence which aggregative fimbriae (SERI7/TAR) nucleation dependence which aggregative fimbriae coli and aggregative fimbriae coli and aggregative fimbriae coli and aggregative fimbriae coli and aggregative fimbriae coli and aggregative fimbriae coli and aggregative fimbriae coli and aggregative fimbriae coli and aggregative fimbriae coli and aggregative fimbriae coli and aggregative fimbriae coli and aggregative fimbriae coli and aggregative fimbriae coli and aggregative fimbriae coli and aggregative coli and aggregative fimbriae coli and ag	W0200060102-A2. 12-OCT-2000. 05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UTVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
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WO200060102-A2.  12-OCT-2000. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of this agreement of the moodes a foreign epitope or antigen. Also describ (1) use of thin aggregative fimbriae (SERIJ/TAR) nucleation depends assembly system of strains of Salmonella, Escherichia coli and AgfA. CscA and AgfA. CscA and AgfA. CscA and AgfA. CscA and Scherichia subunits, respectively; (2)	WO200060102-A2.  12-OCT-2000.  05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprocin useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign cannot encodes a foreign epitope or antigen. Also describe segment of the gene has been replaced by a segment of a foreign epitope or antigen. Also describe segment of the gene of faring epitope or antigen. Also describe segment of the gene of faring epitope or antigen. Also describe segmently system of Stains of Salmonella, Escherichia coli and assembly system of Stains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of finbriae contribing.	WO200060102-A2.  12-OCT-2000.  05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-P8DB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Apropriate; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign English.  The present invention describes a recombinant agfA gene (I) where segmence which encodes a foreign epitope or antigen. Also describe sequence which encodes a foreign epitope or antigen. Also describe in use of thin aggregative fimbriae (SERI/TAR) nucleation dependence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Sanhonella, Escherichia coli and Enracharteria ease for the production of fimbriae comprising recomprising recompanies.	WO200060102-A2.  12-OCT-2000. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White Ab, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esquence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salmonella, Escherichia recombination dependent assembly system of strains of Salmonella, interior coli and	Synchetic. W0200060102-A2. 12-OCT-2000. 05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
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WO200060102-A2.  12-OCT-2000.  05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65.  N-PSDB; AAC64628  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of thin aggregative fimbriae (SEFI7/TAF) nucleation dependence which necodes a foreign epitope or antigen. Also describ(1) use of thin aggregative fimbriae (SEFI7/TAF) nucleation dependence which aggregative fimbriae (SEFI7/TAF) nucleation dependence which aggregative fimbriae (SEFI7/TAF) respectively: (2) and AgfA. CseA and AgfA-homologue fimbrian subunits, respectively: (3)	WO200060102-A2.  12-OCT-2000. 05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant protein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign cannot be segment of a foreign epitope or antigen. Also describe segment of the gene has been replaced by a segment of a foreign epitope or antigen. Also describe segment of the gene of farina epitope or antigen. Also describe segment of the gene of farina epitope or antigen. Also describe segmently system of Stains of Salmonella, Escherichia coli and assembly system of Stains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of finbriae comprising reconstricting the production of finbriae contribution.	WO200060102-A2.  12-OCT-2000. 05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprocessing to the present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign English of the gene has been replaced by a segment of a foreign English of the sequence which encodes a foreign epitope or antigen. Also describe the assembly system of strains of Salmonella, Escherichia coli and Enracharteria case for the production of finbriae comprising recomprising recomprising recompanies.	WO200060102-A2.  12-OCT-2000. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esquence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salmonella, Escherichia recombination dependent assembly system of strains of Salmonella, interior coli and c	MO2000661102-A2. 12-OCT-2000. 05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UTVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
W0200060102-A2.  12-OCT-2000.  05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfa gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfa gene (I) where segment of the gene has been replaced by a segment of a foreign Esement of the gene has been replaced by a segment of a foreign esement of thin aggregative fimbriae (SERI7/TAF) nucleation dependance which neodes a foreign epitope or antigen. Also describ(1) use of thin aggregative fimbriae (SERI7/TAF) nucleation dependance which aggregative fimbriae (SERI7/TAF) respectively recombinant Apfa. CseA and Agfa-homologue fimbria subunits, respectively; (2)	W0200060102-A2.  12-OCT-2000.  05-APR-1999, 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign cannot encodes a foreign epitope or antigen. Also describe segment of the gene has been replaced by a segment of a foreign epitope or antigen. Also describe segment of the gene of fariance of Salmanonla, Escherichia coll and assembly system of Strains of Salmanonla, Escherichia coll and Enterobacteriaceae for the production of fimbriae comprising reconstricting to the production of fimbriae contribution.	W0200060102-A2.  12-OCT-2000.  05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprocessing protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign English of the gene has been replaced by a segment of a foreign Esequence which encodes a foreign epitope or antigen. Also describe the assembly system of strains of Salmonella, Escherichia coli and Enrachatement for the production of finbriae comprising recomprising recompressions.	W0200060102-A2.  12-OCT-2000. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfa gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfa gene (I) where segment of the gene has been replaced by a segment of a foreign Esquence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salmonella, Escherichia recombination dependence which aggregative fimbriae (SERI7/TAR) nucleation dependence which aggregative fimbriae (SERI7/TAR) nucleation dependence which aggregative fimbriae (SERI7/TAR) nucleation dependence which aggregative fimbriae (SERI7/TAR) nucleation dependence which aggregative fimbriae (SERI7/TAR) nucleation dependence which aggregative fimbriae coli and aggregative fimbriae coli and aggregative fimbriae coli and aggregative fimbriae coli and aggregative fimbriae coli and aggregative fimbriae coli and aggregative fimbriae coli and aggregative fimbriae coli and aggregative fimbriae coli and aggregative fimbriae coli and aggregative fimbriae coli and aggregative fimbriae coli and aggregative fimbriae coli and aggregative fimbriae coli and aggregative coli and aggregative fimbriae coli and ag	W0200060102-A2. 12-OCT-2000. 05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UTVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
W0200060102-A2.  12-OCT-2000.  05-APR-2000; 2000WO-CA0000356.  05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White Ab, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-P8DB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DWA which encodes foreign epitope or antigen, expresses recombinant Approtein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the production of the production of finbriae contains assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and aster. CacA and AcfA-homologue finbrin subunits, respectively; (2)	WO200060102-A2.  12-OCT-2000.  05-APR-1999, 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign E segment of the gene has been replaced by a segment of a foreign epitope or antigen. Also describe segment of the gene of strains of sample of Salmbriae Conprising recombinate conpacteriaceae for the production of fimbriae comprising recombinations.	W0200060102-A2.  12-OCT-2000.  05-APR-1999; 99US-0127888P.  (UYVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esequence which encodes a foreign epitope or antigen. Also describe thin aggregative fimbriae (SERIYTAR) nucleation dependence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salmonella, Escherichia coli and Enrachateria rease for the production of fimbriae comprising reachers.	W2200060102-A2.  12-OCT-2000.  05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign emplope or antigen, expresses recombinant Aprocessin useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esement of the gene has been replaced by a segment of a foreign assembly system of strains of Salmonella, inscherichia recombination dependence which aggregative fimbriae (SERI7/TAR) nucleation dependence which aggregative fimbriae (SERI7/TAR) nucleation dependence which aggregative fimbriae (SERI7/TAR) nucleation dependence which aggregative fimbriae (SERI7/TAR) nucleation dependence which aggregative fimbriae (SERI7/TAR) nucleation dependence which aggregative fimbriae coli and aggregative fimb	WO200060102-A2. 12-OCT-2000. 05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
WO200060102-A2.  12-OCT-2000. 05-APR-1099; 99US-0127888P. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-P8DB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprocein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the gene foreign epitope or antigen. Also describ (1) use of thin aggregative fimbriae (SEFI)/TAR) nucleation dependance which encodes a foreign epitope or antigen. Also describ (1) use of thin aggregative fimbriae (SEFI)/TAR) nucleation dependance and AcfA-homologue fimbriae insubmitts, respectively; (2) AcfA. CscA and AcfA-homologue fimbrin submitts, respectively; (2)	WO200060102-A2.  12-OCT-2000. 05-APR-1999, 99US-0127888P. (UTVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign E segment of the gene has been replaced by a segment of a foreign epitope or antigen. Also describe segment of the gene of Stains of Salmbriae Compliand assembly system of Stains of Salmbriae comprising recomplacteriaceae for the production of fimbriae comprising recomplication of fimbriae comprising recompliants.	WO200060102-A2.  12-OCT-2000.  05-APR-1999; 99US-0127888P.  (UYVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW;  WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esequence which encodes a foreign epitope or antigen. Also describe thin aggregative fimbriae (SEFI)/TAR) nucleation dependence which encodes a foreign epitope or antigen. Also describe assembly system of strains of Salmonella, Escherichia coll and Enrachateria rease for the production of fimbriae comprising reachers.	WO200060102-A2.  12-OCT-2000. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the neodes a foreign epitope or antigen. Also describe use of thin aggregative fimbriae (SERI)/TAR) nucleation deperation assembly system of strains of Salmonella.	WO200060102-A2. 12-OCT-2000. 05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
WO200060102-A2.  12-OCT-2000. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the gene foreign epitope or antigen. Also describ (1) use of thin aggregative fimbriae (SEFI)/TAR) nucleation dependance which encodes a foreign epitope or antigen. Also describ (1) use of thin aggregative fimbriae (SEFI)/TAR) nucleation dependance and AcfA-homologue fimbriae insubmitts, respectively; (2) AcfA. CscA and AcfA-homologue fimbrin submitts, respectively; (2)	WO200060102-A2.  12-OCT-2000. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White Ab, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant A protein useful for eliciting immune response in animal.  Disclosure; Page 138; 139pp; English.  The present invention describes a recombinant agfA gene (1) where segment of the gene has been replaced by a segment of a foreign E segment of the gene has been replaced by a segment of a foreign epitope or antigen. Also describe segment of the gene of Stains of Stains of Stains of Stains of Stains of Stains of Stains of Stains contains assembly system of Stains of Stains contains and and assembly system of Stains of Stains contains and the production of finbriae comprising recontains assembly system of Stains of	WO200060102-A2.  12-OCT-2000.  05-APR-1999; 99US-0127888P.  (UVVI-) UNIV VICTORIA.  White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65.  N-PSDB; AAC64628.  Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aproperties or antigen, expresses recombinant Aproperties or antigen, expresses recombinant Aproperties or antigen, expresses recombinant Aproperties or antigen, expresses recombinant Aproperties page 138; 139pp; English.  The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esequence which encodes a foreign epitope or antigen. Also describe the assembly system of strains of Salmonella, Escherichia coll and Enrachateria rease for the production of finbriae comprising recomprising recomprising rease.	WO200060102-A2.  12-OCT-2000. 05-APR-1999; 99US-0127888P. (UVVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK, Kay WW; WPI; 2000-672631/65. N-PSDB; AAC64628. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant Aprotein useful for eliciting immune response in animal. Disclosure; Page 138; 139pp; English. The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign Esegment of the gene has been replaced by a segment of a foreign Esegment of the neodes a foreign epitope or antigen. Also describe use of thin aggregative fimbriae (SERI)/TAR) nucleation deperation assembly system of strains of Salmonella.	WO200060102-A2. 12-OCT-2000. 05-APR-2000; 2000WO-CA000356. 05-APR-1999; 99US-0127888P. (UYVI-) UNIV VICTORIA. White AP, Doran JL, Collison SK,
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comprising separating an amino acid polymer comprising a recombinant Agfa protein containing a replacement segment or segments of foreign amino acid sequence in containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or the containing a replacement segment on a Salmonella, E. coli or the contained for the north of the contained in the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the contained of the present family in the present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%;
Matches 151; Conservative 0.
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                                                                                                                                                                                                                                                                                     Sequence 151 AA;
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The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA segment of thin aggregative finbriae (SEP17/TAR) incleation depended assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and antercobacteriaceae for the production of fimbriae comprising recombinant GT AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively, (2) directing recombinant gene into the chromosome of the homologous species, replacing the native comprising separating a recombinant and minmal, we comprising separating an amino acid polymer response in an animal, comprising separating an amino acid polymer comprising a recombinant and introducing the protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, B. coli or acid sequence or sequences grown on a Salmonella, B. coli or acid sequence host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or dilutent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for a useful contains the inserted epitops, and hybrid fimbrine are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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Pred. No. 1.8e-62;
0; Mismatches 0; Indels
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ilarity 91.1%;
Conservative
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Best Local Similarity
Matches 144; Conserv
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AAB36355
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(UYVI-) UNIV VICTORIA.

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Salmonella; AgfA; vaccine.
                                                                                                                                             Query Match
Best Local Similarity 89.9
Matches 143; Conservative
         WPI; 2000-672631/65.
                                                                                                                                       Sequence 151 AA;
             N-PSDB; AAC64631
                                                                                                                                                                                                                                        AgfA sequence.
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26-JUN-1995
                                                                                                                                                                                                                                                      Salmonella
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   White AP,
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SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Salmonella AgfA protein and DNA are used in vaccine and genetic immunization compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
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Pred. No. 4.1e-60;
                                                                                                                                                                                                                                                                                                                                                                                          Doran JL;
                                                                                                                                                                                                                                                                                  VICTORIA INNOVATION & DEV CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 7B; 95pp; English.
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Best Local Similarity 91.4
Matches 138; Conservative
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                                                                 10-NOV-1994.
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                                                                                                                                                                                                                                                                                  (UYVI-)
(KING/)
                                                                                                                                                                                                                                                                                                                                                                                              Kay WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA control bencodes a foreign epicope or antigen. Also described are: (1) use of thin aggregative finbried (SPET)/TAP) nucleation depended assembly system of strains of Salmonella, Escherichia coli and control system of strains of Salmonella, Escherichia coli and control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control control c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---YDQLVTRVVT 112
                                                                                                                                                                                                                Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 700; DB 3; Length 151;
Pred. No. 4.2e-61;
0; Mismatches 0; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNAT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 HEMAHAGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                          Kay WW;
                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 139; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR74625 standard; protein; 151 AA
                                          Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.3%;
89.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
                                              Doran JL,
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Kay WW;

Collison SK,

Doran JL,

White AP,

WPI; 2000-672631/65

(UYVI-) UNIV VICTORIA

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are:

(I) use of thin aggregative fimbriae (SEP1/TAR) nucleation depended assembly system of strains of Salmonella Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant of directing recombinant by the combination of a recombinant gene are the chromosome of the homologous species, respectively; (2) directing recombinant gene accombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal. Copy of that gene; and (4) eliciting an immune response in an animal protein containing a replacement segment or segments of foreign amino and segment or segments of foreign amino and segment or segments of foreign amino and sequence or sequences grown on a Salmonella, B. coli or Enterobacteriaceae host cell, from the host cell and inroducing the polymer into the animal in conjunction with a carrier or diluter. (I) is useful for the expensesion of recombinant AgfA protein which is useful for useful for the expense in an animal. In a finitial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copples/cell), the hybrid fimbrin protein possesses both the immunogens, which may be important for directing an immune response in municed epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                    Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGUHHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.0%; Score 690; DB 3;
llarity 91.4%; Pred. No. 4.1e-60;
Conservative 2; Mismatches 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                              Disclosure; Page 135; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 138; Conserv
  N-PSDB; AAC64617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 27655-3b. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic 25-MAR-2003 to correct PF field.)

Sequence 151 AA;

Isolated Salmonella gene agfA - used for diagnosis of Salmonella or enteropathogenic bacteria of the Enterobacteria family.

Example 2; Fig 7; 85pp; English.

(UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.

Kay WW,

Collinson SK,

WPI; 1997-309886/28. N-PSDB; AAT74142.

94US-00233788 93US-00054452

26-APR-1994; 26-APR-1993;

US5635617-A. 03-JUN-1997

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                                                                                                                                 61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                            SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
                                                                                  60
                                                       1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                          1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                          Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
  Length 151;
                           Indels
88.9%; Score 689; DB 2;
llarity 91.4%; Pred. No. 5.2e-60;
Conservative 2; Mismatches 11
                                                                                                                                                                                                                                                                                                                                               AgfA::PT3#1 amino acid sequence SEQ ID NO:12.
                                                                                                                                                                  121 HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                             151
                                                                                                                                                                                          121 NNPALVNOTASDSSVMVRQVGFGNNATANOY
                                                                                                                                                                                                                                                                                                                                                                                       vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                               AAB36346 standard; protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-APR-2000; 2000WO-CA000356.
                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella enteritidis.
             Local Similarity
ses 138; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                Sscherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200060102-A2.
                                                                                                                                                                                                                                                                                                                     26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                           AAB36346;
  Query Match
                 Best Loca
Matches
                                                                                                                                                                                                                                      RESULT 7
                                                                                                                                                                                                                                                  AAB36346
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Enteropathogenic bacteria, enterobacteria, S.enteritidis, antibody.

Salmonella enteritidis 27655-3b agfA.

(revised)
(first entry)

25-MAR-2003 29-SEP-1997 AAW23570;

AAW23570 standard; protein; 151 AA

AAW23570

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В

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유 à /note= "Encoded by GCC"

Location/Qualifiers

Misc-difference

Salmonella enteritidis

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA cases a foreign epicope or antigen. Also described are: (1) use of thin aggregative finbriae (SPENJ/TAP) nucleation depended assembly system of strains of Salmonella, Escherichia coli and cassembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and correct of the production of finbriae comprising recombinant of directing recombination of a recombination of a recombinant gene into the chromosome of the homologous species, (3) directing recombination of a recombinant gene comprising separating an amino acid polymer comprising a recombinant pact of the homologous species, replacing the native comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or seful for the expression of recombinant and introducing the carrier for system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response conservable in a manner and epicope, and hybrid fimbriae are easy and given in expensive to purify in large amount. The present sequence is given in the exemplificatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAK------ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                         Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 655, DB 3; Length 151;
Pred. No. 1.2e-56;
0; Mismatches 0; Indels 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----NYDQLVIRVVIHEMAHANQIASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 NNAALVNYDQLVTRVVTHEMAHA--------NNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AgfA::PT3#8 amino acid sequence SEQ ID NO:26.
                                                                                                        Collison SK, Kay WW;
                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 135; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.5%;
79.8%;
99US-0127888P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 134; Conservative
                                                    (UYVI-) UNIV VICTORIA.
                                                                                                        White AP, Doran JL,
                                                                                                                                                         WPI; 2000-672631/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                  N-PSDB; AAC64622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-2001
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA comparison encoded assembly system of strains of Salmonella. Bischerichia coli and assembly system of strains of Salmonella. Escherichia coli and context of the production of fimbriae comprising recombinant of a recombination of a recombinant gene into the chromosome of the compositions recombination of a recombinant gene composition services and (4) aliciting an immune response in an animal. Composition generates and (4) eliciting an immune response in an animal. Composition sequence or sequences grown on a salmonella, E coli or acid sequence or sequences grown on a Salmonella, E coli or acid sequence or sequences grown on a Salmonella, E coli or acid sequence or sequences grown on a Salmonella, E coli or acid sequence or sequences grown on a Salmonella, E coli or acid sequence or sequences grown on a Salmonella, E coli or acid sequence or sequences grown on a Salmonella, E coli or acid sequence or sequences grown on a Salmonella, E coli or acid sequence or sequences grown on a Salmonella, E coli or acid sequence or sequences grown on a Salmonella, E coli or acid sequence or sequence in an animal. In a fimbrial presentation containing an aminon acid polymer cell and introducing the carrier frabrial submit protein possesses both the corresponse the heterologous antigens are presented in high numbers (up to vaccine, the carrier fimbrial submit proteins are usually strong immunogens, which may be important for an efficient live vaccine, the carrier fimbrial submit proteins are easy and manner of inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                 Kay ww;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 138; 139pp; English.
                                                                                                                                                                                                                                                                                                                               Collison SK,
                                                                                                                                                                                               05-APR-2000; 2000WO-CA000356.
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                     Salmonella enteritidis.
                                                                                                                                                                                                                                                                                    (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                 Doran JL,
                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-672631/65.
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                                        Escherichia coli
                                                                                                          WO200060102-A2
                                                                                                                                                                                                                                            05-APR-1999;
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                                                                                                                                                     12-OCT-2000
                                                                                                                                                                                                                                                                                                                                 White AP,
                                                             Synthetic.
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Gaps

151

121

vaccine; immune response; immunogen.

The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA comparison that control is sequence which encodes a foreign epicope or antigen. Also described are: (1) use of thin aggregative finbries (SET)/TAE) nucleation depended assembly system of strains of Salmonella. Escherichia coli and control is the production of fimbriae comprising recombinant of a recombinant gene into the chromosome of the directing recombination of a recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the colymer into the animal in conjunction with a carrier of diluter. (1) is cuseful for the expression of recombinant AgfA protein mind to useful for the expression of recombinant AgfA protein mind to useful for system the heerologous antigens are presented in high numbers (useful for the expression of recombinant AgfA protein possesses both the immune the harbrid fimbrial subunit protein possesses both the immuneration which may be immortant for an immuneration which an immuneration which may be immortant for an immuneration an immuneration an immuneration an immuneration an immuneration an immuneration an immuneration an immuneration an immuneration an immuneration an immuneration an immuneration an immuneration and adhesion properties relevant for an immuneration and immineration immineration immineration immineration immineration immineration immineration im Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal. against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention directing an immune response Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; Length 151; AgfA::PT3#6 amino acid sequence SEQ ID NO:22. Kay WW; immunogens, which may be important for Disclosure; Page 137; 139pp; English. vaccine; immune response; immunogen. AAB36351 standard; protein; 151 AA Collison SK, 05-APR-2000; 2000WO-CA000356 99US-0127888P 26-FEB-2001 (first entry) Salmonella enteritidis. (UYVI-) UNIV VICTORIA. Doran JL, WPI; 2000-672631/65. Escherichia coli. Synthetic. N-PSDB; AAC64627 Sequence 151 AA; WO200060102-A2. 05-APR-1999; 12-OCT-2000 White AP, AAB36351; 

Query Match
78.6%; Score 609; DB 3; Length 151;
Best Local Similarity 73.6%; Pred. No. 4.2e-52;
Matches 128; Conservative 0; Mismatches 0; Indels 46; Gaps 2;

1 WKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSGPDSTLSIYQYGSANAALALQ 60

8 8

MKLLKVAAFAAIVVSGSALAGVVPQWGGGGGININGGGNSSGPDSTLSIYQYGSANAALALQ 60

The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA segment which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative finbriae (SEPI)/TAPP) mucleation depended assembly system of strains of Salmonella, Escherichia coli and therefore the production of fimbriae comprising recombinant of the production of fimbriae comprising recombinant of directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid polymer comprising a replacement segment or segments of foreign amino acid polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a finbrial presentation system the heterologous antigens are presented in high numbers (up to sourcine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immunogens, which may be important for directing an immunogens, against the inserted epitope, and public fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal. 61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120 -----NYDQLVTRVVT 97 98 HEMAHADQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151 Salmonella, agfA, chromosomal gene replacement, fimbrin, epitope, vaccine, immune response, immunogen. -NOTASDSSVMVRQVGFGNNATANOY AgfA::PT3#4 amino acid sequence SEQ ID NO:18. 3 Kay 61 SDARKSETTITQSGYGNGADVGQGAD-Disclosure; Page 136; 139pp; English AAB36349 standard; protein; 151 AA Collison SK, 05-APR-2000; 2000WO-CA000356. 99US-0127888P (first entry) Salmonella enteritidis. Escherichia coli. (UYVI-) UNIV VICTORIA, White AP, Doran JL, WPI; 2000-672631/65. N-PSDB; AAC64625. 121 HEMAHA-W0200060102-A2. 05-APR-1999; 26-FEB-2001 12-OCT-2000 Synthetic. AAB36349; RESULT 10 AAB36349 d ö g 

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2000-672631/65
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N-PSDB; AAC64630
                                                                                                                                                             Sequence 151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                         Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen.
                                                                         .;
                                                 Length 151;
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                                                                         22;
                                                 Score 608; DB 3;
Pred. No. 5.2e-52;
5; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                    AgfA::PT3#5 amino acid sequence SEQ ID NO:20.
 of the present invention
                                                                                                                                                                                                     121 HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kay WW;
                                                                                                                                                                                                                      NNAALVNOTASDSSVMVRQVGFGNNATANQY
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                                                                                                                                                                                                                                                                                           AAB36350 standard; protein; 151 AA
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                                                 / Match
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les 124; Conservative
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N-PSDB; AAC64626.
the exemplification
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Escherichia coli
                          Sequence 151 AA;
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) useful for the expression of recombinant AgfA protein which is useful eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 606, DB 3; Length 15
Pred. No. 8.2e-52;
5; Mismatches 22; Indels
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cc assembly system of strains of Salmonella, Bscherichia coli and Enterobacteriaceae for the production of finbriae comprising recombinant of Enterobacteriaceae for the production of finbriae comprising recombinant composed and Agfa-homologue finbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologue species, replacing the enteropous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologue species, replacing the native comprising separating an amino acid polymer comprising a recombinant Agfa protein containing a replacement segment or segments of foreign amino comprising separating a replacement segment or segments of foreign amino cord sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant Agfa protein which is useful for celliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to copies/cell), the hybrid fimbrin protein see usually strong communogens, which may be important for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response dimensors to purify in large amount. The present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 600; DB 3;
Pred. No. 3.2e-51;
3; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AgfA::PT3#3 amino acid sequence SEQ ID NO:16.
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Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-672631/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200060102-A2.
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AAB36348
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA control of the encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SPEPA/TAP) mucleation depended assembly system of strains of Salmonella. Bscherichia coli and control of the strains of Salmonella bscherichia coli and depended assembly system of strains of Salmonella. Bscherichia coli and dependent of a recombination of a recombination of a recombinant gene into the chromosome of the homologous species, 'replacing the native copy of that gene; and (4) eliciting an immune response in an animal, copy of that gene; and (4) eliciting an immune response in an animal, protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences in an animal in a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which and adhesion properties relevant for an efficient live vaccine, the carrier finbrial subunit proteins are easy and immunogens, which may be important for directing an immune response in manimal invention of the present invention in s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                            Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli CsgA amino acid sequence SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74.2%; Score 575; DB 3;
llarity 81.5%; Pred. No. 9.5e-49;
Conservative 5; Mismatches 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 NNAALVNOTASDSSVMVRQVGFGNNATANQY
                                                                                                                                               Page 136; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine; immune response; immunogen.
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N-PSDB; AAC64624.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 151 AA;
                                                                                                                                               Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Simi
hes 123;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative finbried (SERIATAR) nucleation depended assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and acceptatore of the production of finbriad congrafaty recombinant of AgfA. CsgA and AgfA-homologue finbrin subunits, respectively; (2) directing recombination of a recombinant gene comprising seperation of a recombinant gene into the chromosome of the homologous species, replacing the native back into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or seconominant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for system the hererologous antigens and animal. In a fimbrial presentation system the hererologous antigens are presented in high numbers (up to solo, 00 copies/cell), the hybrid fimbrin protein sere usually strong immunogens, which may be important for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                               Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                Kay WW;
                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 135; 139pp; English.
                                                                                                                                              Collison SK,
05-APR-2000; 2000WO-CA000356.
                                               99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 70.2
Matches 106; Conservative
                                                                                                 (UYVI-) UNIV VICTORIA
                                                                                                                                                Doran JL,
                                                                                                                                                                                                WPI; 2000-672631/65.
                                                                                                                                                                                                                        N-PSDB; AAC64619.
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                                               05-APR-1999;
                                                                                                                                                White AP,
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                                                                                                 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGHHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
Gaps
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                                                                                                                                                          121 HEMAHANQTASDSSVMVRQVGFGNNATANQY
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Search completed: August

Job time : 44.9 secs

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E. coli CsgA subunit 15 kDa protein
                 Ä
                 ABR82651 standard; protein; 151
                                                  (first entry)
                                                  04-DEC-2003
                                 ABR82651;
RESULT 15
         ABR8265
                 SEXEXEX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated peptide capable of binding a mammalian plasma protein, useful in the manufacture of a medicament for the prevention and/or treatment of a bacterial infection, such as Escherichia coli, Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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Plasma protein; immune response; antibacterial; vaccine; gene therapy
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69.5%; Pred. No. 4.2e-44;
ive 18; Mismatches 28;
                                                                                                                                                                                                                                               Herwald H;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 41-42; 42pp; English
                                                                                                                                                                                                                                                 Wikstroem M,
                                                                                                                                            30-JAN-2003; 2003WO-EP000943.
                                                                                                                                                                               31-JAN-2002; 2002GB-00002275
                                                                                                                                                                                                                (HANS-) HANSA MEDICAL RES AB
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                                                                                                                                                                                                                                                                                                                                                                                       Shigella infections.
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                                        Escherichia coli
                                                                         WO2003064446-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 105;
                                                                                                          07-AUG-2003
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Appl Appli

Sequence (

Sequence 4 Sequence 7 Sequence 7 Sequence 3

ALIGNMENTS

73, Apj 5005,

Sequence Seq

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MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Doran, James L.
APPLICANT: Kay, William W.
APPLICANT: Callinson, Karen S.
APPLICANT: Callinson, Karen S.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TITLE OF INVENTION: OF SALMONBLIA
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSER: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STREET: U.S.A.
ZIP: 98104-7092
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88.9%; Score 689; DB 1; Length 151;
Best Local Similarity 91.4%; Pred. No. 1.8e-60;
Matches 138; Conservative 2; Mismatches 11; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: BM PC Compatible
COMPUTER: BM PC Compatible
COMPUTER: BM PC Compatible
COMPUTER: BM PC Compatible
COMPATION WINGER: PC COMPATION
APPLICATION NDATA:
APPLICATION NDATA:
APPLICATION NUMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION NUMBER: 35.570
REGISTRATION NUMBER: 35.570
REFERENCE/DOCKET NUMBER: 920043.403C2
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-490
TELEPHONE: (206) 622-490
TELEPHONE: (206) 622-6031
TELEX: 3723836 SEEDANBERY
INFORMATION FOR SEO ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: amino acids
TYPE: amino acid
US-09-328-352-7735
US-09-489-8039-7973
US-09-495-8039-42
US-09-919-172-41
US-09-073-898-6
US-09-073-898-6
US-09-073-898-6
US-09-134-001C-5005
US-09-134-001C-5005
US-09-134-001C-5005
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US-08-130-19
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    TOPOLÓGY: linear
MOLECULE TYPE: protein
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GENERAL INFORMATION:
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US-08-233-788A-59

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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                      GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-252-991A-3023

US-09-489-039A-1899

US-09-252-991A-26438

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US-09-478-675-3

US-09-595-6848-39
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Listing first 45 summaries
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                                                                                                                                               61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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Patent No. 5635617
CENERAL INFORMATION:
CENERAL INFORMATION:
APPLICANT: Collinson, Karen S.
APPLICANT: Clouthier, Sharon C.
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Pred. No. 1.7e-42;
2; Mismatches 11; Indels
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ADDRESSEE: Seed and Berry
STREET: Seatle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104-7092
COMPUTER: EADDRES FROM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DG/MS-DS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/23,788A
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 920043.403C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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                                                                                                                                                                                                                                                                                                                                 RESULT 3
US-09-196-387-8
Sequence 8, Application US/09196387
Patent No. 6277613
GENERAL INFORMATION:
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Matches 99; Conservative
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CORRESPONDENCE ADDRESS:
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US-08-233-788A-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82
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65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
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                                                                                                                                                                                                                BINDS TO TRF1 AND METHODS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER EACH EFORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC COMPATIBLE
COMPUTER: EN PC COMPATIBLE
COMPUTER: DEACH FOCH EN FOCH EN FOCH EN FOCH EN FOCH EN FOCH EN FOCH EN FOCH EN FOCH EN FOLK EN FOCH EN FOCH EN FOCH EN FOCH EN FOCH EN FOCH EN FOCH EN FORM EN FOCH EN FOCH EN FOCH EN FOCH EN FOCH EN FOCH EN FOCH EN FORM EN FOCH EN FOCH EN FOCH EN FOCH EN FOCH EN FOCH EN FOCH EN FORM EN FOCH EN FOCH EN FOCH EN FOCH EN FOCH EN FOCH EN FOCH EN FORM EN FOCH EN FOCH EN FOCH EN FOCH EN FOCH EN FOCH EN FOCH EN FORM EN FOCH EN FOCH EN FOCH EN FOCH EN FOCH EN FOCH EN FOCH EN FORM EN FOCH EN FOCH EN FOCH EN FOCH EN FOCH EN FOCH EN FOCH EN FORM EN FOCH EN FOCH EN FOLK EN FORM EN FOCH EN FORM EN FOCH EN FORM EN FOCH EN FORM EN FOCH EN FORM EN FOLK EN FORM EN FOLK EN FORM EN FOLK EN FORM EN FOLK EN FORM EN FOLK EN FORM EN FOLK EN FORM EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FORM EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FORM EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FORM EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FORM EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FORM EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FORM EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FORM EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FORM EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FORM EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FORM EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FOLK EN FO
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Best Local Similarity 28.4%; Pred. No. 1.1;
Matches 42; Conservative 16; Mismatches 61;
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Sequence 8, Application US/09841835

Patent No. 6506587

GENERAL INFORMATION:

APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan

TITLE OF INVENTION: OF USE THEREOF

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSE: Klauber & Jackson

STREET: Hackensack

CITY: Hackensack

COUNTRY: USA
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: ATT
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
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99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNG------DVSRVKRLVDA--- 204
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APPLICATION NUMBER: US/09/841,835
                                                                                                                                                                                                                                                                                                                                                                                                                           11.7%; Score 90.5; DB 3; 28.4%; Pred. No. 1.8; tive 16; Mismatches 61;
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Fatent No. 6506587
GENERAL INFORMATION
APPLICANT: GELANGE, Titia
APPLICANT: Smith, Susan
ITILE OF INVENTION: A PROTEIN THAT BINDS TO TITIE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 411 Hackensack Avenue, 4th Floor
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNES JACKSON BEG., DAVIG A.
RAGISTRATION NUMBER: 26,742
REPERRNCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-580
TELEPHONE: 201-487-580
TELEPHONE: 201-487-580
TELEPHONE: 201-487-580
TELEPHONE: CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 949 mmino acids
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ATTORNEY/AGENT INFORMATION:
NAME: Jackson Bsq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 ----ANVNAKDMAGRKSSPLHFAAGFG 227
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CLASSIFICATION
PRICH APPLICATION
APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
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ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DC
                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 28.4 Matches 42; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear;
MOLECULE TYPE: protein
US-09-196-387-10
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STATE: New Jersey
CONNTRY: USA
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3Y: linear
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US-09-841-835-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
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US-09-196-387-10
Sequence 10, Application US/09196387
Patent No. 6277613
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THERROF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.7%; Score 90.5; DB 4; Length 673; 28.4%; Pred. No. 1.1; tive 16; Mismatches 61; Indels 2
                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRATION DATA:
APPLICATION NUMBER: US/09/841,835
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELEPHONE: 201-487-5800
TELEPHONE: 201-343-1684
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 HEMAHANQTASD----SSVMVRQVGFG 143
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APPLICATION NUMBER: 09/196,387
FILING DATE:
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Best Local Similarity 28.43
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 673 amino acids TYPE: amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
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PRIOR APPLICATION DATA:
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: New Jersey
RY: USA
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                                                                                                                            99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                                                                                                                                                                                  65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
                                                                                                                                                                                                                                                                                                                   ----DVSRVKRLVDA--- 204
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                                                                            6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: de Lange, Titia
APPLICANT: de Lange, Titia
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 1.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jacker
STREET: 411 Hand
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Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
61;
                                                                                                                                                                                                                                                                                                                   158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNG---
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFRENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFRAX: 201-343-1684
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     121 HEMAHANOTASD----SSVMVROVGFG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----ANVNAKDMAGRKSSPIHFAAGFG 227
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APPLICATION NUMBER: US/09/841,835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-841-835-2; Sequence 2, Application US/09841835; Sequence 2, Application US/09841835; Patent No. 6506587; GENERAL INFORMATION:
    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible Obersharm
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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        42; Conservative
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MEDIUM TYPE: Floppy
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HYPOTHETICAL: NO
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: USA
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STATE: New Jerse
COUNTRY: USA
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Best Local Similarity
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Patent NO. 6277613
GENERAL INFORMATION:
APPLICANT: General Titia
APPLICANT: General Smith, Susan
ITILE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES:
ADDRESSEE: Klauber & Jackson
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FILING DATE:
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PRIOR APPLICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/ABENT INFORMATION:
NAME: Jackson Esq., David A
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 411 Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY: Hackensack Avenue, 4th Floor CITY
                                                                                                                                                                                                                                                                                                                                                                               16; Mismatches
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Z01-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 1327 amino acids
TYPE: amino acid
STRANDEDNESS: sir-
TOPOLOGY:
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28.48;
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NO
            SEQUENCE CHARACTERISTICS LENGTH: 949 amino acids
                                                   949 amino acids
amino acid
                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
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Best Local Similarity
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Best Local Similarity
Matches 42; Conserv
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HYPOTHETICAL:
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Sequence 171, Application US/09198452A

Patent No. 655924

GENERAL INFORMATION:
APPLICANT; Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment:
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, previring REPERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT FILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 LLKVAAFAAIVVSGSALAGVVPQWGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD 62
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Best Local Similarity 35.4%; Pred. No. 1.6;
Matches 29; Conservative 4; Mismatches 26; Indels 2:
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APPLICATION NUMBER: US/08/864,038A
FILING DATE: MAY 28, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 8-184459
FILING DATE: 15-UJY-1996
ATTORNEY/AGENT INFORMATION:
NAME: C. BRUCE HAMDURG
REGISTRATION NUMBER: 22,389
REGISTRATION NUMBER: P-5610
TELEPHONE: (212)966-2340
TELEPHONE: (212)966-2340
TELEPHONE: (212)966-2340
TELEPHONE: (212)966-2340
TELEPHONE: (212)966-2340
SEQUENCE CHARACTERISTICS:
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CELL TYPE: mantle epithelial cell
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ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: peptide
LOCATION: from 1 to 738
IDENTIFICATION METHOD: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-198-452A-171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-198-452A-171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-864-038A-3
                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Patent No. 6001592
GENERAL INFORMATION:
APPLICANT: Kunio NAKASHIMA et al.
TITLE OF INVENTION: NOVEL POLYBEPTIDE GENE CDNA, VECTOR
TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
TITLE OF INVENTION: ALD POLYPEPTIDE PRODUCED THEREBY, MITH SAID
TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
TITLE OF INVENTION: TO SAID POLYPEPTIDE
NUMBER OF SECUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 KSETTIT; --- QSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNG------DVSRVKRLVDA--- 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 1327;
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MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage COMPUTER: IBM Compatible OPERATING SYSTEM: Microsoft Windows 95 SOFTWARE: Word Perfect 6.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                         APPLICANT: Geron Corporation
APPLICANT: Geron Corporation
APPLICANT: Gregg, Morin B.
APPLICANT: Walter, Funk D.
APPLICANT: Maczyslaw, Piatyszek A.
TITLE OF INVENTION: A Second Mammalian Telomerase
FILE REPERENCE: 080/003C
CURRENT PELING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/128,577
PRIOR APPLICATION NUMBER: US 60/129,123
PRIOR FILING DATE: 1999-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.7%; Score 90.5; DB 28.4%; Pred. No. 2.8; ative 16; Mismatches
                                121 HEMAHANQTASD----SSVMVRQVGFG 143
                                                                                ----ANVNAKDMAGRKSSPLHFAAGFG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 HEMAHANQTASD----SSVMVRQVGFG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----ANVNAKDMAGRKSSPLHFAAGFG 227
                                                                                                                                                                                                   Sequence 8, Application US/09972115A Patent No. 6599728 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     812-5 Hirano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 28.4%
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Tsu-city
STATE: Mie-prefecture
COUNTRY: JAPAN
ZIP: 514-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-115A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isshinden
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                                                                                                                                                                                US-09-972-115A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
US-08-864-038A-3
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58 HIYGVDAPSAFYGYGWAQARSQGDNILRLYGEAR------GKGAEYWGPDYEQTT 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 IELTQNGFRNNATIDQWNAK-----NYDQLVTRVVTHEMAHANQTASDSSVMVRQV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OFERATIONS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PERCENTED RELEASE #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA: PC-DOS/MS-DOS
RPELICATION NUMBER: US/07/731,157A
FILING DATE: 19910509
CLASSIFICATION: 435
RICH APPLICATION DATA:
APPLICATION NUMBER: EP 90200962
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
RAB-VENTER PH.D. BARBARA
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: GBRO-027/00US
TELEPHONE: 415-494-7663
TELEPHONE: 415-494-7663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                APPLICANT: Misset, Onno
APPLICANT: Misset, Onno
APPLICANT: Misset, Onno
APPLICANT: Wan der Laam, Jan M.
APPLICANT: Van der Laam, Jan M.
TITLE OF INVENTION: Mutated beta-lactam acylase genes
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS: ADDRESS: COOLEY GODWARD CASTRO HUDDLESON & TATUM
STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.5%; Score 81.5; DB 1;
ilarity 25.8%; Pred. No. 9.5;
Conservative 17; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKLLKVAAFAAIVVSGSALAGVV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
126 ANOTASDSSVMVRQVGFGNN 145
                                                                                                                                                                          Sequence 2, Application US/07731157A, Patent No. 5457032, GENERAL INFORMATION:
                                             180 ANOATGESSTV---AGGSNN 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08541780; Patent No. 5935831; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 380816 COOLEY PA
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 720 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: FIVE PALO CITY: PALO ALTO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                       US-07-731-157A-2
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TELEX: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-541-780-2
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                                                                                   APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPREMENTE: 107196.136
CURRENT APPLICATION NUMBER: US 60/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32096
LENGTH: 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 ALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQ---- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 -----TSVLQSGYGNTLNNYSNPNTASLSNSANNVSGNLGVNV-AAGNFNQQKND 163
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US-09-316-447A-15
US-09-316-447A-15
Sequence 15, Application US/09336447A
Sequence 15, Application US/09336447A
Patent No. 6310190
GENERAL INFORMATION:
APPLICANT: AEB1, CHRISTOPH
APPLICANT: ACOUNT, LESLIE D.
APPLICANT: TOOPE, LESLIE D.
APPLICANT: FREEDENBURG, ROSE A.
APPLICANT: FREEDENBURG, ROSE A.
APPLICANT: FREEDENBURG, ROSE A.
APPLICANT: FREEDENBURG, ROSE A.
APPLICANT: FREEDENBURG, ROSE A.
APPLICANT: FREEDENBURG, ROSE A.
APPLICANT: FREEDENBURG, ROSE A.
APPLICANT: FREEDENBURG, ROSE A.
APPLICANT: FREEDENBURG, ROSE A.
APPLICANT FILING NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID LOSE: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 KVAAFAAIVVSGSALAGVVPQWGG-----GGNHNGGGNSSGPDSTLSIYQYGSANAAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
10.9%; Score 84.5; DB 4; Length 339;
Best Local Similarity 21.5%; Pred. No. 1.8;
Matches 34; Conservative 32; Mismatches 67; Indels 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 LVTRVVTHEMAHANQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAAAVSNGQYSTAGSAASQTSTGNTTVNSANYAYGGTY 201
                        Sequence 32096, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Moraxella catarrhalis
US-09-336-447A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 889
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Best Local Similarity
Matches 39; Conserv
        US-09-252-991A-32096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-252-991A-32096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 25.8%; Pred. No. 9.5;
Matches 46; Conservative 17; Mismatches 56; Indels 59; Gaps
APPLICANT: Quax, Wilhelmus J.
APPLICANT: Misset, Onno
APPLICANT: Waset, Onno
APPLICANT: Van der Laan, Jan M.
APPLICANT: Van der Laan, Jan M.
APPLICANT: Lenting, Herman B.M.
TITLE OF INVENTION: Mutated beta-lactam acylase genes
NUMBER OF SEQUENCES:
SOCHEN ADDRESS:
ADDRESSEE: COCLEY GODWARD CASTRO HUDDLESON & TATUM
STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR
CITY: PALO ALTO
CITY: PALO ALTO
COUNTY: DALO ALTO
STATE: CALIFORNIA
COUNTY: USA
ZIF: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BAR PC Compatible
COMPUTER: BAR PC Compatible
COMPUTER: BAR PC Compatible
COMPUTER: BAR PC COMPAT:
MEDIUM TYPE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,780
FILING DATE: 18-ARP.1990
ATTORNEY AGENT INFORMATION:
APPLICATION NUMBER: BY 91.00062
FILING DATE: 18-ARP.1990
ATTORNEY AGENT INFORMATION:
TELECHMONICATION NUMBER: 32,750
REFERENCY DOCKET NUMBER: GBRO-027/00US
TELECHMONICATION NUMBER: A3,750
REFERENCY DOCKET NUMBER: A3,750
REFERENCY DOCKET NUMBER: A3,750
REFERENCY DOCKET NUMBER: A3,750
REFERENCY DOCKET NUMBER: A3,750
REFERENCY DOCKET NUMBER: A3,750
REFERENCY DOCKET NUMBER: B2,750
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REFERENCY DOCKET NUMBER: B2,750
REFERENCY DOCKET NUMBER: B2,750
RELECOMMUNICATION PROPAMATION:
TELECOMMUNICATION POR B2.00062
TELECOMMUNICATION POR B2.00062
TELECOMMUNICATION POR B2.00062
TELECOMMUNICATION POR B3.00060
REPORTER A30016 COOLEY PA
INFORMATION POR SEQ ID NO: 2:
SEQUENCE TELECOMMUNICATIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 720 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-541-780-2
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Search completed: August 2, 2004, 14:58:35 Job time: 12 secs

(0108N) YUD18 860d S141

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August 2, 2004, 14:54:48; Search time 36.8 Seconds (without alignments) 1287.123 Million cell updates/sec
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775
1 MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151
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16: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCCMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	-	Description	Sequence 4, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2	Sequence 7876, Ap	Sequence 49960, A	Sequence 8, Appli	Sequence 10, Appl	Sequence 2, Appli	Sequence 8, Appli	Sequence 4, Appli		8 Sequence 275468,	Sequence 57763, A
SUMMARIES	;		US-09-741-873B-4	US-09-741-873B-4	US-09-741-873B-2	US-09-741-873B-2	US-10-369-493-20638	US-10-032-585-7876	US-10-425-114-49960	US-09-841-835-8	US-09-841-835-10	US-09-841-835-2	US-09-972-115A-8	US-10-199-937-4	US-10-425-114-56041	US-10-424-599-275468	US-10-425-114-57763
		DB	12	12	12	12	15	14	12	σ	σ	ഗ	10	14	12	12	12
	% Query	Length	151	151	131	131	445	688	263	673	949	1327	1327	1327	369	486	507
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48 Segue	Ψ	Seguenc	12 Seque	Seque	4	9	<b>0</b> 1	S	3	Seguence	Seque	Seguenc	Seguence	S	79 Sequence	S	Seguenc	9	43 Seguenc	Segue	Seguenc	3	9	9	S	78 Sequenc	ഗ	Ø	S
-10-437-963-147	-10-156-	-10-289-762-17	-10-282-122A-494	-10-156-761-876	-10-282-122A-59	-10-437-963-122	-10-156-761-117	-10-282-122A-4	-10-437-963-115	-09-880-748-113	-09-880-748-116	-10-293-418-113	-10-293-418-116	-10-156-761-131	-10-437-963-163	-10-425-114-615	-09-952-267-1	-10-282-122A-506	-10-437-963-1191	-09-880-748-12	-10-293-418-122	-10-282-122A-645	-10-282-122A-426	-10-437-963-1707	-10-156-761-1197	-10-437-963-1246	4-599-2854	-10-425-114-4839	-10-425-114-4940
45 1	38 1	56 1	86 1	82 1	62 1	70 1	71 1	57 1	78 1	54 1	54 1	54 1	54 1	50 1	94 1	42 1	89 1	74 1	14 1	54 1	54 1	78 1	83 1	89	56 1	29 1	49 12	09	29 1
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## ALIGNMENTS

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RESULT 1
Sequence 4, Application US/09741873B
Sequence 4, Application US/09741873B
Sequence 4, Application US/09741873B
Sequence 4, Application US/090081722A1
GENERAL INFORMATION:
APPLICANT: ON NO. US20020081722A1
APPLICANT: Olsen, Area
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084
CURRENT PILING DATE: 10289-054
FRICH APPLICATION NUMBER: US/09/741,873B
CURRENT PILING DATE: 1998-05-06
FRICH APPLICATION NUMBER: US 08/978,878
FRICH APPLICATION NUMBER: US 07/347,189
FRICH APPLICATION NUMBER: US 07/789,437
FRICH APPLICATION NUMBER: US 07/789,437
FRICH APPLICATION NUMBER: US 07/789,437
FRICH APPLICATION NUMBER: US 07/789,437
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60

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58.3%; Score 452;
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, ORGANISM: Escherichia coli
US-09-741-873B-2
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, ORGANISM: Escherichia coli
US-09-741-873B-2
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Sequence 4, Application US/09741873B

Publication No. US20040096965A9

GENERAL INFORMATION:
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084

CURRENT APPLICATION NUMBER: US/09/741,873B

CURRENT APPLICATION NUMBER: SE 880172-1

PRIOR APPLICATION NUMBER: SE 880172-1

PRIOR PLING DATE: 1998-05-06

PRIOR FILING DATE: 1998-05-06

PRIOR FILING DATE: 1999-11-26

PRIOR PRILOR APPLICATION NUMBER: US 07/347,189

PRIOR PRILOR NUMBER: US 07/347,189

PRIOR PRILOR DATE: 1991-11-06

PRIOR PLING DATE: 1991-11-06

PRIOR FILING DATE: 1991-11-06

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-10-05

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn version 3.0

SEQ ID NO 4

LENGTH: 151
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                                                                61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
                                                                                          61 SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
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Publication No. US20020081722A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Orsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012899-048
CURRENT APPLICATION NUMBER: US/09/741,873B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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68.4%; Score 530; DB 12; Length 1:
Best Local Similarity 69.5%; Pred. No. 7.2e-46;
Matches 105; Conservative 19; Mismatches 27; Indels
                                                                                                                                               121 HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                       121 HEMAHANOTASDSSVMVRQVGFGNNATANOY 151
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US-09-741-873B-2
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US-09-741-873B-2

J Sequence 2, Application US/09741873B

Sequence 2, Application NO. US20040096965A9

GENERAL INFORMATION:

APPLICANT: Normark, Staffan

APPLICANT: Olsen, Arne

TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation

TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation

TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation

TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation

TITLE OF INVENTION WHERE US/09/741,87B

PRIOR FILING DATE: 1998-05-06

PRIOR FILING DATE: 1997-11-26

PRIOR FILING DATE: 1997-11-26

PRIOR FILING DATE: 1997-11-103

PRIOR FILING DATE: 1997-11-06

PRIOR FILING DATE: 1997-11-06

PRIOR FILING DATE: 1997-11-05

PRIOR FILING DATE: 1997-10-05

PRIOR FILING DATE: 1994-10-05

PRIOR FILING DATE: 1994-10-05

PRIOR PLING DATE: 1994-10-05

NUMBER OF SEQ ID NOS: 10

SEQ ID NO 2

LENGTHAE: PATENTIN 131

TYPE: DPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 VGGGSDDSSIDLIQRGFGNSATLDQWNGKNSEMTVKQFGGGNGAAVDQTASNSSVNVTQV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GVVPQYGGGGNHGGGGNNSGPNSELNTYQYGGGNSALALQTDARNSDLTITQHGGGNGAD
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Best Local Similarity 66.4%; Pred. No. 5e-38;
Matches 87; Conservative 18; Mismatches 26;
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 08/978, 878
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1989-05-04
PRIOR FILING DATE: 1989-05-04
PRIOR RELIGATION NUMBER: US 07/789,437
PRIOR PELING DATE: 1991-11-06
PRIOR PELING DATE: 1991-11-06
PRIOR FILING DATE: 1994-11-03
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-00-28
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 10
SSOFWARE: PALENT UN VERSION 3.0
SSOFWARE: PALENT UN VERSION 3.0
LENGTH: 131
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DB 12; Length 131;

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APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 49960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 SALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSG-- 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                              545 KSKKKSNFDNNSNS---ALNNLDKSKLKINTWEITNISETTSNSSSPVINLNHGGRSS 599
                                                                                                                                                                                                                                                                                                                                                                                                                                 90 IELTQNGFRNNATIDQWNAKNYDQLVTRVVTHEMAHANQTASDSSVMVRQVGFGNNAT 147
                                                                                                                                                                                                                                                                                                                                                                             488 GNNNGSGNSSGTTNNSNNYNNKSISKKNEIDDGDDLNPISITNN---TGLINNNNSKSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 -----YGNGA--DVGQGADNSTIEL--TQNGFRNNATID 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.7%; Score 90.5; DB 12; 27.9%; Pred. No. 0.62;
                                                                                                                                                                                                                             Query Match
11.7%; Score 91, DB 14;
Best Local Similarity 23.7%; Pred. No. 1.9;
Matches 28; Conservative 25; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; CTHER INFORMATION: Clone ID: 700071884_FLI.pep
US-10-425-114-49960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/09841835;
Patent No.:US20020076795A1
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Genie, Titia
TITLE OF INVENTION: A PROTEIN THAT BIN
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 49960, Application US/10425114; Publication No. US20040034888A1; GENERAL INFORMATION:
     CURRENT FILING DATE: 2001-12-2
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3:1
SEQ ID NO 7876
LENGTH: 688
                                                                                                                                  i TYPE: PRT

   ORGANISM: Candida albicans
US-10-032-585-7876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-425-114-49960
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US-09-841-835-8
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US-10-369-493-20638

US-10-369-493-20638

Sequence 20638, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Goo, Yongwei
APPLICANT: Gladman, Barry S.
APPLICANT: Chen, Xianfeng
ITILE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
ITILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
ITILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT PILING DATE: 2003-02-28

PRIOR PLING DATE: 2002-02-11

NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                 140
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J Sequence 7876, Application US/10032585

Publication No. US2030180953A1

GENERAL INFORMATION:

APPLICANT: Perry, Roemer D.

APPLICANT: Bo, Jiang

APPLICANT: Howard, Bussey

TITLE OF INVENTION Gene Disruption Methodologies for Drug Target Discovery

FILE REFERENCE: 10182-005-999

CURRENT APPLICATION NUMBER: US/10/032,585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 GNSNSV-----GRDIQGKQSGAGNSAAIFQEGTGSDVELQQTGTSNGAVPSGWNWTN 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 GSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKN 110
                                                                                                                               09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 AAFAADSNTVYLNQTGNDQQANITQSGNGNSVGAFNGNSGFLQENGTLSGA-NLLTVKQS 77
                                                                                                          1 GVVPQYGGGGNHGGGGNNSGPNSELNTYQYGGGNSALALQTDARNSDLTITQHGGGNGAD
                                                                                                                                                                                                           21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
                                                                                                                                                                                 81 VGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVTHEMAHANQTASDSSVMVRQV
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68; Indels 30; Gaps
                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 YDQLVTRVVTHEMAHAN----QTASDSSVMVRQVGFGNNATANQ 150
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5e-38;
----- 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1)..(445)
CTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-20638
          ; Pred, No. 5e-38
18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Rhodopseudomonas palustris
          66.48;
     Best Local Similarity 66.4%
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42; Conservative
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Best Local Similarity
Matches 42; Conserv
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Gaps

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CAPPUTER FALSE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC Compatible
COMPUTER: EN PC Compatible
COMPUTER: DatentIN Selease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE:
APPLICATION NUMBER: 09/196,387
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: AGCKSON ESQ., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/COKET NUMBER: 600-1-230 CIP1
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
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FILING LAALD.
CLASSERICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE:
ATTORNEY JACKSON ESG., David A.
REGIETRATION NUMBER: 26/742
REFERENCE/DOCKET NUMBER: 600-1-230 CIPI
TELECOMMUNICATION INFORMATION:
TELETAK: 201-349-5800
TELETAK: 201-349-1684
TELETAK: 201-343-1684
TELEX: 133521
INFORMATION FOR SEG ID NO: 10:
SEQUENCE CHARACTERISTICS:
LEBUGHH: 949 amino acid
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16, Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 28.4%
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear;
MOLECULE TYPE: protein
US-09-841-835-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNG------DVSRVKRLVDA--- 204
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Sequence 10, Application US/09841835
Patent No. US20020076795A1
GENERAL INFORMATION:
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Ralease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 28.4%; Pred. No. 2;
Matches 42; Conservative 16; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                   NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 HEMAHANQTASD----SSVMVRQVGFG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----ANVNAKDMAGRKSSPLHFAAGFG 227
                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
FILICATION NUMBER: 09/196,387
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 13351
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
    Hackensack
New Jersey
YY: USA
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                                                  COUNTRY:
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158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNG------DVSRVKRLVDA--- 204
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                                                                                                                                                                                                                                    65 KSETTIT----OSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-841-835-2

US-09-841-835-2

Sequence 2, Application US/09841835

Patent No. US20020076795A1

SEQUERAL INFORMATION:

APPLICANT: de Lange, Titia

APPLICANT: Smith, Susan

TITLE OF INVENTION: OF USE THEREOF

NUMBER OF SEQUENCES:

CORRESPONDENCE ADRESS:

ADDRESSEE: Klauber & Jackson
11.7%; Score 90.5; DB 9; Length 949; 28.4%; Pred. No. 3.1;
                                                          Indels
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US-10-199-937-4
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                                                                                                                                                                                                                                                                                                                                         99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                                                                                                                                                                                                                                                                                                                                        65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                   158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNG------DVSRVKELVDA--- 204
                                                                                                                                                                                                                                                                                                                 6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
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                                                                                                                                                                                                                                         Length 1327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61; Indels
                                                                                                                                                                                                                                                                              61; Indels
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Sequence 8, Application US/09972115A

PUBLication No. US20030032769A1

GENERAL INFORMATION:

APPLICANT: Geron Corporation

APPLICANT: Greogy, Morin B.

APPLICANT: Malter, Funk D.

APPLICANT: Malcayslaw, Piatyszek A.

TITLE OF INVENTION: A Second Mammalian Telomerase

FILE REFERENCE: 080/003C

CURRENT APPLICATION NUMBER: US/09/972,115A

CURRENT PILING DATE: 2001-10-05

PRIOR PILING DATE: 2000-04-10

PRIOR FILING DATE: 1999-04-13

NUMBER OF SEQ ID NOS: 64

SOFTWARE: Patentin version 3.1

SEQ ID NO
                                                                                                                                                                                                                                           DB 9;
                                                                                                                                                                                                                                         ; Score 90.5; DE; DE; Pred. No. 4.8; 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.7%; Score 90.5; DE 28.4%; Pred. No. 4.8; iive 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 HEMAHANQTASD----SSVMVRQVGFG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 ----ANVNAKDMAGRKSSPLHFAAGFG 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 ----ANVNAKDMAGRKSSPLHFAAGFG 227
TELEFAX: 201-5...
TELEX: 133521
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1327 amino acids
"VPE: amino acid
"TPE: amino acid
                                                                                                                                                                                                                                     11.7%;
Local Similarity 28.4%;
ses 42; Conservative 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 28.4%
Matches 42, Conservative
                                                                                                                          SS: single
linear
                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-972-115A-8
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US-09-841-835-2
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Matches
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RESULT 12 US-10-199-937-4

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Sequence 56041, Application US/10425114

Sequence 56041, Application No. US200400348881

Sequence 56041, Application No. US200400348881

Sequence 56041, Application No. US200400348881

APPLICANT: Liu, Jingdong

APPLICANT: Chou, Yihua

APPLICANT: Screen, Steven E

APPLICANT: APPLICANT: Apaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21 (5313) B

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 56041

LENGTH: 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNG-------DVSRVKRLVDA--- 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 VRSSASKG-KPPLSAGNNNNGGWDNWDPDD----GFGSARGG----ADLRRNQSTGDVR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPBAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR
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Best Local Similarity 26.3%; Pred. No. 1.4;
Matches 36; Conservative 20; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                 APPLICANT DeMaggio, Anthony J.
APPLICANT Goldman, PMyllis S.
APPLICANT Goldman, PMyllis S.
APPLICANT Goldman, PMyllis S.
TITLE GOT INVENTION: TANKTRASE2 MATERIALS AND METHODS
FILLS REPERENCE: 27866/36559
CURRENT APPLICATION NUMBER: US/10/199,937
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/141,582
PRIOR APPLICATION NUMBER: 60/141,582
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-29
SEQ ID NOS: 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.7%; Score 90.5; DB 14;
llarity 28.4%; Pred. No. 4.8;
Conservative 16; Mismatches 61;
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US-10-425-114-56041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 HEMAHANQTASD----SSVMVRQVGFG 143
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Sequence 4, Application US/10199937
Publication No. US20030190739A1
GENERAL INFORMATION:
APPLICANT Christenson, Erik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Glycine max
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Best Local Similarity
Matches 42; Conserv
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US-10-425-114-56041
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Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Acvalic David K

APPLICANT: Acvalic David K

APPLICANT: Cac Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

CURRENT APPLICATION NUMBER: US/10/424,599

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 275468

LENGTH: 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
                         GFGGGGNV-----SRSKSTQDMY-TRAELEASAANKEDFFARKRAENESRPEGLPPSQG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 GFGGGGNV-----SRSKSTQDMY-TRAELEASAANKEDFFARKRAENESRPEGLPPSQG 232
GYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVTHEMAHANQTASDS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 VSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 GYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVTHEMAHANQTASDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.5%; Score 89; DB 12; Length 486; 26.3%; Pred. No. 1.9;
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; OTHER INFORMATION: Clone ID: UC-GMFLMINSOY049H04_FLI.pep
US-10-425-114-57763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT3847_90769C.l.pep
US-10-424-599-275468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 57763, Application US/10425114 Publication No. US20040034888A1 GENERAL INFORMATION:
                                                                                 134 SVMVROVGFGNNATANO 150
                                                                                                                 : ||||:
116 G---KYVGFGSGPAPNQ 129
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 36, Conserv
                                                                                                                                                                                              RESULT 14
US-10-424-599-275468
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US-10-425-114-57763
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LENGTH: 507
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Sequence 14, Sequence 30,

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Run on:

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Total number of

Searched:

Minimum DB Maximum DB

Maximum

Database :

Scoring table:

Perfect score:

Sequence:

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Sequence 5, Appl
Sequence 20, Appl
Sequence 22, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 27, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 27, Appl
Sequence 2834, Ap
Sequence 2834, Ap
Sequence 35, Appl
Sequence 3634, Appl
Sequence 34, Appl
Sequence 36, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 2033, Appl
Sequence 2033, Appl
Sequence 2033, Appl
Sequence 2033, Appl
Sequence 2033, Appl
Sequence 2033, Appl
Sequence 2033, Appl
Sequence 5833, Appl
Sequence 5833, Appl
Sequence 5833, Appl
Sequence 5833, Appl
Sequence 5833, Appl
Sequence 5833, Appl
Sequence 5833, Appl
Sequence 5833, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                            6 US-09-233-642A-55

6 US-09-252-691-5834

6 US-09-252-691-5834

6 US-09-252-691-5834

9 US-09-543-407-34

9 US-09-543-407-35

1 US-09-543-407-35

1 US-09-543-407-35

1 US-09-543-407-35

1 US-09-543-407-35

1 US-09-543-407-37

1 US-09-543-407-38

1 US-09-543-407-8

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1 US-09-543-407-8

1 US-09-614-150-24084

1 US-09-614-150-24084

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1 US-09-614-150-14916

1 US-06-167-114918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: White, Aaron P.
APPLICANT: White, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEP
FILE REPERBURE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF.SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 151
US-09-543-407-24

US-09-543-407-30

US-09-543-407-30

US-09-543-407-12

US-09-543-407-12

US-09-543-407-12

US-09-543-407-12

US-09-543-407-12

US-09-543-407-18

US-09-543-407-18

US-09-543-407-16

US-09-543-407-16

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US-09-543-407-16

US-08-543-407-16

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     US-09-543-407-24
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248.5
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775
1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                    hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                    6019581 seqs, 976053577 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                    using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length DB
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Score

Result Š.

Sequence 24084, Sequence 24179, Sequence 19019,

Sequence Sequence Sequence

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APPLICANT: Kay, William W.
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US-09-543-407-30
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                                                                                                TYPE: PRT
                                                                                                                                      FEATURE:
                                                                          LENGTH:
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                                                                                                                                                                                                                                    61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDARKSETTITOSGYGNGADVGQGADNSTIELTONGFRNNATIDOWNAKNSDITVGQYDQ 120
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                                                                                                                                             1 MKLLKVAAFPAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                  SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT
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                                                                             Gaps
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Col. William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REPERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILIG DATE: 2000-04-05
SOFTWARE: FASTSEQ for Windows Version 4.0
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GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Octainson, S. Karen
APPLICANT: Collinson, S. Karen
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 92043.407
CURRENT APPLICATION NUMBER: US/09/543,407
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                                      Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 92.1%; Score 714; DB 19; Length 151; Best Local Similarity 91.1%; Pred. No. 9.2e-68; Matches 144; Conservative 0; Mismatches 0; Indels 14
                                                                             Indels
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                                  100.0%; Score 775; DB 19;
100.0%; Pred. No. 2.7e-74;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                               HEMAHANOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                           HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
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GENERAL INFORMATION:
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                                                                             Conservative
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                                      Query Match
Best Local Similarity
Matches 151; Conserv
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US-09-543-407-30
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US-09-543-407-24
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LENGTH: 151
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                                                                                                                                                                                                                                                                                                                                                                                               16;
                                                                                                                                                                                                         OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                             Length 151;
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                                                                                                                                                                                                                                                                                                                                                                                               Indels
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APPLICANT: White, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGGOUS PEP'
FILE REFERENCE: 920043,407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                          90.3%; Score 700; DB 19;
89.9%; Pred. No. 2.9e-66;
tive 0; Mismatches 0;
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ilarity 91.4%; Pred. No. 3.4e-65;
Conservative 2; Mismatches 11;
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NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
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US-08-233-642A-57
Sequence 57, Application US/08233642A
, GENERAL INFORMATION:
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                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 89.9
Matches 143; Conservative
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Best Local Similarity
Matches 138; Conserv
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121 NNAALVNYDQLVTRVVTHEMAHA-----
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 79.8%;
Matches 134; Conservative 0
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ORGANISM: Artificial Sequence
                                  ORGANISM: Artificial Sequence
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US-09-543-407-26
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GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Doran, James L.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Ray, William W.

TITLE OF INVENTION: BRETERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: BRETERIATION OF HETEROLOGOUS PEPTIDE SEQUENCES

FILE REFERENCE: 920043.406

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 12

LENGTH: 151
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                              APPLICANT: Clouthier, Sharon C.
APPLICANT: Clouthier, Sharon C.
APPLICANT: Doran, James L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
NUMBER OF SEQUENCES: 58
NUMBER OF SEQUENCES: -
CORRESPONDENCE ADDRESS: -
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 91.4%; Pred. No. 4.4e-65;
Matches 138; Conservative 2; Mismatches 11; Indels
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CIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ATTCRNEY/AGENT INFORMATION:
NAME: ATTCRNEY/AGENT INFORMATION:
NAME: KING JOSHUE: 35,570
REFERENCE/DOCKET NUMBER: 35,570
TELEPRATION NUMBER: 35,570
TELECOMMUNICATION INFORMATION:
TELEPRATION CATENTINENTED THE COMPATION INFORMATION:
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TELEX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
Collinson, S. Karen
Clouthier, Sharon C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 151 amino acids
amino acid
3Y: linear
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STATE: Washington
COUNTRY: U.S.A.
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US-09-543-407-12
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61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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SEQUENCE 22, Application US/09543407

GENERAL INFORMATION:

APPLICANT White, Aaron P.

APPLICANT Collinson. S. Karen

APPLICANT Kay, William W.

TITLE OF INVENTION: BRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

FILE REFERENCE: 920043.406

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 22

LENGTH: 151
                                                                                                                                                                                                                                                                                                                  1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEMAHADOWNAKUSDITVGOYGGNNAALVNOTASDSSVMVROVGFGNNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46;
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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Best Local Similarity 73.6%; Pred. No. 1.6e-56;
Matches 128; Conservative 0; Mismatches 0; Indels 40
                                                                                                                                                      Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                       61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAK-
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                                                                                                                                                  Score 655; DB 19;
Pred. No. 1.9e-61;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ 60
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APPLICANT: White, Aaron P.
APPLICANT: White, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT PILLING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SEQ ID NO 18
LENGTHAR: 151
APPLICANT: Collinson, S. Karen
APPLICANT: KAY, William W.
TITLE OF INVENTION: PRESENTALION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILLE REFERENCE: 92043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASISEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 609; DB 19;
Pred. No. 1.6e-56;
4; Mismatches 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 78.6%;
Best Local Similarity 82.1%;
Matches 124; Conservative
                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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ORGANIT
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61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
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                                                                                                                                                                                                                                     APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PASSENTATION OF HETEROLOGGUS PEPTIDE SEQUENCES
FILE REPERENCE: 920043.466
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTRARE: PastSEQ for Windows Version 4.0
LENGTH: 151
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GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REPERENCE: 920043.4466
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILE SECTION NOWEST.
SOFTWARE: FastSEQ for Windows Version 4.0
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82.1%; Pred. No. 3.4e-56;
live 5; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.8%; Score 603; DB 19;
ilarity 90.1%; Pred. No. 5.9e-56;
Conservative 2; Mismatches 11;
                                   121 HEMAHANQTASDSSVMVRQVGFGNNATANQY 151
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TYPE: BRT
ORGANISM: Salmonella enteritidis
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Best Local Similarity 82.1:
Matches 124; Conservative
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Best Local Similarity
Matches 118; Conserva
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                                                                    81 VGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVTHEMAHANQTASDSSVMVRQV 140
                                                                                                  61 VGÇGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVWVRQV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SDARKSETTITOSGYGNGADYDQLVTRVVTHEMAHAPRNNATIDOWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGFDSTLSIYQYGSANAALALQ 60
MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
SOFTWARE: FactSEQ for Windows Version 4.0
SQITWARE: FactSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Tollinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
77.4%; Score 600; DB 19;
Best Local Similarity 81.5%; Pred. No. 1.5e-55;
Matches 123; Conservative 3; Mismatches 25;
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                                                                                                                                                                                                                                                                                     US-09-543-407-28; Sequence 28, Application US/09543407; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-543-407-16; Sequence 16, Application US/09543407; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                           GFGNNATANOY 151
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OTHER INFORMATION:
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US-09-543-407-28
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GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: NORMARK, Staffan
APPLICANT: OLSEN, Arne
TITLE OF INVENTION FIRENOMECTIN BINDING PROTEIN AS WELL AS ITS PREPARATION
FILE REFERENCE: 012889-081
CURRENT FILING DATE: 1997-11-26
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: SE 8801723-1
EARLIER FILING DATE: 1988-05-06
                                                                                                                                                                                                                                   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                 MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT; White, Aaron P.

APPLICANT; Collinson, S. Karen

APPLICANT; Collinson, S. Karen

APPLICANT; Collinson, S. Karen

APPLICANT; Collinson, S. Karen

APPLICANT; Collinson, S. Karen

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

FILE REFERENCE: 9200433,406

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0
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Recombinant Salmonella enteritidis 3b afgA sequence containing the replacement fragment encoding PT3 from GP63 of Leishmania major.
                                                                                                                            Length 151;
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                                                                                                                         Score 575; DB 19; 1
Pred. No. 7.2e-53;
5; Mismatches 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 NNAALVNQTASDSSVWVRQVGFGNNATANQY 151
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                                                                                                                            Query Match
Best Local Similarity 81.5%;
Matches 123; Conservative
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Best Local Similarity 70.2<sup>3</sup>
Matches 106; Conservative
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-09-543-407-16
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US-09-543-407-7
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Search completed: August 2, 2004, 15:26:45 Job time : 167.9 secs

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RESULT 1
US-09-741-873C-4
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Sequence 17559, A
Sequence 300390,
Sequence 312468,
Sequence 35751, A
Sequence 25751, A
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Sequence 7907, Ap
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 285216,
Sequence 285216,
Sequence 21109, A
Sequence 319662,
Sequence 319662,
Sequence 319662,
Sequence 345256,
Sequence 295, Appl
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88, Appl
2, Appli
346132,
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49, Appl
301334,
                                                         2, 2004, 14:49:38 ; Search time 17.8 Seconds (without alignments) 888.146 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
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Sequence 4
Sequence 3
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                                                                                                                           1 MKLLKVAAFAAIVVSGSALA......bssvmvrqvgFGNNATANQY
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1: /cgn2_6/ptcdata/2/paa/USO5_NEW_COMB.pep:*

2: /cgn2_6/ptcdata/2/paa/USO5_NEW_COMB.pep:*

3: /cgn2_6/ptcdata/2/paa/USO7 NEW_COMB.pep:*

4: /cgn2_6/ptcdata/2/paa/USO9_NEW_COMB.pep:*

5: /cgn2_6/ptcdata/2/paa/USO9_NEW_COMB.pep:*

5: /cgn2_6/ptcdata/2/paa/USO9_NEW_COMB.pep:*

7: /cgn2_6/ptcdata/2/paa/USO9_NEW_COMB.pep:*
version 5.1.6
- 2004 Compugen Ltd.
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US-09-741-873C-4

US-09-748-73C-2

US-09-425-115-300359

US-10-425-115-312468

US-10-470-205E-35751

US-10-470-205E-35751

US-10-470-205E-3751

US-10-470-205E-741

PCT-USO4-02338-49

US-10-470-205E-741

PCT-USO4-02338-49

US-10-425-115-30334

US-10-425-115-346132

US-09-952-2678-15

US-10-872-768-15

US-10-872-768-15

US-10-872-768-15

US-10-872-768-15

US-10-872-768-15

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US-10-425-115-285216

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US-10-425-115-285216
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Maximum Match 100%
Listing first 45 summaries
                                         protein search, using sw model
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Gapop 10.0 , Gapext 0.5
GenCore
Copyright (c) 1993
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seq length: 200000000
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44, Appli
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574, App
570, App
570, App
571, App
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602, App
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609, App
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Sequence 1
Sequence 5
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PCT - USO4 - 09385-4

US-10-864-439-41

US-10-724-972A-4638

US-60-566-425-574

US-60-566-425-574

US-60-566-425-571

US-60-566-425-571

US-60-566-425-571

US-60-566-425-571

US-60-566-425-571

US-60-566-425-571

US-60-566-422-575

US-60-576-812-602

US-60-576-812-602

US-60-576-812-603

US-60-576-812-603

US-60-576-812-603

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US-60-576-812-603
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## ALIGNMENTS

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Sequence 4; Application US/09741873C

Sequence 4; Application US/09741873C

GENERAL INFORMATION:

APPLICANT: Normark, Staffan

APPLICANT: Olean, Arne

ITILE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation

FILE REFERENCE: 012889-084

CURRENT APPLICATION NUMBER: US/09/741,873C

CURRENT FILING DATE: 198-05-06

PRIOR FILING DATE: 1989-05-06

PRIOR FILING DATE: 1989-05-06

PRIOR FILING DATE: 1999-05-04

PRIOR FILING DATE: 1999-05-04

PRIOR FILING DATE: 1991-05-04

PRIOR FILING DATE: 1991-05-04

PRIOR FILING DATE: 1991-01-06

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-10-05

PRIOR FILING DATE: 1994-10-05

PRIOR FILING DATE: 1994-10-05

PRIOR FILING DATE: 1994-10-05

PRIOR FILING DATE: 1994-10-05

PRIOR FILING DATE: 1994-10-05

PRIOR FILING DATE: 1994-10-05

PRIOR FILING DATE: 1994-10-05

PRIOR PAPLICATION NUMBER: US 08/187,865

PRIOR FILING DATE: 1994-10-05

PRIOR APPLICATION NUMBER: US 08/187,865

PRIOR FILING DATE: 1994-10-05

PRIOR PAPLICATION NUMBER: US 08/187,865

PRIOR PAPLICATION NUMBER: US 08/187,865

PRIOR PAPLICATION NUMBER: US 08/187,865

PRIOR APPLICATION NUMBER: US 08/187,865

PRIOR PAPLICATION NUMBER: US 08/187,865
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69.5%; Pred. No. 1.8e-39;
cive 19; Mismatches 27;
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ORGANISM: Escherichia coli
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Best Local Simi:
Matches 105;
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APPLICANT: In revenic.

APPLICANT: APPLICANT: Goveric, David K.

APPLICANT: Kovalic, David K.

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Dants

TITLE OF INVENTION: Dants

FILE REFERENCE: 38-21(5322)B

CURRENT APPLICATION NUMBER: US/10/425,115

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 312468

LENGTH: 295
                                                                                                                                                                                                                                                                                                                   APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Avalic, David K.
APPLICANT: Avalic, David K.
APPLICANT: Cao, Yinua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE OF INVENTION: Plants
FILE REFERENCE: 38-21(5)322B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 369326
SEQ ID NOS: 369326
LENGTH: 258
                                             519 GNNNGSGNSSGTTNNNSNNYNNKSISKKWEIDDGDDLNPTSITNN---TGLTNNNNSKSPA 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 GNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNST 89
                                                                                               90 IELTQNGFRNNATIDQWNAKNYDQLVTRVVTHEMAHANQTASDSSVMVRQVGFGNNAT 147
                                                                                                                               17 SALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.7%; Score 90.5; DB 6; Length 258; illarity 27.9%; Pred. No. 2.1; Conservative 15; Mismatches 39; Indels 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: MRT4577_37025C.1.pep
US-10-425-115-300390
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; OTHER INFORMATION: Clone ID: WRT4577_48027C.1.pep
US-10-425-115-312468
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Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: unsure at all Xaa locations FEATURE:
                                                                                                                                                                                                                                                                         Sequence 300390, Application US/10425115 GENERAL INFORMATION:
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; Sequence 312468, Application US/10425115
; GENERAL INFORMATION:
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Best Local Similarity
Matches 29; Conserv
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Best Local Similarity
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ORGANISM: Zea mays
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ORGANISM: Zea mays
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US-10-425-115-300390
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GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: 1899-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
                                                            GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
FILE REPERENCE: 0.2899-084
CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 1999-0.22
PRIOR APPLICATION NUMBER: US 08/978,878
FRICK PILING DATE: 1999-05-06
FRICK FILING DATE: 1999-05-06
FRICK FILING DATE: 1999-05-07
FRICK PILING DATE: 1999-05-04
FRICK PILING DATE: 1999-05-04
FRICK PILING DATE: 1999-11-06
FRICK PILING DATE: 1991-11-06
FRICK APPLICATION NUMBER: US 07/99,437
FRICK APPLICATION NUMBER: US 07/99,437
FRICK APPLICATION NUMBER: US 07/99,437
FRICK APPLICATION NUMBER: US 08/918,865
FRICK APPLICATION NUMBER: US 08/187,865
FRICK APPLICATION NUMBER: US 08/187,865
FRICK APPLICATION NUMBER: US 08/318,519
FRICK APPLICATION NUMBER: US 08/318,519
FRICK FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN VETSION 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GVVPQYGGGGNHGGGGNNSGPNSELNTYQYGGGNSALALQTDARNSDLTITQHGGGNGAD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.7%; Score 91; DB 5; Length 719; llarity 23.7%; Pred. No. 6.2; Conservative 25; Mismatches 59; Indels
                          Sequence 2, Application US/09741873C GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Candida albicans
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Best Local Similarity
Matches 87; Conserv
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Best Local Similarity
Matches 28; Conserv
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US-09-248-796A-17559
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; ORGANISM: Candid
US-09-248-796A-17559
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LENGTH: 719
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APPLICANT: EXELIXES, INC.

TITLE OF INVENTION: MAPCAXS AS MODIFIERS OF THE APC AND AXIN PATHWAYS AND METHODS OF TITLE OF INVENTION: USE
FILE REPERENCE: EXO4-003C-PC
CURRENT APPLICATION NUMBER: PCT/US04/02338
CURRENT APPLICATION NUMBER: D604/43,484
PRIOR APPLICATION NUMBER: US60/447,358
PRIOR PELING DATE: 2003-01-29
PRIOR PELING DATE: 2003-01-10
PRIOR PELING DATE: 2003-01-10
PRIOR PELING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: US60/461,789
PRIOR PELING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: US60/470,684
PRIOR APPLICATION NUMBER: US60/470,684
PRIOR PILING DATE: 2003-05-14
PRIOR PILING DATE: 2003-05-14
PRIOR PILING DATE: 2003-06-19
NUMBER OF SEQ ID NOS: 54
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PATENTIN VERSION 3.2
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APPLICANT' ADAMS, Mark

TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN

TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF

FILE REPERBACE: CL001381

CURRENT APPLICATION NUMBER: US/10/170,205E

CURRENT FILING DATE: 2002-06-13

NUMBER OF SEQ ID NOS: 40312

SOFTWARE: Patentin version 3.2

SEQ ID NO 741

LENGTH: 1203
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                                                                347 AGAGAAAAASAGAGAGAGGYGYGVAGGSS----ISYGATSSSATSSSTASSSRSGIVTSG 402
                                                                                                                                                                             403 GYGAGAAAGAGAGAGAGSYSG----SISRLSSA---EAVNRVSSNIGAVASGGASAL 454
                                                                                                                                     GYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVTHEMAHANQTASDS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
15 SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSET-TITQS 73
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11.7%; Score 90.5; Di
Best Local Similarity 28.4%; Pred. No. 13;
Matches 42; Conservative 16; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 741, Application US/10170205E; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                          455 PGVISNIFSGVSSSAGSY 472
                                                                                                                                                                                                                                                                       134 SVMVRQVGFGNNATANQY 151
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US-10-170-205E-741
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PCT-US04-02338-49
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Matches
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GENERAL INFORMATION:
APPLICANT: ADAMS, Mark
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
FILE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE REPERENCE: CL001381
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: Patentin version 3.2
SEQ ID NO 35551
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GENERAL INFORMATION:
APPLICANT: Bond A. Roth
APPLICANT: Randolph V. Lewis
APPLICANT: Randolph V. Lewis
TITLE OF INVENTION:
TITLE OF INVENTION EXPRESSION OF Spider Silk Proteins in Higher Plants
FILE REFERENCE: WYO. 02-0004US
CURRENT APPLICATION NUMBER: US/10/479,638
CURRENT FILING DATE: 2003-12-03
FRIOR APPLICATION NUMBER: FCT/US02/18256
FRIOR APPLICATION NUMBER: 6/296,184
FRIOR APPLICATION NUMBER: 6/296,184
FRIOR FILING DATE: 2001-06-06
FRIOR FILING DATE: 2001-06-06
FRIOR FILING DATE: 2001-06-06
FRIOR FILING DATE: 2001-06-06
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FRIOR FILING DATE: SOUNDESSION FOR FULL STANDARD: FASTER FASTER FASTER FASTER FASTER FOR FOR FOR FULL STANDARD: FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER FASTER 
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                                                                                                                                            138 YGGGGYSSGGGYSSG-GYAANGYGVGSGSGNYSNASGGGYSGS----DGYGNGAASGGYA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
                                                                           26 WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGA 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 90.5; DB 6; Length 299;
; Pred. No. 2.5;
16; Mismatches 61; Indels 2:
              44; Indels
              Mismatches
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Best Local Similarity 28.4%;
Matches 42; Conservative 1.
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              29; Conservative
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US-10-170-205E-35751
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Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
US-10-170-205E-35751
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SNGTH: 299
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US-10-479-638-21
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LENGTH: 520
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PCT-USO4-21492-88
Sequence 88, Application PC/TUSO421492
Sequence 88, Application PC/TUSO421492
GENERAL INFORMATION:
APPLICANT: Steer, Brian
APPLICANT: Callen, Walter
APPLICANT: Callen, Walter
APPLICANT: GLOCANASES, NUCLEIC ACIDS ENCODING THEM AND METHODS FOR MAKING AN TITLE OF INVENTION: GLUCANASES, NUCLEIC ACIDS ENCODING THEM AND METHODS FOR MAKING AN TITLE OF INVENTION: THEM
TITLE OF INVENTION: THEM
TITLE OF INVENTION: THEM
TITLE DATE: 2004407-20
CURRENT RELING DATE: 2004-07-20
PRIOR FILING DATE: 2003-07-20
PRIOR FILING DATE: 2003-07-20
NUMBER OF SEQ ID NOS: 518
SOFTWARE: Patent In version 3.1
                                                                                                              9
                                                                                                                                                                                                                                                                      54 NAALALQSDARKSETTITQ-----SGYGNGADVGQGADNSTIELT-QNGFRNNATIDQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 IVVNGQTRQAENQSVNTGVWANNQCGGSGNSEWLHCNGYISFGNVSGSSSSSSSSSSSSSSS 420
                                                                                                                                                        30 GNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNST 89
                                                                                                                                                                                                                                             ---FRNNATIDQWNAKNYDQL-VTRVV--THEMAHANQTAS-DSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 IVVSG-----SALAGVVP--QWGGGGN----HNGG----GNSSGPDSTLSIYQYGSA
                                                                                                           29;
                                                                                                                                                                                  ; Score 85; DB 1; Length 535;
; Pred. No. 15;
19; Mismatches 62; Indels
                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Obtained from an environmental sample.
                                                             Score 85.5; DB 5;
Pred. No. 9.4;
16; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 WNAKNYDOLVTRVVTHEMAHANQTASDSSVMVRQVG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 WGVSNFTGRTISV-----TVNGSGTAVTTIG 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Syngenta Participations AG APPLICANT: Sainz, Manuel APPLICANT: Salmeron, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-491-733-2; Sequence 2, Application US/10491733; GENERAL INFORMATION:
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Best Local Similarity 27.9%;
Matches 38; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 11.0%;
Best Local Similarity 25.0%;
Matches 39; Conservative 15
                                                                                                                                                                                                                                                                                                                                 136 MVRQVGFGNNATANQY
; ORGANISM: Candida albicans
US-09-248-796A-17306
                                                                                                                                                                                                                                             90 IELTQNG---
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; NAME/KEY: SIGNAL
; LOCATION: (1)...(27)
PCT-US04-21492-88
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ORGANISM: Unknown
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GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR PILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 301334, Application US/10425115
GRNERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Con, Yongwei
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 301334
LENGTH: 256
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                                                                                                                                                                                65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
                                                                                                                                                                                                                                                                                       ----- DVSRVKRLVDA--- 204
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                                                                                                              29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21; Gaps
                                                                 Length 1327;
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Best Local Similarity 27.9%; Pred. No. 2.6;
Matches 29; Conservative 14; Mismatches 40; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 SGYGNGAD------VGQGADNSTIEL--TQNGFRNNATID 104
                                                                                                           Indels
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                                                                                                           61;
                                                             Query Match 11.7%; Score 90.5; DB 1; Best Local Similarity 28.4%; Pred. No. 14; Matches 42; Conservative 16; Mismatches 61;
                                                                                                                                                                                                                                                                                     158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: MRT4577_37894C.1.pep
US-10-425-115-301334
                                                                                                                                                                                                                                                                                                                                                                           ----ANVNAKDMAGRKSSPLHFAAGFG 227
  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Zea mays
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US-10-425-115-301334
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US-09-248-796A-17306
    ; OKGANISH: 11000-
PCT-US04-02338-49
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LENGTH: 388
TYPE: PRT
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                                                St
APPLICANT: Weislo, Laura J.

TITLE OF INVENTION: Nucleic Acid Molecules from Rice Encoding Proteins for Abiotic STITLE OF INVENTION: Resistance, Yield, Disease Resistance and Nutritional Quality & FILE REFERENCE: 60127WOPT.

CURRENT APPLICATION NUMBER: US/10/491,733

CURRENT PILING DATE: 2004-04-05

PRIOR APPLICATION NUMBER: 60/334,501

PRIOR PILING DATE: 2001-11-30

NUMBER OF SEQ ID NOS: 64

SOFTWARE: PATENTIN VERSION 3.1
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| Sequence 346132, Application US/10425115
| Sequence 346132, Application US/10425115
| GENERAL INFORMATION: Thomas J.
| APPLICANT: Evalic, David K.
| APPLICANT: Cao, Yongwei
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Multiple Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucleic Nucl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 SALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQS--DARKSETTITQSG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 SALAG-----GGGG--GGGGGGGGGKD-----FGSMAMDELLRSIWTAEESQAMASASG 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Gaps
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10.8%; Score 84; DB 6; Length 376;
Best Local Similarity 31.5%; Pred. No. 12;
Matches 34; Conservative 15; Mismatches 39; Indels
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US-10-491-733-2
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Matches 28; Conserv
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ORGANISM: Zea mays
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LENGTH: 179
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LENGTH: 376
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APPLICANT: Munyikwa, Tichifa R. I.
APPLICANT: Roberts, James K.
APPLICANT: Roberts, James K.
APPLICANT: Waw, Wei
APPLICANT: Any, Bei
TITLE OF INVENTION: Compositions Thereof
TITLE OF INVENTION: Compositions Thereof
FILE REFERENCE: 38-21(53403) B
CURRENT APPLICATION NUMBER: US/60/565,632
CURRENT FILING DATE: 2004-04-27
NUMBER OF SEQ ID NOS: 15449
SOFTWARE: Patentin version 3.2
SEQ ID NO 7907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 AAADNNGSADAA-----QGNDNRAAAENNANADAQTDAAQ-GSANEANAENNANADAQND 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 ARKSETTITQSGYGNGADVGQGADN-STIELTQN----GFRNNATID------QMNAK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209 AAQANDNGAAAENNGNADAAQGTDNEAAAENSGNENGTGAENNANADAQTDVAQGSTNEA 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 AAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 NAENNANADVQNDAAQANENGAAAENSGNADAAQGTDNGAAA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 NYDOLVTRVVTHEMAHANO---TASDSSVMVRQVGFGNNATA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
10.8%; Score 83.5; D
Best Local Similarity 27.8%; Pred. No. 22;
Matches 45; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2, 2004, 15:29:54
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TYPE: PRT
ORGANISM: Diabrotica virgifera
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Job time : 17.8 secs
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(0108N) YUD18 860d 5141

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 2, 2004, 14:39:53 ; Search time 9.4 Seconds (without alignments) 1545.204 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-543-407-24 775 1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

PIR 78:\*
1: Dirl:\*
2: Dir2:\*
3: Dir3:\*
4: Dir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	fimbrin protein ag	major curlin chain	curlin protein csg	curlin major subun	hypothetical prote	hypothetical prote	cnjB protein - Tet	fimbrin protein ag	nucleation compone	n nucl		nor	probable PPE prote	10	ng pr	ovo protein - frui	conserved hypothet	hypothetical prote	merozoite 45K surf	glycine-rich prote	tail fiber protein	F3F19.21 protein -	hypothetical glyci	NA-bind	sin (	leishmanolysin (EC	eishmanolysin (	shmanolysin (	leishmanolysin (EC
SUMMARIES	ΩI	JC6039	AI0635	S70788	D90806	H85665	T20847	842136	JC6040	AH0635	S70787	290806	G85665	D70604	AD1539	A56038	S16356	AD3143	H98144	B39112	T03371	800275	C86266	E95965	A47369	A45621	B42049	A44951	22	91
	DB	73	N	N	~	~	0	7	~	~	7	7	7	N	7	~	7	7	(7)	Ø	8	N	73	7	7	Н	7	0	-	Н
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	Result No.		2	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

	CT147 hypothetical	conserved hypothet	probable disease r	probable PPE prote	probable secreted	protein C05B5.3 [i	protein kinase sgg	hypothetical prote	hypothetical prote	probable sugar ABC	hypothetical prote	hypothetical prote	hemolysin [importe	leishmanolysin (EC	hypothetical prote	probable outer mem
	F86509	C81558	G84687	F70675	T35789	C88571	835327	866852	A83401	AC1182	H71607	T19581	AI0452	C42049	T05221	F90892
	7	(1)	~	7	~	N	7	(1	0	7	7	C)	~	N	N	0
	1537	1537	447	582	438	401	575	196	340	439	764	423	1635	639	343	382
	11.2	11.2	11.1	11.1	11.0	11.0	11.0	11.0	10.9	10.8	10.8	10.8	10.8	10.7	10.6	10.6
12.5	87	87	86	.86	85.5		85	82	84.5	84	.84	83.5	83.5	83		82
	30	31	32	33	34	35	36	37	38	თ ო	40	41	42	43	44	45

## ALIGNMENTS

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Gaps

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Indels

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A)Description: major component of wild-type curli, interaction between CsgA and CsgB A;Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli th and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers Fi-20(Domain: signal sequence #status predicted <SiG>F:21-151/Product: curlin #status experimental <MAT>
A,Title: The RpoS sigma factor relieves H-NS-mediated transcriptional repression of A,Reference number: S31202, MUID:93211294, PMID:8459772 A,Accession: S31202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 curlin major subunit CsgA [imported] - Escherichia coli (strain O157:H7, substrain R C;Species: Bscherichia coli (c)Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C;Accession: D90806 R; Advanti, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishli, K.; Yokoyama, K.; Han, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res 8, 11-22, 2001 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and (A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                             A; Molecule type: DNA
A; Residues: 1-6, V', 8-151 < OLS1>
A; Accession: S34560
A; Accession: S34560
A; Accession: S44540
A; Accession: S44540
A; Residues: 21-42; 44-50 < OLS2>
B; Olsen, A.N.; Arnqvist, A.M.
Submitted to the EMBL Data Library, October 1992
A; Reference number: S34559
A; Molecule type: DNA
A; Residues: 1-133, RQRDSGWLW' < OLS3>
A; Residues: 1-133, RQRDSGWLW' < OLS3>
A; Residues: EMBL: L04979; NID: g290424; PIDN: AAA23616.1; PID: g290425
A; Experimental source: strain K-12, substrain W3110
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-152 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34843.1; PID:g13360880; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 151;
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llarity 68.4%; Pred. No. 4.6e-36;
Conservative 19; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.8%; Score 533; DB 2; 70.2%; Pred. No. 7.1e-38; iive 18; Mismatches 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY
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C; Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Simi
hes 106;
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Best Local Simi
Matches 104;
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NiAlternate names: csgA protein; major curlin protein
C;Specias: Escherichia coli
C;Date: 12-Peb-1998 #sequence revision 20-Peb-1998 #text_change 01-Mar-2002
C;Accession: S70788; G64846; S31202; S34560; S34559
R;Hammar, M.; Arnqvist, A.; Blan, Z.; Olsen, A.; Normark, S.

Mol. Microbiol. 18, 661-670, 1995
A.Title: Expression of two csg operons is required for production of fibronectin- and CA;Recession: S70788; MUID: 96414468; PMID: 8817489
A;Accession: S70788
A;Accession: S70788
A;Accession: S70788
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A;Accession: S70788
A;Accession: BMB:X90754; NID: 91147558; PIDN: CAA62282.1; PID: 91147564
A;Accession: Sanduce: EMB:X90754; NID: 91147558; PIDN: CAA62282.1; PID: 91147564
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                                                                                                                                                                                           major curlin chain precursor [imported] - Salmonella enterica subsp. enterica serovar Typhi (;Species: Salmonella enterica subsp. enterica serovar Typhi (;Ancies: Salmonella enterica subsp. enterica serovar Typhi (;Ancies: Os-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 (;Accession: A10635 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 (;Arcession: A10635 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 (;Arcession: A10635 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 (;Arcession: A) Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronnin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; OʻGaora, P.
Nature 413, 848-852, 2001
A,Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A,Athcher Complete genome sequence of multiple drug resistant Salmonella enterica serova A,Reference number: AB0502; MUID:21534947; PMID:11677608
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R;Olsen, A.; Arnqvist, A.; Hammar, M.; Sukupolvi, S.; Normark,
Mol. Microbiol. 7, 523-536, 1993
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Pred. No. 4.7e-51;
2; Mismatches 11
        NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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91.4%;
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Matches 138; Conserv
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A;Molecule type: DNA
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---SNQTNNESS--- 1722
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               -ATIDOWNAK 109
                                                192 YONNOGRHQGGGGHSSSSNSVMSNNGYSSNSGYGNNNGPTPSFLNNVSSSAAQDYYNIV 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----CQSNVQESTITSSGGWGSSGSGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
12.8%; Score 99; DB 2; Length 1748;
Best Local Similarity 28.0%; Pred. No. 3.1;
Matches 37; Conservative 16; Mismatches 31; Indels 4
                                                                                                              NNKSLTINGINEQ----ASNWASANSVQAQYIQYETNRSA 287
                                                                                     110 NYDOLVTRVVTHEMAHANQTASDSSVMVRQVGFGNNATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1686 QTGGGWGSNDN----QQQQNENTGGGGWGSSN---
                 YGN--GADVGQGADNSTIE---LTQNGFRNN
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                                                                                                                                                                    hypotherical protein csqA [imported] - Escherichia coli (strain O157:H7, substrain EDL93 C; Species: Escherichia coli C; Species: Escherichia coli C; Species: Escherichia coli C; Species: L6.Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C; Accession: H85665
R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew liler, L., Grotheck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Accession: H8565
A; Status: preliminary
A; Residues: DNA
A; Residues: L-152 <STO>
A; Cross-references: GB:AE005174; NID:g12514574; PIDN:AAG55788.1; GSPDB:GN00145; UWGP:216
C; Genetics:
C; Genetics: A; Gene: csgA
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A;Experimental source: clone F13E9
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F13E9.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Aug-2002
C;Accession: T20847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKLLKVAAIAAIVFSGSALAGVVPQYGGGGGNHGGGGNNSGPNSELNIYQYGGGGNSALAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.0%; Score 511.5; DB 2; Length 152; 68.4%; Pred. No. 4.6e-36; ive 19; Mismatches 28; Indels 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 GGNGAAVDQTASNSTVNVTQVGFGNNATAHQY 152
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                                                    120 THEMAHANQTASDSSVMVRQVGFGNNATANQY 151
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Matches 104; Conservative
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A,Introns: 32/1; 275/3; 337/3
C,Superfamily: loricrin
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Matches 37; Conservative
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A; Experimental source: strain K12, substrain W3110
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.A.; Rose, D.G.; Mau, B.; Shao, Y.
A;; Rose, D.G.; Mau, B.; Shao, Y.
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
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A;Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli that
and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers
F;1-21/Domain: signal sequence #status predicted <51G>
F;22-151/Product: minor curlin chain #status predicted <MAT>
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A;Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74125.1; PID:g1787278;
A;Experimental source: strain K-12, substrain MG1655
N;Alternate names: csgB protein; curlin nucleation component; minor curlin protein C;Species: Escherichia coli C;Datei 12-Feb-1998 #text_change 01-Mar-2002 C;Date 12-Feb-1998 #text_change 01-Mar-2002 C;Accession: S70787; F64846 R;Hammar, M.; Arngvist, A.; Bian, Z.; Olsen, A.; Normark, S. Mol. Microbiol. 18, 661-670, 1995 A;Telle: Expression of two csg operons is required for production of fibronectin- and A;Reference number: S70783; MUID:96414468; PMID:8817489
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-151 <HAM>
A;Cross-references: EMBL:X90754; NID:g1147558; PIDN:CAA62281.1; PID:g1147563
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A;Status: nucleic acid sequence not shown; translation not shown
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12.5%; Score 96.5; DB 2;
Best Local Similarity 25.6%; Pred. No. 0.31;
Matches 30; Conservative 24; Mismatches 46;
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.larity 25.6%; Pred. No. 0.31;
Conservative 24; Mismatches
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Best Local Similarity
Matches 30, Conserv
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                                                                                                                                                       C,Accession: JC6040

R;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.
J. Bacteriol. 178, 662-667, 1996

A;Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fimbriae.

A;Reference number: JC6039; MUID:96146512; PMID:8550497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Description: minor component of thin aggregative fimbriae
A,Note: fimbriae bind to fibronectin, plasminogen, tissue plasminogen activator C;Keywords: fimbria
F,1-21/Domain: signal sequence #status predicted <SIG>F,22-151/Product: fimbrin protein agfB #status predicted <MAT>
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                 imbrin protein agfB precursor - Salmonella enteritidis
Species: Salmonella enteritidis
Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999
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S70787
curlin nucleator protein csgB precursor - Escherichia coli (strain K-12)
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Matches 34; Conserv
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Page 5

OY 51 GSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQ 105	QY 64 RKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
Qy 106 WNAKNYDQLVTRVVTHEMAHANQTASDSSVMVRQVGFGNNATANQY 151 	Cy 121 HEMAHANQTASDSSVMVRQVGFGNNAT 147  Db 463DSGLTNSGFGNTGT 476
RESULT 12  G8565  Curlin minor chain precursor, CsgA homolog [imported] - Escherichia coli (strain O157:H7  C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001  C;Accession: G8565  B;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  B;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  B; Britle: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.  A;Reference number: A85480; MUID:21074935; PMID:11206551  A;Recession: G8566  A;Residues: 1-151 <sto> A;Cross-references: GB:AE005174; NID:g12514573; PIDN:AAG55787.1; GSPDB:GN00145; UWGP:Z16 C;Genetics: C;Genetics: A;Gene: csgB</sto>	RESULT 14 AD1539 probable sugar ABC transporter, periplasmic sugar-binding protein homolog lin0852 [impo C;Species: Listeria innocua C;Species: Listeria innocua C;Accession: AD1539 R;Glaser, P; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke.; Dominguez-Bernal, G.; Duchaud, E.; Durand, A.; Baquero, F.; Berche, P.; Bloecke.; Dominguez-Bernal, G.; Duchaud, E.; Durand, E.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U. Science 294, 649-9852, 2001 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M. A;Authors: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland A;Atlele comparative genomics of Listeria species. A;Reference number: AB1077; MulD:21537279; PMID:11679669 A;Residues: L-440 cdLA> A;Residues: L-440 cdL
Query Match  12.5%; Score 96.5; DB 2; Length 151;  Best Local Similarity 25.6%; Pred. No. 0.31;  Matches 30; Conservative 24; Mismatches 46; Indels 17; Gaps 4;  Qy 51 GSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIBLTQNGFRNNATIDQ 105  14 GAPGIAAAAGYDLANSENNEAVNEAKSSRYBAALIGQAGTNNSAQLSGGSSKLLAVVAQ 73	Abxperimental Bource: Strain Clipitzez A;Genetics: A;Gene: lino852 Query Match Best Local Similarity 23.8%; Bred. No. 2.3; Matches 39; Conservative 23; Mismatches 59; Indels 43; Gaps 5;
<b>.</b>	1 MKLLKVA-AFAAIVVSGSALAGVVPQWGGGRNHNGGGN
RESULT 13  D70604  probable PPE protein - Mycobacterium tuberculosis (strain H37RV)  C;Species: Mycobacterium tuberculosis  C;Date: 17-7ul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000  C;Date: 17-7ul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000  C;Accession: D70604  R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Comor, R.; Davises, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998  A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MulD:98295987; PMID:9614230	Db 57 AKAYEKENPDVTVEVSQMKESPSSEATIQSALASKTAPTMSENINRSFAAQLADSKAI-V 115  Qy 93 TQNGFRNNATIDQWNAKAYDQLVTRVVTHEMAHA 126  116 PLNDVKGLDDVVKERKMSETMDSWKFSDGNQYVLPVYSNPILFA 159  RESULT 15  A56038  DNA-binding protein ovo - fruit fly (Drosophila melanogaster)  C;Species: Drosophila melanogaster  C;Date: 0.Dec-1995 #sequence_revision 01-Dec-1995 #text_change 21-Jul-2000  C;Accession: A56038  R;Garfinkel_M.D.; Wang, J.; Liang, Y.; Mahowald, A.P.
377289	MOIL Cell. Diol. 14, 8027-8080, 1934 A;Title: Multiple products from the shavenbaby-cvo gene region of Drosophila melanogast A;Reference number: A56038, MUID:95021209; PMID:7935398 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-1028 <gar> A;Cross-references: GB:U11383; NID:g520526; PIDN:AAB60216.1; PID:g520527 C;Genetics:</gar>
Query Match Best Local Similarity 27.9%; Pred. No. 2.4; Matches 41; Conservative 11; Mismatches 58; Indels 37; Gaps 7;  Qy 15 SGSALAGVVPQWGGGNANGGRSGPDSTLSIYQYGSANAALALQSDA 63  Db 353 SGSGNIGVFNTGANTLVPGDLNNLGVGNSGNANIGFGNAGULNTGFGNASILNTGLG 409	A;Gene: ovo A;Cross-references: FlyBase:FBgn0003028 Query Match Query Match Best Local Similarity 26.7%; Pred. No. 5.9; Matches 40; Conservative 14; Mismatches 61; Indels 35; Gaps 6; Qy 3 LLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD 62

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2, 2004, 14:36:12; Search time 5.3 Seconds (without alignments) 1483.508 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

scription	P55225 salmonella P5327 escherichia Q827m3 salmonella P5526 ascherichia Q827m3 salmonella P5526 salmonella P5526 salmonella P5527 descherichia Q8271 homo sapien Q03646 plasmonia P03870 leishmania P15706 leishmania P63120 leishmania P63120 leishmania P63120 leishmania P63120 leishmania P6327 couter mem P3429 cachorhabdi Q03297 drosophila Q80429 chosophila Q80429 homo sapien P2662 pseudomonas Q0525 homo sapien P2674 oryza sativ Q47502 escherichia Q15241 drosophila Q1070 mycobacteri P07184 drosophila Q175780 escherichia Q475780 escherichia Q475780 escherichia P75780 erwinia her P20469 pantoea ana P16239 erwinia her
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1 PIMD ECOLI NPA3 HUMAN 1 FLGE_HELPJ 2 I FLGE HELPY 3 I FLGE HELPY 3 GG DROME MBN_DROME 1 YHC3 YEAST 1 YHC3 YEAST 1 YZ17 AQUAE 1 YZ17 AQUAE 1 I CEV FSESX 1 I CEV FSESX	ALIGNMENTS	reated) ast sequence update) ast sequence update) ast annotation update) cecursor (Fimbrin SEF17). OR STY1181 OR T1776.  ia, Gammaproteobacteria; monella.  STRAIN=SR-11; STRAIN=SR-11; Ad=9457880; mmar M., Sierralta W.D., mmar M., Sierralta W.D., mmar M., Sierralta W.D., y conserved between Salf espect to operon structu 71 (1998).	Heltz / SGSC1412 7609; X., Foler M., Cl id., Dante M., X., Holmes A., iiller W., Stone Salmonella ente Salmonella ente K.D., Thomson ntley S.D., Hol I., Chillingwort X.D., Hien T.T., X., Moule S., mmonds M., Skel a multiple drug; ATCC 700931; 4504; G. III, Mayhew G. III, Mayhew
79 10.2 878 78.5 10.1 718 78.5 10.1 718 78.5 10.1 1067 77 9.9 1146 77 9.9 1690 76.5 9.9 348		ITY 325; 525; 525; 527-1996 (Rel. 34, 0.007-1996 (Rel. 34, 1.007-1996 (R	J. Bacteriol. 180:722-731(1998).  [2] SEQUENCE FROM N.A. SPECIES=S.179phimurium; STRAIN=LTZ , MEDLINE=21534948; PubMed=11677609; MCClelland M., Sanderson K.E., Spicourtney L., Porvollik S., Ali J., Leomard's., Nguyen C., Scott K., H. Gromplete genome sequence of salmon "Complete genome sequence of salmon "Complete genome sequence of salmon "Complete genome sequence of salmon "Tal"; Nature 413:852-856(2001).  [3] Nature 413:852-856(2001).  [4] MEDLINE=21334947; PubMed=11677608; Parkhill J., Dougan G., James K.D., Churcher C., Mungall K.L., Bentley Barker S., Basham D., Brooks K., Churcher C., Mungall K.L., Bentley Barker S., Basham D., Brooks K., Churcher C., Mungall K.L., Bentley Barker S., Basham D., Brooks K., Churcher C., Mungall K.L., Bentley Barker S., Basham D., Brooks K., Simmond Whitchead S., Barrell B.G.; Leather S., Quail M.A., Rutherford K., Simmond Whitchead S., Barrell B.G.; Complete genome sequence of a multentica serovar Typhi CT18."; Nature 413:848-852(2001).  [4] Nature 413:848-852(2001).  [5] SEQUENCE FROM N.A. SPECIESES. Typhi; STRAIN=TY2 / ATCC MEDLINE=2531367; PubMed=12644504; Dung W., Liou SK., Plunkett G. I. Dung W., Liou SK., Plunkett G. I. Dung W., Liou SK., Plunkett G. I. Dung W., Liou SK., Plunkett G. I. Dung W., Liou SK., Plunkett G. I. Dung W., Liou SK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella enteritidis.";
J. Bacteriol. 173:4773-4781(1991)
-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN.
'Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECTES=S_enteritidis; STRAIN=27655-3B; MEDLINE=91310586; PubMed=1677357; Collinson S.K., Emoedy L., Mueller K.-M., Trust T.J., Kay W.W.; "Purification and characterization of thin, aggregative fimbriae from
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MEDLINE-S6746512, PubMed-8550497,
Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W.W.;
"Salmonella enteritidis agfBAC operon encoding thin, aggregative
                                                                                                                                                                                                                                                                                                                                                                                              SPECIESES.enteritidis; STRAIN=27655-3B; MEDLINE=94013373; PubMed=8104955; Doran J.L., Collinson S.K., Burian B.K., Sarlos G., Todd E.C.D., Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., Kay W.W.; "DNA-based diagnostic tests for Salmonella species targeting agfA, the structural gene for thin, aggregative fimbriae."; J. Clin. Microbiol. 31:2263-2273(1993).
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SVMVRQVGFGNNATANQY -> DSYTQVAS
REF. 6).
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B7DAC0D16B621359 CRC64;
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PIR; JC6039, JC6039.
StyGene; SG10608; csgA.
Finbria; Signal; Complete proteome.
SIGNAL 1 20 MAJOR CU
CHAIN 21 151 SYMYRQVG
                                                             Bacteriol. 185:2330-2337(2003)
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EMBL, AE008749; AAL20074.1; -.
EMBL, AL627269; CAD08268.1; -.
EMBL, AE016640; AA069399.1; -.
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SEQUENCE OF 21-31.

**A MEDLINE-91310586; PubMed=1677357;

**RA Collinson S.K., Emoedy L., Trust T.J., Kay W.W.;

**RT "Purification and characterization of thin, aggregative fimbriae from RT Salmonella entertidis.";

**RL J. Bacteriol. 173:4773-4781(1991).

**RL J. Bacteriol. 173:4773-4781(1991).

**C. I. FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES. CURLIN. AT GROWTH

C. TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mortomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T., Tagami H., Takemoto K., Wada C., Yamamoto Y., Anda Y., Saito N., Sano M., Horiuchi T., Tagami H., Takemoto K., Wada C., Yamamoto Y., Jaskb DNA sequence of the Escherichia coli K-12 genome Corresponding to the 12.7-28.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96414468; PubMed=8817489; Hammark S.; Arrqvist A., Bian Z., Olsen A., Normark S.; Expression of two csg operons is required for production of fibronectin- and congo red-binding curli polymers in Escherichia coli
                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
SEQUENCE PROM N.A.
MEDLINE=92211264; PubMed=8459772;
Olsen A., Arnqvist A.;
"The Rpos sigma factor relieves H-NS-mediated transcriptional repression of csgA, the subunit gene of fibronectin-binding curli in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-KI2 / MG1655;
MEDLINE-97426617; PubMed=9278503;
MEDLINE-97426617; PubMed 11, Bloch C.A., Perna N.T., Burland V. Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.,
                                                                                                                                                                          Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
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MEDLINE=99023873; PubMed=1357528;
MEDLINE=91023873; PubMed=1357528;
Arrayvist A., Olsen A., Pfeifer J., Russell D.G., Normark S.;
"The Crl protein activates cryptic genes for curli formation and fibronectin binding in Escherichia coli HB101.";
Mol. Microbiol. 6:2443-2452(1992).
                                                                  01-DEC-1992 (Rel. 24, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-PBS-2003 (Rel. 41, Last annotation update)
Major curlin subunit precursor.
CSGA OR B1042.
                                 151 AA.
                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli.";
Mol. Microbiol. 7:523-536(1993)
                                 STANDARD;
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SEQUENCE FROM N.A.
STRAIN=K12 / MC4100;
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                                                                                                                                                                Escherichia coli.
                                                                                                                                                                                                                    NCBI_TaxID=562;
RESULT 2
CSGA_ECOLI
ID _CSGA_ECOLI
AC P28307;
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NCBI_TaxID=601;
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                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformetics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=21218556; PubMed=11319125;
Uhlich G.A., Keen J.E., Elder R.O.;
"Mutations in the csgD promoter associated with variations in curli
expression in certain strains of Bscherichia coli 0157:H7.";
Appl. Environ. Microbiol. 67:2367-2370(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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7 7 A -> E (IN REF. 1).
AA; 15049 MW; C003470D208D395F CRC64;
  SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY
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EMBL; X90754; CAA62282.1; -.
EMBL; AB000255; AAC7426.1; -.
EMBL; D90741; BAA35832.1; -.
EMBL; D90742; BAA35840.1; -.
PTR; S70788; S70788.
EcoGene; EG11489; csgA.
Finbria; Signal; Complete proteome.
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28-FEB-2003 (Rel. 41, Last sequ
28-FEB-2003 (Rel. 41, Last anno
Major curlin subunit precursor.
CSGA OR Z1676 OR ECS1420.
Escherichia coli 0157:H7.
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SEQUENCE FROM N.A.
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Q93U24;
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P SEQUENCE FROM N.A.

STAIN=0157:H7 / RIMD 0509952;

CSTAIN=0157:H7 / RIMD 0509952;

RA Hayashi'T. Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., RA Hayashi'T. Makino E., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., RA Hayashi'T. Makino E., Sasakawa C., Ogasawara N., Tobe T., RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., RA Kuhara S., Shiba T., Hattori M., Shinagawa H.; Romplete genome sequence of enterchemorrhagic Escherichia coli RT "Complete genome sequence of enterchemorrhagic Escherichia coli RT "Complete genome comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001).

RI DNA Res. 8:11-22(2001).

CC "EDNERATURES BELOW 37 DEGRBES CELSIUS. CURLI CAN BIND TO TENTERCHEMORPHICE PREFERENTIALLY AT GROWTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLLKVAAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALAL
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MAJOR CURLIN SUBUNIT.
EE2D2D94DDE91243 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FIBRONECTIN. SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.0%; Score 511.5; DB 1 68.4%; Pred. No. 1.5e-36;
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Minor curlin subunit precursor.
Salmonella typhi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ā
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EMBL, AE005315; AAG55788.1; -.
EMBL, AP002554; BAB34843.1; -.
EMBL, F. D90806; D90806.
PIR, H85665; H85665.
Fimbria; Signal; Complete proteome.
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MEDLINE=21534947; PubMed=11677608;
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Best Local Similarity 68.45
Matches 104; Conservative
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Local Similarity
hes 34; Conserv
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CSGB_ECOLI
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                                                                                                                SEQUENCE FROM N.A.
STRAILE-TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.,
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                       J. Bacteriol. 185:2330-2337(2003).

-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBROMECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF CURLIN MONOMERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES=S.typhimurium, STRAIN=SR-11,
MEDLINE=98117058; PubMed=9457880;
Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;
"Curli fibers are highly conserved between Salmonella typhimurium and
Escherichia coli with respect to operon structure and regulation.";
J. Bacteriol. 180:722-731(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 GSANAALALQSDARKSE----TTITQSGYGNGADVGQ-GADNST-----IELTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAPGIATATNYDLARSEYNFAVNELSKSSFNQAAIIGOVGTDNSARVROEGSKLLSVISO
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Feltwell T., Hamlin N., Hague A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitchhead S., Barrell B.G.;
Woomplete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
MCBI_TaxID=602, 592;
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01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Minor curlin subunit precursor (Fimbrin SEF17 minor subunit).
CSGB OR AGFB OR STW1143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.7%; Score 98.5; DB 1; Length 151; 28.8%; Pred. No. 0.099; cive 17; Mismatches 48; Indels 19
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                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Mismatches
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EMBL; AE016840; AAO69400.1; -.
Fimbria; Signal; Complete proteome.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 GAPGIATATNYDLARSEYNFAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISQ
                                                               McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriol. 178:662-667(1996).
- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARCOLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES Senteritidis; STRAIN=27655-3B; MEDLINE=96146512; PubMed=950497; PubMed=950497; Collinson S.K., Clouther S.C., Doran J.L., Banser P.A., Kay W.W.; "Salmonella enteritidis agfBAC operon encoding thin, aggregative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli, and
Escherichia coli 0157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 151;
SPECIES=8.typhimurium, STRAIN=LT2 / SGSC1412 / ATCC 700720,
MEDLINE=21534948, PubMed=11677609;
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MINOR CURLIN SUBUNIT.
, COFC5430E6DD361D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.7%; Score 98.5; DB 28.8%; Pred. No. 0.099;
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01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Minor curlin subunit precursor.
CSGB OR B1041 OR Z1675 OR ECS1419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Z
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EMBL; AE008749; AAL20073.1; -.
EMBL; U43280; AAC43598.1; -.
FIR; JC6040; JC6040.
StyGene; SG10609; csgB.
Fimbria; Signal; Complete proteome.
Fimbria; Signal; Complete Proteome.
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NCBI_TaxID=562, 83334;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
SEQUENCE FROM N.A.
STRAIN=K12 / MC4100;
MEDLINE=9641466; PubMed=8817489;
MEDLINE=9641466; PubMed=8817489;
MEDLINE=9641466; PubMed=8817489;
"Expression of two csg operons is required for production of fibronectin- and congo red-binding curli polymers in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97061202; PubMed=8905232;
Oshima T., Abba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ishama T., Abba H., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIDEALZ / MG1658.
STRAIDEALZ / MG1658.
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arnqvist A., Olsen A., Normark S.;
"Sigma S-dependent growth-phase induction of the csgBA promoter in Escherichia coli can be achieved in vivo by sigma 70 in the absence of the nucleoid-associated protein H-NS.";
Mol. Microbiol. 13:1021-1032(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=21074935, PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rosefai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N. W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.", DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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MEDLINE=95157246; PubMed=7854117;
                                                                                                                                        Mol. Microbiol. 18:661-670(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 GSANAALALQSDARKSE----TTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 EGSSNRAK-IDQIGDYNLAYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mevel-Ninio M.T.M., Terracol R., Kafatos F.C.;

"The ovo gene of Drosophila encodes a zinc finger protein required floor ovo gene of Drosophila encodes a zinc finger protein required floor female germ line development.";

-I. FUNCTION: REQUIRED FOR SURVIVAL AND DIFFERENTIATION OF FEMALE GERM LINE CELLS. PLAYS A ROLE IN GERM LINE SEX DETERMINATION.

-I. SUBCELULAR LOCATION: NUCLEAR (POCENTIAL).

-I. DEVELOPMENTAL STAGE: FIRST APPEARS IN THE GERMARIUM AND ACCUMULATES IN UNRASE CELLS DURING OCCENESIS. STORED IN THE EGG, BUT, IS RAPIDLY LOST IN THE EMBRYOS EXCEPT FOR ITS CONTINUED PRESENCE IN THE GERM LINE PRECURSOR POLE CELLS.

-I. SIMILARITY: Contains 4 C2H2-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---MVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Ovary;
MEDLINE=95021209; PubMed=7935338;
MEDLINE=95021209; PubMed=7935338;
MAICHINES M.D., Wang J., Liang Y., Mahowald A.P.;
"Multiple products from the shavenbaby-ovo gene region of Drosophila melanogaster: relationship to genetic complexity.";
Mol. Cell. Biol. 14:6809-6818(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     17;
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                           Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                            MINOR CURLIN SUBUNIT.
B18D266B964014B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 46;
                                                                                                                                                                                                                                                                                                                                                                                                           12.5%; Score 96.5; DB 1; 25.6%; Pred. No. 0.15; ive 24; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 WNAKNYDQLVTRVVTHEMAHANQ--TASDSSV-----
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P51521; G9XZU4;
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                             PIR; C90806; C90806.
PIR; G85665; G85665.
PIR; S70787; S70787.
PICGene; EG12621; csg8.
Fimbria; Signal; Complete proteome.
SIGNAL
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MEDLINE-91293102; PubMed=1712294;
                                                                                                        EMBL, X90754; CAA62281.1; -.
EMBL, AE00205; AAC74125.1; -.
EMBL, D90741; BAA35831.1; -.
EMBL, AE002315; AAG55787.1; -.
EMBL, AP002554; BAB34842.1; -.
                                                                                                                                                                                                                                                                                                                                                                     15882 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                     151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 ARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVTHE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GGNGYINCGGVG-GPNNS---LDGNNLLNFASVSNYNESN----SKFHNHH 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD
                                                                                                                                                       FlyBase; FBG00001028; ovo.
InterPro; IPR007087; Znf C2H2.
End: FPC00096; Zf C2H2; SM00355; Znr C2H2; 4.
PROSITE; PS00028; ZINC FINGER C2H2 1; 3.
PROSITE; PS05017; ZINC FINGER C2H2 2; 3.
Zinc-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein; Transcription regulation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.9%; Score 92.5; DB 1; 26.7%; Pred. No. 2.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 MAHA----NQTASDSSVMVRQVGFGNNATA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | : | : | : HHHQHNNNNNNNGGQTSMMGHPFYGGNPSA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Mismatches
                                                                        EMBL; X59772; CAB36921.1; ALT_SEQ. PIR, A56038; A56038.
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1028 AA;
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Best Local Similarity
Thes 40; Conserve
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ZN_FING
CONFLICT
SEQUENCE
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ac numen telomeres.";

Mol. Cell. Biol. 22:332-342(2002).

1. FUNCTION: May regulate vesicle trafficking and modulate the subcellular distribution of SLC244/GLUT4-vesicles. Has PARP activity and can modify TRF1, and thereby contribute to the activity and can modify TRF1, and thereby contribute to the regulation of telomere length.

1. CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribosy1}(N)-acceptor = nicotinamide + {ADP-D-ribosy1}(N+1)-acceptor = nicotinamide + {ADP-D-ribosy1}(N+1)-acceptor = nicotinamide + ADP-D-ribosy1}(N+1)-acceptor = nicotinamide + ADP-D-D-ribosy1}(N+1)-acceptor = nicotinamide + ADP-D-ribosy1}(N+1)-acceptor = nicotinamide + nicotinamide + ADP-D-ribosy1}(N+1)-acceptor = nicotinamide + nicotinamide + nicotinamide + nicotinamide + nicotinamide + nicotinamide + nicotinamide + nicotinamide + nicotinamide + nicotinamide + nicotinamide + nicotinamide + nicotinamide + nicotinamide + nicotinamide + nicotinamide + nicotinamide + nicotinamide + nicotinamide + nicotinamide
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Cook B.D., Dynek J.N., Chang W., Shostak G., Smith S.;
"Role for the related poly(ADP-Ribose) polymerases tankyrase 1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION, AND PHOSPHORYLATION.
MEDLINE=20556282; PubMed=10989299;
Chi N.-W., Lodish H.F.;
"Tankyrase is a Golgi-associated mitogen-activated protein kinase substrate that interacts with IRAP in GLUT4 vesicles.";
J. Biol. Chem. 275:38437-38444(2000).
                                                                                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith S., Giriat I., Schmitt A., de Lange T.; "Tankyrase, a poly(ADP-ribose) polymerase at human telomeres."; Science 282:1484-1487(1998).
Tankyrase 1 (EC 2.4.2.30) (TANK1) (Tankyrase I) (TNKS-1) (TRF1-interacting ankyrin-related ADP-ribose polymerase).

TNKS OR TNKS1 OR TIN1 OR TINF1 OR PARPL.

Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by MAPK kinases.
PTM: ADP-ribosylated (-auto).
SIMILARITY: Belongs to the PARP family.
SIMILARITY: Contains 15 ANK repeats.
SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
                                                                                                                                                                                                                                   Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
TISSUB=Testis;
MEDLINE=99040105; PubMed=9822378;
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MEDLINE=99454782; PubMed=10523501;
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                                                                                                           SEQUENCE FROM N.A.
MEDLINE-91156685; Pubmed=2000383;
Smythe J.A., Coppel R.L., Day K.P., Martin R.K., Oduola A.M.J.,
Kemp D.J., Anders R.F.;
"Structural diversity in the Plasmodium falciparum merozoite surface
                                                                                                                                                                                                          (Potential).
                                                                                                                                                                                        (POTENTIAL). (POTENTIAL). (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                    Plasmodium falciparum (isolate Nig32 / Nigeria).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.6%; Score 90; DB 1; Length 347; 24.3%; Pred. No. 1.3; ive 16; Mismatches 71; Indels
                                                                                                                                                           antigen 2.",
Proc. Natl. Acad. Sci. U.S.A. 88:1751-1755(1991).
-!- FUNCTION: May play a role in the merozoite attachment
                                                                                                                                                                                                                                                                                                                                   InterPro; IPR01136; MSA_2.
Pfam; PF00985; MSA_2; 1.
Malaria; Membrane; Glycoprotein; Antigen; Signal; Repeat; SIGNAL .
                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
MERGACITE SURFACE ANTIGEN 2.
HYDROPHOBIC, REMOVED DURING I (BY SIMILARITY).
POLYMORPHIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABCF24BB560BF537 CRC64;
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N-LINKED (GLCNAC.
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(GLCNAC.
                      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Merozoite surface antigen 2 precursor (MSA-2)
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22 N-
22 N-
224 N-
226 N-
320 N-
321 N-
33786 MM,
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Best Local Similarity 24.3%
    STANDARD;
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347
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347 AA;
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H->A: LOSS OF ACTIVITY, WHEN ASSOCIATED
WITH A-1291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASSOCIATED
                                                                                           MIM; 603303; -. Golfnomosome, telomeric region; IDA. GO; GO:0000781; C:chromosome, telomeric region; IDA. GO; GO:0003515; F:MAD ADP-ribosyltransferase activity; IDA. GO; GO:0005515; F:protein binding; IPI. GO:0007004; P:telomerase-dependent telomere maintenance; NAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 1327;
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Missing (in isoform 2).
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113.
114.
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EMBL, AF082558; AAC79843.1; -.
EMBL, AF082559; AAC79844.1; -.
HSSP, Q00420; LAWC.
Genew; HGNC:11941; TNKS.
MIM; 603303; -.
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122 AGNGAGNGAGNGAGNGAGNGAGNGAGNGAGNGAGNGAVASAGNGAVAERSSSTPATTTT 181 AGNGAVASAGNGAGNGAGNGAGNGAGNGAG-------NGAGNGA---GNGAGNG ETTITQSGYGNGA--DVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQ-----LVTR Ā 262 PRT; STANDARD; RESULT 10 VG38\_BPT2 ID VG38\_BPT2 AC P07875;

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RESULT 9 MSA2\_PLAF2

Gaps

28;

MATURATION

to the

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SEQUENCE FROM N.A.
MEDLINE=90205976; PubMed=2320059;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 GGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGAD 86
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                                                                                                                                                                                                                             MEDLINES READ N.A.

MEDLINES STABLI; PubMed=3302276;

Ridde I., Drexler K., Eschbach M.L., Henning U.;

Ridde I., Drexler K., Eschbach M.L., Henning U.;

"DNA sequence of genes 38 encoding a receptor-recognizing protein of bacteriophages T2, K3 and of K3 host range mutants.";

J. Mol. Biol. 194:31-39(1987).

-!- FUNCTION: Vg38 is at the tip of the long tail fibers and serves as the phage recognition site for the cellular receptor.

-I. MISCELLANEOUS: THIS PHAGE USE OUTER MEMBRANE PROTEINS OMPF AND TTRAS RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Gaps
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MEDLINE=22107220; PubMed=1762629;
MEDLINE=22107220; L.L., McMaster R.W.;
"Heterogeneity of the genes encoding the major surface glycoprotein of Leishmania donovani.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GP63_LBIDO STANDARD; PRT; 590 AA.
P23223;
D1-NOV-1991 (Rel. 20, Last sequence update)
O1-NOV-1991 (Rel. 20, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
                                                                                                                     Bacteriophage T2.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
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25801 MW; 0567366918F6C745 CRC64;
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  01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-AUG-1990 (Rel. 15, Last annotation update)
Receptor recognizing protein (Protein Gp38).
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InterPro; IPR007932; Tail_fibre_GP38.
Pfam; PF05268; GP38; 1.
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Best Local Similarity 34.43
Matches 32; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262 AA;
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                                                                                                                                                            T4-like viruses.
NCBI_TaxID=10664;
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SEQUENCE 262
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MESCPS; PO8148; LLUL.

DR MESCPS; MO8.001;
DR OMESCPS; MO8.001;
DR InterPro; IPRO01657; Peptidase_M8.

DR FARM; PPO1457; Peptidase_M8.

DR PRINTS; PRO0782; LSHAMADINES.

DR PRO0172; DSTOC PROTEASE; 1.

DR PRO0172; PRO0782; LSHAMADINES.

DR PRO0172; PRO0182; LSHAMADINES.

DR PRO0172; PRO0782; LSHAMADINES.

NW Aydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc;

NW Aymogen; Signal; Cell adheelon; GPI-anchor; Lipoprotein.

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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
                                    P1' and basic residues at P2 and P3'. A model nonapeptide is cleaved at -Ala-Tyr-|-Leu-Lys-Lys-...COFACTOR: Binds 1 zinc ion per subunit (By similarity)...: SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor... SIMILARITY: Belongs to peptidase family M8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (BC 3. 4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
CATALYTIC ACTIVITY: Preference for hydrophobic residues at P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M60048; AAA29244.1; -. HSSP; P08148; 1LML.
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STANDARD;

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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania
KII TaxID=5664;
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                                                                         P08148; P15906;
01-AUG-1988 (Rel. 08, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 101-123.
MEDLINE-88154764; PubMed=3346625;
Button L.L., Andaster W.R.;
"Molecular cloning of the major surface antigen of leishmania.";
J. Exp. Med. 167:724-729(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91009116; PubMed=2145267; Schneider P., Ferguson M.A.J., McConville M.J., Mehlert A., Schneider P., Ferguson M.A.J., McConville M.J., Mehlert A., Structure of the glycosyl-phosphatidylinositol membrane and the Leishmania major promasiigote surface protease."; J. Biol. Chem. 265:16955-16964(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Button L.L., McMaster W.R.;
J. Exp. Med. 171:589-589(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proteins 22:58-66(1995)
                                                                                                                                                                                                                                     Leishmania major
                                                                                                                                                                                                endopeptidase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  major."
                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                        Wilson M.E., "Three distinct RNAs for the surface protease gp63 are differentially
                                                                                                                MEDLINE=92112918; PubMed=1370484;
Ramamoorthy R., Donelson J.E., Paetz K.E., Maybodi M., Roberts S.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIVATION PEPTIDE.
LEISHYANOLYSIN.
ENGOVED IN MATURE FORM (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
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Miller R.A., Reed S.G., Parsons M.;
"Leishmania gp63 molecule implicated in cellular adhesion lacks
Arg-Gly-Asp sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR001577; Peptidase_M8.
Pfam; PF01457; Peptidase_M8.
PROSTE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Prosite; Metalloprotease; Glycoprotein; Metal-binding; Zinc; Zymogen; Signal; Cell adhesion; GPI-anchor; Lipoprotein.
39 POTENTIAL.
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Pred. No. 4.4;
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746730AE8E2A2E7C CRC64;
                                      Arg-Gly-Asp sequence."; Mol. Biochem. Parasitol. 39:267-274(1990).
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89.5%;
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membrane anchor of

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                                                                                                                                                                                                                                                                -!- FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.
-!- CATALYTIC ACTIVITY: Preference for hydrophobic residues at Pl and Pl', and basic residues at P2 and P3'. A model nonapeptide is cleaved at -Ala-Tyr-|-Leu-Lys-Lys-.
-!- CORACTOR: Binds 1 zinc ion per subunit.
-!- SUBGELLUIAR LOCATION: Attached to the membrane by a GPI-anchor.
-!- PTM; THE PHOSPHATIDYLINOSITOL MOIETY OF THE GPI-ANCHOR CONTAINS A FULLY SATURATED, UNBRANCHED 1-O-ALKYL CHAIN (MAINLY C24:0) AND A MIXTURE OF FULLY SATURATED UNBRANCHED 2-O-ACYL CHAINS (C12:0, C14:0, C16:0, AND C18:0).
                                  MEDLINE=98416698, PubMed=9739094,
Schlagenhauf E., Etges R., Metcalf P.,
"The crystal structure of the Leishmania major surface proteinase
Leishmanolysin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Belongs to peptidase family M8.
X-RAY CRYSTALLOGRAPHY (1.86 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, Y00647; CAA68673.1; -. PIR; PL0221; PL0221. PDB; 1LML; 17-SEP-97. MEROPS; M08.001; -.
                                                                                                                                                                                                                             Structure 6:1035-1046(1998)
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Gaps

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Mismatches

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Similarity

108 AKNYDQLVTRVVTHEMAHA 126 ASRYDQLVTRVVTHEMAHA 266

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Gaps
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Length 602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            63953 MW; 982EF3245D87C43E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.2%; Score 87; DB 189.5%; Pred. No. 4.5; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 AKNYDQLVTRVVTHEMAHA 126
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602 AA;
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InterPro; IPR006025; Pept M Zn BS.

InterPro; IPR001577; Peptidase_M8.

Refam; PR01457; Peptidase_M8: 1.

Refam; PR01457; Peptidase_M8: 1.

Refam; PR0142; ZINC_PR0TBASE; 1.

Refaciase; Metalloprotease; Glycoprotein; Metal-binding; Zinc;

M ydxodase; Metalloprotease; Glycoprotein; Metal-binding; Zinc;

M ydxodase; Metalloprotease; Glycoprotein; Metal-binding; Zinc;

M Zymogen; Signal; Cell adhesion; GPI-anchor; 3D-structure; Lipoprotein.

T ROPEP 40 10 10 ACTIVATION PEPTIDE.

T CHAIN 101 577 LEISHWANDLYSIN.

T ROPEP 578 602 REMOVED IN MATTRE FORM.

T MATTAL 264 264 ZINC (CATALYTIC).

T ACT SITE 265 268 ZINC (CATALYTIC).
                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
GPI-anchor amidated asparagine.
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NCBI_TaxID=35790;
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                                                                                                                              Uchiyama T.;
                                                                                                                                                    japonica.";
                                                                                                                    STRAIN=YH;
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                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMB. outstainnthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mol. Biochem. Parasitol. 57:31-46(1993).
-!- FUNCTION: Has an integral role during the infection of macrophages
in the mammalian host.
                             CATALYTHIS ACTIVITY: Preference for hydrophobic residues at P1 and P1' and basic residues at P2 and P3'. A model nonapeptide is cleaved at -A1a-Tyr-|-Leu-Lys-Lys-
COFACTOR: Binds 1 zinc ion per subunit (By similarity).

DEVELOPMENTAL STAGE: Expressed in both the promastigote and the
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                                                                                                                                                                                                                                                                                       PRINTS; PR00782; LSHWANOLYSIN.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc; Zymogen; Signal; Cell adhesion; Multigene family.
1 39 POTENTIAL.
PROPEP 40 102 ACTIVATION PEPTIDE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                     LEISHMANOLYSIN CI.
ZINC (CATALYTIC) (BY SIMILARITY)
BY SIMILARITY:
ZINC (CATALYTIC) (BY SIMILARITY)
ZINC (CATALYTIC) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                          ACTIVATION PEPTIDE (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
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                                                                                  amastigote forms.
-!- SIMILARITY: Belongs to peptidase family M8.
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Last annotation update)
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InterPro; IRR006025; Pept M_Zn BS.
InterPro; IPR001577; Peptidase_M8.
Pfan; PP01457; Peptidase_M8, 1.
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PIR; S19916; S19916.
HSSP; PO8148; 1LML.
MEROPS; MO8.001; -
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llarity 89.5%;
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(Rel. 40, I
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646 AA;
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AC O06653;
DT 30-MAY-2000 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---TLTLGGANIISANGGTINFQANGGTIKLTST--QNNIVVDCDLAIATDQ--TGVVDA 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: THE 32 KDa BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR (By similarity).
-!- SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a S-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 VAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GAÁLQSITLANDÁTK
Outer membrane protein B precursor (168 kDa surface-layer protein) (Surface protein antigen) (Cell surface antigen 5) (Sas5) (TompB) (Tomp B) (Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptidel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   'Sequencing of the gene encoding the protein rOmp B of Rickettsia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (By
                                                                                                                                                              Rickettšia japonica.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 kDa SURFACE-EXPOSED PROTEIN.
32 kDa BETA PEPTIDE.
POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          layer with hexagonal symmetry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2%; Score 87; DB 1; Length 1656; 6%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    628
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CHAIN 1 1338
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EMBL; AJ000514; CAAA4151.1; -.
NON TER: 152 ... MM. 918714606 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmoneila typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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Last sequence update)
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Pred. No. 2e-46;
3; Mismatches 1
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                                                Q89JIS
Q88HG0
Q7Z8HG0
Q8HIV1
Q8HIV1
Q9NGF6
Q9NGF7
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01-JAN-1998 (TrEMBLrel. 0
01-DEC-2001 (TrEMBLrel. 1
AgfA protein (Fragment).
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Best Local Similarity 90.1
Matches 136; Conservative
 PRELIMINARY;
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11222
12222
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Q80w63 escherichia
Q95355 enterobacte
Q95355 escherichia
Q86ih4 shewanella
Q86ih3 shewanella
Q19403 bradyrhizob
Q19403 bradyrhizob
Q7x238 enterobacte
Q89ii3 bradyrhizob
Q89ii3 bradyrhizob
Q89ii3 bradyrhizob
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Q7x243 citrobacter
Q7x240 citrobacter
                                                                                                                                  (without alignments)
1604.150 Million cell updates/sec
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775
1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY
                                                                                                                2, 2004, 14:39:17 ; Search time 29.7 Seconds
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                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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07X238
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07X243
07X240
08CW63
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08EIH4
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08UH38
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sparchea:*
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sp.manal:*
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Match Length DB
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Post-processing:

Database

Minimum DB : Maximum DB :

score:

Sequence:

OM protein

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Scoring table:

Gaps

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121 HEMAHANQTASDSSVMVRQVGFGNNATANQY 151

61

Score

27X243;

Q7X243 RESULT 2 Q7X243

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61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAXNYDQLVTRVVT 120
                                                                  SDARKSDVTITOHGRGNGAVVGOGADDSTISLKOTGFONSATIDOWNAKNADISVTOFGG 118
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STRAIN=06:HJ / CFT073 / ATCC 700928;
MEDLINE=2138824; FubMed=12471157;
MEDLINE=2238824; FubMed=12471157;
MELOR R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhaw G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Escherichia.
MCBI_TaxID=217992;
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae, Enterobacter.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Last annotation update)
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STRAIN=Fec39;
Zogaj X., Bokranz W., Nimtz M., Romling
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01-0CT-2003 (TrEMBLrel.
01-0CT-2003 (TrEMBLrel.
Curlin-csgA protein.
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Escherichia coli O6
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SEQUENCE 152 AA;
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Production of Cellulose and Curli Fimbriae by Members of the Family
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 72:4151-4158(2003).
EMBL; AJ515700; CAD566721; -.
SEQUENCE 150 AA; 15016 MW; 1D7141B8D6973DC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zogaj X., Bokranz W., Nimtz M., Romling U.;
"Production of Cellulose and Curli Fimbriae by Members of the Family
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 72:4151-4158 (2003).
EMBL, AJS15701; CAD566751; -
SEQUENCE 149 AA; 15260 MW; 946DD52017F648FD CRC64;
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
                                                                                                                                                                                                                                 Citrobacter sp. Fec2.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
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Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.3%; Score 591.5; DB 2
78.8%; Pred. No. 2.3e-39;
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Matches 119; Conservative
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                                                                                                                                                                                                     Curlin-csgA protein.
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"Production of Cellulose and Curli Fimbriae by Members of the Family Enterbacteriaceae Isolated from the Human Gastrointestinal Tract."; Infect. Immun. 72:4151-4158 (2003).
EMBL; AJSIS702; CADS66781; -. SEQUENCE 150 AA; 15112 MW; 5D8BS2D872DF15F3 CRC64;
                                                                                          Gaps
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Enterobacteriaceae; Salmonella.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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Pred. No. 2.1e-23;
                                                         55.7%; Score 431.5; DB 2; Leny...
59.6%; Pred. No. 1e-26;
... wiematches 33; Indels
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Cox J.M., Eglezos S., Woolcock J.B.;
Cox J.W. Eglezos S., Woolcock J.B.;
Wirulence of Salmonella enteritidis in chickens correla
colony morphology and expression of SE17 fimbriae.";
Submitted (APR-1996) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 AA; 7704 MW; 2FD5411241A7BCB1 CRC64;
                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                             120 INGALVDQTASNSTVNVTQIGFGNHATAHQY 150
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                                                                             Similarity 59.6
90; Conservative
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                                                                                                                                                                                                                                                                                                                                                      Salmonella enteritidis.
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                                                                 Query Match
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MEDINE-22297686; PubMed=12368813; Melson K.E., Gaidos E.J., Nelson W.C., Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadir R., Ward N., Methe B., Clayton R.A., DeBoy R.T., Tasapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Manathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., "Genome: sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis."
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                                                                                                                                                                                                                                                                                                                                                                                2; Indels
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EMBL, AR015532; AAN53941.1; -.

TIGR, S00865; -.

Hypotherical protein; Complete proteome.

SEQUENCE 502 AA; 52441 MW; D08CA23D6C46B62D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Conservéd hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                 15.7%; Score 122; DB 2;
89.7%; Pred. No. 0.0042;
ive 1; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Best Local Similarity
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Gaps

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4048 GDGNHGTLGGGVASQEPTRSSYSVGEDGTLSV---SVGNGLLANDIEMDGDSLTITEIN- 4103
                                                                                                                                                                      GNGADVGQG---ADNSTIBLTQNGFRNNATIDQWNAKNYDQLVTRVVTHEMAHANQTASD 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 ALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATI-----DQWNAKNYDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 STNSAQTQSPSSTGQSAAGQTTNSGTGT-NTTQAPTSNNSTNQAQTSQPSNQTNAPS-DQ
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                                                              28 GGGNHN--GGGNSS------GPDSTLSIYQYGSANAALALQSDARKSETTITQSGY
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002).
EMBL; AP005962; BAG52907.1; -:
Hypothetical protein; Complete proteome.
SEQUENCE 362 AA; 39058 MW; D447EE0D4E8433EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.3%; Score 103; DB 16; Length 362; 31.6%; Pred. No. 2.6;
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Bradyrhizobiaceae, Bradyrhizobium.
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                         Indels
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Last annotation update)
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Last annotation update)
                         57;
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      29.1%; Pred. No. 81; ative 18; Mismatches
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MEDLINE=22484998; PubMed=12597275;
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                                                                                                                                                                                                                                   SSVMVRQVGFGNNA 146
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                            39; Conservative
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Best Local Similarity
Matches 39; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Cladwig W., Gade D., Beck A., Borzwa K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhardt R., "Complete genome sequence of the marine planctomycete Pirellula sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNATIDOWNAKNYDOLVTRVVTHEMAHANGTASDSSVMVROVGFGNNATANOY 151
                                                                                                                                                                                            Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Alteromonadaceae, Shewanella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 30.1%; Pred. No. 0.28;
Matches 34; Conservative 19; Mismatches 46; Indels 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).

BMBL, BX294135, CAD72214.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 7716 AA; 797868 MM; D391A25BD96405C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome.
SEQUENCE 139 AA; 14811 MW; 41ECICFA76957920 CRC64;
                                                                         01-NAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Last annotation update)
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EMBL; AE015532; AAN53942.1; -.
                                                                                                                                        Minor curlin subunit CsgB, putative
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MEDLINE=22735913; PubMed=12835416;
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MEDLINE=22297686; PubMed=12368813;
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25,
                                  PRELIMINARY;
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01-OCT-2003 (TrEMBLrel.
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Hypothetical protein.
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RESULT 10

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strain 1.

Query Match

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TPTIKKEVSLSGALSKIYDANKSTSDLIAEDIKANPTNYFDNGEALKDLIKDATVSVNGG 120
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MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
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DNA Res: 9:189-197(20102)
EMBL; AP005954; BACS0555.1; -.
                                                                                                                                                                                                                       Mycoplašma penetrans.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; DB 16; Length 362; 4.5;
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EMBL; AP0404172. BAC4476.1; -
InterPro; IPR000437; Prok lipoprot S.
Lipoprotein; Complete Proceome.

Elipoprotein; Complete Proceome.

Elipoprotein; Complete Proceome.
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Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales;
Bradyrhizobiaceae, Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63; Indels
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                                                                                   Created)
Last sequence update)
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Last annotation update)
                                  362 AA
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                                  PRT;
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(TrEMBLrel. 23, I
(TrEMBLrel. 25, I
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01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
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                                  PRELIMINARY;
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                                                                                                                                                                P35 lipoprotein homolog.
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CSGA OR:BLL5300.
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                                                                                01-MAR-2003
01-MAR-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                           STRAIN=HF-2;
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Q89JI3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 SGOQASGSMNSFGGQGGYGQNQNGFGGQSGFSGQSGWGSNSLSSANSNGNNNQG--SSSG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 YONNOGRHOGOGGGHSSSSNSVMSNNGYSSNSGYGNNNGPTPSFLNNVSSSAAQDYYNIV 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSG
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"Production of Cellulose and Curil Fimbriae by Members of the Fami Enterobacteriaceae Isolated from the Human Gastrointestinal Tract. Imfect. Timmun. 72.4151-488(2003).
EMBL, AJ515702; CAD56677.1; -. SEQUENCE 151 AA; 15985 MW; FOBRARDAA7784797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Enterobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.0%; Score 101; DB 5; Length 409; 23.3%; Pred. No. 4.3; ive 26; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45; Indels
                                                                                                             to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                           Genome sequence of the nematode C.elegans: A platform
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SEQUENCE 409 AA; 43231 MW; B07DF0E4175C5739 CRC64;
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Last annotation update)
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1-OCT-2003 (TrEMBLrel. 25, Last sequenc
01-OCT-2003 (TrEMBLrel. 25, Last annotat
Nucleation component of curlin monomers.
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InterPro; IPR003677; Onchocerca_Ag.
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23.3%; Pic.
                                                                                                                                                                                                                                                                     investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z69383; CAA93412.1; -.
PIK; T20847; T20847.
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                                                                             McMurray A.A.;
Submitted (FEB-1996)
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Les 37; Conserv
                                                SEQUENCE FROM N.A.
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NCBI_TaxID=6239;
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T., Furuya K.,

DB 16; Length 171; Score 99.5; Pred. No. 2; 12.8%; 25.8%; Local Similarity

4,	09	78	116	138			
Gaps	AALALQ :	GSSVTQ	YDQLVT	NGSALT			
31;	YGSAN	SVGLVN	ZWNAKN 	QVAFGN			
63; Indels 31; Gaps	PDSTLSIYQYGSA : :	NİSTIVQVĞLVNGSSVIQ 78	-NSTIELTQNGFRNNATID	VONSATIG			
63;	GGNSSG	-	ELTONG	TVNOAG	0 150	7 2 168	
Mismatches	VPQWGGGGNHNG	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	OGADNSTI	QGTSSPSLNNVS	OVGFG-NNATAN	OLSFGINTSTVS	4:54:40
21;	SALAGV	AAQAA-	GADVG	NGASTM	SSVMVR	 	104, 1
40; Conservative 21; Mismatches	1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60	40 MRKLFFASVAVLALSSAAQAA	61 SDARKSETTITQSGYGNGADVGQGADNSTIELFQNGFRNNATIDQMNAKNYDQLVT 116	79 NGLTNDSSSTTQIGILNGASTMQGTSSPSLNNVSTVNQAGVQNSATTGQVAFGNNGSAIT 138	117 RUVTHEMAHANOTASDSSVMVRQVGFG-NNATANO 150	139 GNSFGPPALQNNSASVGQLSFGINTSTVSQ 168	Search completed: August 2, 2004, 14:54:40 Job time : 29.7 secs
40;	T W	40 MF	61 SI	79 NG	117 R	139 Q1	pleted 29.7
Matches	λŏ	Db	6	qa	λō	qa	Search completed: Au Job time : 29.7 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:
August 2, 2004, 14:35:42; Search time 44.9 Seconds

(without alignments)
950.215 Million cell updates/sec
Perfect score: 782
Sequence:
1 MKLLKVAAFAAIVVSGSALA.........DSSVMVRQVGFGNNATANQY 151
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched:
1586107 seqs, 282547505 residues
Total number of hits satisfying chosen parameters: 1586107
Minimum DB seq length: 0
Maximum DB seq length: 0
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description Control of the Control o	33		74625	41 Salmon	3570	36349	5354	36346 AgfA::	Aab36347 AgfA::PT3	36352 AgfA::	86351	36355 AgfA::	Aab36348 AgfA::PT3	5343	651 I	2761 A	0,	52664 Fibronec	52663 FNB curl	=	36318 Salmonel	1 Sal	36326 Salmonel	8 Sal	Abr82644 E. coli c
SUMMARIES	£	77	AAB36353	535	AAR74625	AAB36341	357		AAB36354	4	AAB36347	535	35	AAB36355	AAB36348	m	265	76	56	AAR52664	997	AAB36316	AAB36318	AAB36321	AAB36326	AAB36338	ABR82644
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AAB36344	AAB36322	AAB36327	AAB36337	AAB36342	AAU08231	ABR82649	AAW64378	AAW81745	AAY39032	AAY39175	ABU36445	AAW56163	ABB65764	ABB62708	AAG29728	AAG29727	AAB36323	AAB36336	AAB36328
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112	111	111	111	107	105	102		100		100	100	98.5	97.5	97.5	96.5	96.5	96	96	96
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

X Y X	AAB36353,
	26-FBB-ç001 (first entry)
	AgfA::Pṛ3#8 amino acid sequence SBQ ID NO:26.
	Salmonella, agfA, chromosomal gene replacement, fimbrin, epitope, vaccine, immune response, immunogen.
	Salmonella enteritidis. Escherichia coli. Synthetic.
	WO200060102-A2.
	12-OCT-2000.
	05-APR-2000; 2000WO-CA000356.
	05-APR-1999; 99US-0127888P.
	(UYVI-) UNIV VICTORIA.
	White AP, Doran JL, Collison SK, Kay WW;
	WPI; 2000-672631/65. N-PSDB; AAC64629.
	Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
PS PS	Disclosure, Page 138, 139pp, English.
	The present invention describes a recombinant agfA gene (I) where a segment, of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative fimbriae (SEFI7/TAF) nucleation depended assembly system of strains of Salmonelia, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CSgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene homologous species; (3) directing recombinant gene homologous species; (3) directing recombinant gene back into the chromosome of the homologous species; replacing the native

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AAR74625
       THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE S
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copy of that gene; and (4) eliciting an immune response in an animal, computising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriacese host cell, from the host cell and introducing the coliting an immune response in an animal. In a finbrial presentation eliciting an immune response in an animal. In a finbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial pubmit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 151;
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100.0%; Score 782; DB 3;
Best Local Similarity 100.0%; Pred. No. 2.3e-67;
Matches 151; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AgfA::PT3#5 amino acid sequence SEQ ID NO:20.
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                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 151 AA;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA segment of this maggregative fimbries (SEPT/TAPF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and directing recombinate comprising recombinant conditions and AgfA, CsgA and AgfA-homologue fimbries in the chromosome of the comprising recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino collymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a finbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogens, which may be important for directing an immune response in an animal protecting are usually strong immunogens, which may be important for directing an immune response in a minal protecting an immune response in a minal protecting an immune response confinent may be important for directing an immune response.
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89.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93US-00054452.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella, AgfA; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 89.9
Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AgfA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09425598-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L0-NOV-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
26-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR74625;
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cc assembly system of strains of Salmonella Escherichia coli and assembly system of strains of Salmonella Escherichia coli and considerably system of strains of Salmonella Escherichia coli and Enterbacteriacaee for the production of fimbriae comprising recombinant composed fince in the chromosome of the combination of a recombination of a recombination of a recombination of a recombinant gene into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising separating an amino acid polymer comprising separating an amino acid polymer comprising a recombinant Agfa comprising separating an amino acid polymer comprising a recombinant of protein containing a replacement sequent or sequents of foreign amino composition of sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or containing a replacement sequent or sequents of foreign amino coli sequence or sequences grown on a Salmonella, E. coli or coli or memory of the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant Agfa protein which is useful for coliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to consect of colicy coll), the hybrid fimbrin protein sare usually strong immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response consecuence in expensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88.5%; Score 692; DB 3; Length 151; 90.7%; Pred. No. 1.1e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNAALVNOTASDSSVMVROVGFGNNATANOY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Encoded by GCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella enteritidis 27655-3b agfA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW23570 standard; protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Doran JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94US-00233788.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity .... Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Collinson SK, Kay WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-APR-1993;
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29-SEP-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                      The Salmonella AgfA protein and DNA are used in vaccine and genetic immunization compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                   Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are:
                                                                                                                                                                                                                                                                                                                                                                                              1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
                                                                                                                                                                                                                                                                                                                                                                                                                         MKLLKVAAFAAIVVSGSALAGVVPQWGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SDARKSETTITOSGYGNGADVGOGADNSTIELTONGFRNNATIDOWNAKNSDITVGOYGG
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                           .
0
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                                                                                                                                                                                                                                                                                                                     Length 151;
                                                                                                                                                                                                                                                                                                                                                        12; Indels
             Doran JL;
                                                                                                                                                                                                                                                                                                                   Score 692; DB 2;
Pred. No. 1.1e-58;
2; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNAALVNOTASDSSVMVRQVGFGNNATANQY
             Clouthier SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ¥.
                                                                                                                                                         Disclosure; Fig 7B; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB36341 standard; protein; 151
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                                                                                                                                                                                                                                                                                                                     88.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                           Matches 137; Conservative
           Collinson SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella enteritidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Doran JL,
                                                WPI; 1994-358275/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-672631/65.
N-PSDB; AAC64617.
                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                 N-PSDB; AAQ87467
                                                                                                                                                                                                                                                                                    Sequence 151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB36341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                       Query Match
           Kay WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB36341
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05-APR-2000; 2000WO-CA000356.
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Best Local Similarity
Matches 136; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200060102-A2
                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-FEB-2001
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                                                                                                                                                                                                                                                                                                                                     120
                                                                                         The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 27655-3b. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic pacteria for the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 93% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PP field.)
                                                                                                                                                                                                                                                                                                                                                          SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA
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                                                                                                                                                                                                                                                                                                         MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                           1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
                                                                                                                                                                                                                                                                                                                                       LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                     Gaps
                                          Isolated Salmonella gene agfA - used for diagnosis of Salmonella or enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosomal gene replacement; fimbrin; epitope;
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0
                                                                                                                                                                                                                                               87.9%; Score 687; DB 2; Length 151; 90.1%; Pred. No. 3.3e-58;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AgfA::PT3#4 amino acid sequence SEQ ID NO:18.
                                                                                                                                                                                                                                                                                                                                                                                 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                      NNPALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Collison SK,
                                                                             Example 2; Fig 7; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB36349 standard; protein; 151
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                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              White AP, Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-672631/65.
N-PSDB; AAC64625.
          WPI; 1997-309886/28
                                                                                                                                                                                                                                                       Best Local Similarity
Matches 136; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     agfA;
                     N-PSDB; AAT74142
                                                                                                                                                                                                                          Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200060102-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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                                                                                                                                                                                                                                                Query Match
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back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, to comprising separating an amino acid polymer comprising a recombinant and comprising a separating an emino acid polymer comprising a recombinant of protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequence or sequence in an animal in a fimbrial presentation system the heterologous antigens are presented in high numbers (up to Succipie, the carrier fimbrial submit protein protein protein protein live vaccine, the carrier fimbrial submit proteins are usually strong immunogens, which may be important for directing an immune response cagainst the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GYGNGADVGQGADNSTIELTQNGFRNNATIDQ 105
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                                                                                                                                                                     The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative finbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of finbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) directing recombination of a recombinant gene homologous species; (3) directing recombinant gene into the chromosome of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30;
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protein useful for eliciting immune response in animal
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                                                                                       Page 136; 139pp; English
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81.98;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epictope or antigen. Also described are: (I) use of thin aggregative finbriae (SEPI)/TAF) mucleation depended assembly system of strains of Salmonella. Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant of AgfA, CobA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising are combinant AgfA protein contraining a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for the expression of recombinant for an efficient live cliciting an immune response in an animal. In a fimbrial presentation of source or sequence or an efficient live cliciting the interred of the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live immunogens, which may be important for directing an immune response in an ability and animal the inserted epicope, and hybrid fimbrine are usually strong immunogens, which may be important for directing an immunogenic properties are usually strong immunogens.
                                                                                                                                                                                                      Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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The present sequence is given in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 RNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 617; DB 3; Length 151;
Pred. No. 1.8e-51;
0; Mismatches 0; Indels 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AgfA::PT3#1 amino acid sequence SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inexpensive to purify in large amount. The pithe exemplification of the present invention
                                                                                           Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                          Disclosure, Page 138; 139pp; English
                                                                                        Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB36346 standard; protein; 151 AA
05-APR-1999; 99US-0127888P
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Best Local Similarity 73.6
Matches 128; Conservative
                                             (UYVI-) UNIV VICTORIA
                                                                                           Doran JL,
                                                                                                                                   WPI; 2000-672631/65.
                                                                                                                                                         N-PSDB; AAC64630
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                                                                                           White AP,
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment. Of the gene has been replaced by a segment of a foreign DNA sequence, which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEPI)/TAF) mucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant of a recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a recombinant gene of the homologous species, replacing the native comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant AgfA protein which is useful for system the hererologous antigens are presented in high numbers (up to system the hererologous antigens are presented in high numbers (up to source, the carrier finbrial submit proteins are usually strong immunogens, which may be important for an efficient live vaccine, the carrier finbrial submit proteins are usually strong against, the inserted epitope, and hybrid fimbriae are usually strong immunogens, the inserted epitope, and hybrid fimbriae are usually strong against, the inserted epitope, and hybrid fimbriae are usually strong immunogens, which may be important for an efficient live the exemplify in large amount. The present sequence is given in the exemplify and adhesion progens invented in sequence is given in the exemplify and adhesion progens.
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                                                                                                                                                                                                                                                                                                                                                               Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Page 135; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                               Collison SK,
                                                                                                                                                                                                                 2000WO-CA000356.
                                                                                                                                                                                                                                                                  99US-01278B8P.
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                    Salmonella enteritidis.
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                                              Escherichia coli
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                                                                                                                 WO200060102-A2.
                                                                                                                                                                                                              05-APR-2000;
                                                                                                                                                                                                                                                                  05-APR-1999;
                                                                                                                                                                12-OCT-2000.
                                                                   Synthetic.
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Best Local S
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120

RESULT 9

vaccine; immune response; immunogen.

61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120

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AAB3635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and
                                                                                                                                                                                                    Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.3%; Score 612; DB 3; Length 151; 81.5%; Pred. No. 5.5e-51; .ive 5; Mismatches 23; Indels
                                                                                                                                                        AgfA::PT3#2 amino acid sequence SEQ ID NO:14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Page 136; 139pp; English
                                                                                                                                                                                                                                 vaccine; immune response; immunogen.
                   AAB36347 standard; protein; 151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-APR-2000; 2000WO-CA000356
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Conservative
                                                                                                              (first entry)
                                                                                                                                                                                                                                                                      Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-672631/65.
N-PSDB; AAC64623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 123; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                      WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-APR-1999;
                                                                                                              26-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     White AP,
                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                               AAB36347;
AAB36347
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ 60 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: sequence which encodes a foreign epitope or antigen. Also described are: or seembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant or AgfA, CogA and AgfA-homologue fimbrin subunite, respectively, (2) directing recombination of a recombinant gene into the chromosome of the homologous species, (3) directing recombinant gene into the chromosome of the homologous species, (3) directing recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene, and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the copy useful for the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant agfA gene having a segment replaced by a foreign DNA seguence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              system the heterologous artigens are presented in high numbers (up to 550,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella, agfA, chromosomal gene replacement, fimbrin, epitope, vaccine, immune response, immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AgfA::PT3#7 amino acid sequence SEQ ID NO:24.
                                                                                                                                   151
                                                                                                                                                                                     .
X
                                                                                                                                   121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kay
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                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB36352 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-APR-2000; 2000WO-CA000356.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             White AP, Doran JL,
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-672631/
N-PSDB; AAC64628.
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White AP,
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                                                                                                                                                       61 SDARKSETTITQSGYGNGADVGQGADNSTIBLTQNGFRNNATIDQWNARNYDQLVTRVVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEFI)/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue finbrin subunits, respectively; (2) directing recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a production and the back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                         1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
                                                                                                              WKLLKVAAFAAIVVSGSALAGVVPQWGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                      61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                           Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                      .;
0
                                                Length 151;
                                                                    23; Indels
                                              Score 609; DB 3;
Pred. No. 1.1e-50;
4; Mismatches 23
                                                                                                                                                                                                                                                                                                                                      amino acid sequence SEQ ID NO:22.
the exemplification of the present invention
                                                                                                                                                                                   NNAALVNQTASDSSVMVRQVGFGNNATANOY 151
                                                                                                                                                                                                  Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 137; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                        vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Collison SK,
                                                                                                                                                                                                                                                                  AAB36351 standard; protein; 151 AA
                                             77.9%;
82.1%;
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                                                        al Similarity 82.1
124; Conservative
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Escherichia coli.
Synthetic.
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N-PSDB; AAC64627.
                       Sequence 151 AA;
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                                             Query Match
                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant Agfa protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVIRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Best Local Similarity 81.5%; Pred. No. 6.3e-50;
Matches 123; Conservative 4; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AgfA::PT3#10 amino acid sequence SEQ ID NO:30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNAALVNOTASDSSVMVRQVGFGNNATANOY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccine; immune response; immunogen.
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 151 AA;
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N-PSDB; AAC64624.
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 assembly system of strains of Salmonalla, Escherichia coli and assembly system of strains of Salmonalla, Escherichia coli and anseembly system of strains of Salmonalla, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the homologous species, replacing the native back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising are combinant AgrA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or the present into the animal in conjunction with a carrier or diluent. (1) is colymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgrA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbria protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response in mexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MXLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella, agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                     76.7%; Score 600; DB 3; Length 151; 81.5%; Pred. No. 7.8e-50; ive 4; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AgfA::PT3#3 amino acid sequence SEQ ID NO:16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB36348 standard; protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-APR-2000; 2000WO-CA000356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 81.5
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYVI-) UNIV VICTORIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-672631/65
                                                                                                                                                                                                                                                                                                                               Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200060102-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB36348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                          Query Match
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AAB36348
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The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA segment of the gene case for the production of the classical assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and casembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant of AgfA, CsgA and AgfA-homologue Imbrin submits; respectively; (2) of directing recombinant gene into the chromosome of the homologues species, respectively; (2) of directing recombinant gene into the chromosome of the homologues species, replacing the native copy of that gene; and (9) eliciting an immune response in an animal, comprising separating an emino acid polymer comprising a replacement segment or segments of foreign amino copy of that gene; and (9) eliciting an immune response in an almanla. E. coli or acid sequence or sequences grown on a Salmonella, E. coli or copy of the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (upper compinity and adhesion properties relevant for an efficient live immunogenicity and adhesion properties relevant for an efficient live immunogenicity and adhesion properties relevant for an efficient live immunogenicity and adhesion properties relevant for an efficient live immunogenicity and adhesion public dimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 577; DB 3;
Pred. No. 1.3e-47;
5; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                              Disclosure, Page 136, 139pp, English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Æ
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80.8%;
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Best Local Similarity 80.8
Matches 122; Conservative
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Plasma protein; immune response; antibacterial; vaccine; gene therapy

Escherichia coli.

WO2003064446-A2

07-AUG-2003

Herwald H;

Wikstroem M,

Bjoerck L, Olsen A,

30-JAN-2003; 2003WO-EP000943. 31-JAN-2002; 2002GB-00002275 (HANS-) HANSA MEDICAL RES AB

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The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epicope or antigen. Also described are: (1) use of thin aggregative fimbries (SEFI)/TAP) nucleation depended assembly system of strains of Salmonella, Bscherichia coli and comparation of strains of fimbries comprising recombinant of Enterobacteriaceae for the production of fimbries comprising recombinant of a recombinant gene into the chromosome of the homologus species, replacing the native composing species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating a main oaid polymer comprising a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino cortain sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the hererologous antigens are presented in high numbers (up to consume, the carrier fimbrial subunit protein sare usually strong immunogens; which may be important for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens; which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and incompanied to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                    Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                   Kay ww;
                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 135; 139pp; English.
                                                                                                                                                             Collison SK,
05-APR-2000; 2000WO-CA000356
                                                    99US-0127888P
                                                                                                         (UYVI-) UNIV VICTORIA
                                                                                                                                                                Doran JL,
                                                                                                                                                                                                                     2000-672631/65.
                                                                                                                                                                                                                                                  N-PSDB; AAC64619
                                                       05-APR-1999;
                                                                                                                                                             White AP,
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Sequence 151 AA;

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                                                                                                                                                                               61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                           61 IDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGRNSEMTVKQFGG 120
                                                                                         1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ 60
                                                                                                                                  1 MKLLKVAAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ 60
                                                 ,
66.9%; Score 523; DB 3; Length 151; 68.9%; Pred. No. 2e-42; ive 18; Mismatches 29; Indels
                                                                                                                                                                                                                                                                      NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                GNGAAVDQTASNSSVNVTQVGFGNNATAHQY
                  Best Local Similarity 68.9
Matches 104; Conservative
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    Query Match
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151

121

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ABR82651 standard; protein; 151 AA (first entry) 04-DEC-2003 ABR82651; RESULT 1 ABR82651 XEXEXEX

E. coli CsgA subunit 15 kDa protein.

The invention relates to an isolated peptide capable of binding a mammalian plasma protein or of generating an immune response in a mammal selected from sequences shown in ABR02642. ABR02648.49. The peptide or antibody is useful for treating a bacterial infection in a human or animal or in the manufacture of a medicament for the prophylactic treatment of a bacterial infection, such as Escherichia coli, salmonella or Shigella infection. The peptide that is immobilized on a solid support is also useful as a reagent for determining the ability of a plasma protein to bind to bacteria. The present sequence represents an E. coli 61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120 61 TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG 120 New isolated peptide capable of binding a mammalian plasma protein, useful in the manufacture of a medicament for the prevention and/or treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infections. 9 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ . 0 66.2%; Score 518; DB 7; Length 151; 68.2%; Pred. No. 6.2e-42; ive 18; Mismatches 30; Indels 151 121 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 121 NNAALVNQTASDSSVMVRQVGFGNNATANQY Disclosure; Page 41-42; 42pp; English. Best Local Similarity 68.2 Matches 103, Conservative WPI; 2003-646136/61. N-PSDB; ACF36153. Sequence 151 AA; Query Match g ò d d à

2, 2004, 14:48:28 completed: August : 45.9 secs Job time Search

(0108N) YUDIB 860d SIUI

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TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-233-788A-59
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Sequence 204, Appl
Sequence 131, Appl
Sequence 131, Appl
Sequence 204, Appl
Sequence 3, Appli
Sequence 5, Appli
Sequence 6167, Appli
Sequence 8, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 2, Appli
Sequence 2, Appli
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Sequence 2, Appli
Sequence 30227, A
Sequence 132, Appli
Sequence 30227, A
Sequence 1073, Appli
Sequence 132, Appli
Sequence 132, Appli
Sequence 13227, A
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Sequence 5130, Ap
Sequence 18, Appl
Sequence 53, Appl
                                                                                                                                                           August 2, 2004, 14:40:48; Search time 12 Seconds (without alignments) 649.627 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                       782
1 MKILKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
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11. (cgn2 6/ptodata/2/iaa/5A_COMB.pep:*
22. (cgn2 6/ptodata/2/iaa/5B_COMB.pep:*
33. (cgn2 6/ptodata/2/iaa/6A_COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-477-135A-131

US-08-336-447A-5

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US-09-328-322-4764

US-09-328-322-4764

US-09-196-387-8

US-09-196-387-8

US-09-196-387-10

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US-09-540-250A-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                             US-09-543-407-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 %
Query
Match Length D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78.5
78.5
77.5
77.5
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                                                                                                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
No.
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9, Appli	9, Appli	10, Appl			10, Appl	5434, Ap	-	2, Appli	•	9, Appli	2, Appli	17, Appl	~	2, Appli	2, Appli	2, Appli	2, Appli	
Sequence 5	Sequence 9	Sequence 1	Sequence 1		Sequence 1		ednence	Sequence	Seguence	Seguence	Seguence	Sequence	Seguence	Sequence	Sequence	Seguence	Seguence	
118-08-728-470-9	-08-719-641-		US-08-719-641-10	US-08-617-697-9	US-08-617-697-10	US-09-543-681A-5434	US-08-458-023B-6	US-08-331-515A-2	US-09-168-406A-2	US-09-336-447A-9	US-08-169-927-2	US-07-792-259-17	US-07-876-280-2	US-07-675-772-2	US-08-063-170-2	US-08-158-232-2	US-08-304-626-2	
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ALIGNMENTS

US-	US-08-233-788A-59
 S	Sequence 59, Application US/08233788A
<u>.</u>	atent No. 5635617
	GENERAL INFORMATION:
	Kay, Willia
	on,
•~	Clouthier, Sharon C.
٠.	O
. •-	NUMBER OF SEQUENCES: 61
•-	CORRESPONDENCE ADDRESS:
. ••	
	STREET: 6300 Columbia Center, 701 Fifth Avenue
	CITY: Seattle
	STATE: Washington
	COUNTRY: U.S.A.
	ZIP: :98104-7092
	COMPUTER READABLE FORM:
	MEDIUM TYPE: Floppy disk
	COMPUTER: IBM PC compatible
	SO
	SOFTWARE: PatentIn Release #1.0, Version #1.25
	LICATION DA
	APPLIÇATION NUMBER: US/08/233,788A
. •	FILING DATE: 26-APR-1994
. •-	CLASSIFICATION: 435
. •-	ATTORNEY/AGENT INFORMATION:
. •-	
	,570
	REFERENCE/DOCKET NUMBER: 920043.403C2
	TELECOMMUNICATION INFORMATION:
	TELEPHONE: (206) 622-4900
••	(506)
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	TO THE CALL OF THE CALL OF

Gaps ., Query Match 87.9%; Score 687; DB 1; Length 151; Best Local Similarity 90.1%; Pred. No. 7e-60; Matches 136; Conservative 2; Mismatches 13; Indels

: 151 amino acids amino acid

LENGTH:

1 MKLLKVAAFAAIVVSGSALAGVVPPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALXDQ

ö 9 N

TREAT

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APPLICANT: TWARDZIK,
APPLICANT: Lodes, Mi
APPLICANT: Hendricks
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JS-09-056-556-204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
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                                                                 61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                               61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 VVPQWGGGGNHNGGCNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGNGADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Patent No. 5635617

GENERAL INFORMATION:
APPLICANT: Clouch and w.
APPLICANT: Clouch and w.
APPLICANT: Clouch and w.
APPLICANT: Clouch and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a control and a contr
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Best Local Similarity 87.5%; Pred. No. 2.1e-42;
Matches 98; Conservative 2; Mismatches 12; Indels
                                                                                                                                                                                                       121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                          121 NNPALVNOTASDSSVMVRQVGFGNNATANQY 151
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amino acid
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
US-08-233-788A-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-233-788A-57
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US-09-056-556-204
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; Sequence 204, Application US/09056556; Patent No. 6350456; GENERAL INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHA
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 GYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        464 GSGNIGVFNVGSGSLGNYNIGSGN-----LGIYNIGFGNVGDY-----
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Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 12.8%; Score 100; DB 4; Length 943; Best Local Similarity 26.0%; Pred. No. 0.2; Matches 40; Conservative 12; Mismatches 52; Indels
                                                                                                                                                     AURESCEE: SEED and BERRI LLE
SCREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle Columbia Center, 701 Fifth Avenue
CITY: Seattle Columbia Center, 701 Fifth Avenue
CUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORDY disk
CCMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION NUMBER: 31.392
REGISTRATION NUMBER: 31.392
REGISTRATION NUMBER: 31.392
REFERENCE/DOCKET NUMBER: 210121.457
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: CARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                       E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 ---NAALVNQTASDSSVM---VRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        554 GTGNSGLFNSGTNNVGIFNAGTGNVGIANSGTGN 587
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Patent No. 6458366
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skeiky, Yasir A.W.
Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      504 GFGNAGDFNQGFANT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 943 amino acids
amino acid
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CITY: S
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----GNNNIGFANTGNNNIGIGLSGDNQQGFNIASGWNS 660
16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos Neto, Antonio
APPLICANT: Campos Neto, Antonio
APPLICANT: Wedvick, Thomas S.
APPLICANT: Wedvick, Thomas S.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Codes, Michael J.
APPLICANT: APPLICANT: Compounds AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; DB 4; Length 943; 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGN--
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                                                                                                                       GYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGN
                                                        571 GSGNIGVFNVGSGSLGNYNIGSGN-----LGIYNIGFGNVGDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT'APPLICATION DATA:
APPLICATION UNMER: US/09/072,967
FILING DATE: 05-MAY-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                   122 ---NAALVNOTASDSSVM---VROVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                        661 GTGNSGLFNSGTNNVGIFNAGTGNVGIANSGTGN 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 12.8%; Score 100; DB Best Local Similarity 26.0%; Pred. No. 0.2; Matches 40; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 204, Application US/09072967
Patent No. 6592877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 21012
REFERENCE/DOCKET NUMBER: 21012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6931
INFORMATION FOR SEQ ID NO: 204:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                611 GFGNAGDFNQGFANT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     943 amino acids
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 6300 Colum
CITY: Seattle
STATE: Washington
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US-09-072-967-204
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                                                                                                                       74
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Sequence 131, Application US/09477135A
Fatent No. 6572865
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.8%; Score 100; DB 4; Length 943; 26.0%; Pred. No. 0.2; vative 12; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             464 GSGNIGVFNVGSGSLGNYNIGSGN-----LGIYNIGFGNVGDY---
                                                                                                                                                                                                              SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/09/072,596
FILING DATE: 0-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAXA, DAVIG J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-6031
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 ---NAALVNQTASDSSVM---VRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 554 GTGNSGLFNSGTNNVGIFNAGTGNVGIANSGTGN 587
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US-09-477-135A-131
                                                        ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 943 amino acids
amino acid
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Best Local Similarity 26.08
Marches 40; Conservative
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Best Local Similarity 26.0°
Matches 40; Conservative
      STATE: Washington
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US-09-072-596-199
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Gaps

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Sequence 4764, Application US/09328352
Patent No. 6563958
GENERAL INPORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 GGGNHN------GGGNSS---GPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGY
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                                                                                                                                                  APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: OCDE, LESLIE D.
APPLICANT: OCDE, LESLIE D.
APPLICANT: MACIVER, ISOBED.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PATCHIN VOS: 2.1
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11.7%; Score 91.5; Di
Best Local Similarity 27.4%; Pred. No. 1.4;
Matches 37; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.9%; Score 93; DB ilarity 27.7%; Pred. No. 0.89 Conservative 14; Mismatches
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CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4764
LENGTH: 975
                                                                          Sequence 5, Application US/09336447A Patent No. 6310190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Moraxella catarrhalis
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Matches 41; Conserv
                                                                                                                                 GENERAL INFORMATION:
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US-09-328-352-4764
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TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR

TITLE OF INVENTION: OVALIAINIG SAID CDNA, HOST CELLS TRANSFORMED WITH SAID

TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID

TITLE OF INVENTION: VECTOR, POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY

TITLE OF INVENTION: TO SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 TRVVTHEMAHAGYGNGADVGQGADNSTIELTQ----NGFRNNATIDQWNAKNSDITVGQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: ISSUAL...

CITY: TSU-city
STATE: Mie-prefecture
COUNTRY: Ma-prefecture
COUNTRY: Ma-prefecture
COMPUTER: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: Diskette, 3.50 inch, 1.44 MB storage
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Mord Perfect 6.1
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US97
FILING DATE: May 28, 1997
FILING DATE: 15-July-1996
ATTORNEY/AGENT INFORMATION:
NAME: C. Bruce Hamburg
RESTERATION NUMBER: 22,389
RESTERATION NUMBER: 22,389
REFERENCE/DOCKET NUMBER: F-5610
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 YGGNNAALVNOTASDSS-----VMVRQVGFGNNATA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        504 LGGGSAAAAAAAAAAGGGGRALRRALRROMRGGGSAAA 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --- GGGGGGGGGGGGGGGG-
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122 ---NAALVNQTASDSSVM---VRQVGFGNNATAN 149
                                                554 GIGNSGLFNSGINNVGIFNAGIGNVGIANSGIGN 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
12.6%; Score 98.5; DE
Best Local Similarity 28.1%; Pred. No. 0.2;
Macches 45; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: from 1 to 738
IDENTIFICATION METHOD: E (by experiment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pinctada fucata
CELL TYPE: mantle epithelial cell
                                                                                                                                                                                    Sequence 3, Application US/08864038A
Patent No. 6001592
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      419 LLKSSASASASASASAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212)953-7733
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         812-5 Hirano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IXPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                US-08-864-038A-3
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99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSPSSPGSSLAESPEAA 157
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                                                                                                                                                                                               RESULT 13
US-09-841-835-8
US-09-841-835-8
Sequence 8, Application US/09841835
Pacent No. 6506587
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.5%; Score 82; DB 3; Length 673; 29.6%; Pred. No. 7.4;
486 GANIGSGASGITVVQ--SQNGANIGSGASGISVVQSQSG 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 107601
ZIP: 107601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT.APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX 133521
INFORMATIÓN FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 29.6
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 673 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Jersey
: USA
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                                                                                                                                              RESULT 12
US-09-196-387-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-196-387-8
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                                                                                                                                                                     Sequence 6167, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: GATA,
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BADMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6167
LENGTH: 273
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Patent No. 6551795

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPBUTICS
TITLE OF INVENTION: NUMBER: US/09/252,991A
TITLE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 RVVTHEMAHAGYG------NGADVGQGADNSTIELTQN------GFRNNATIDQWN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     426 AVQSQSGANIGSGANGISVVQSQNGANIGAGASDISVVQSQNSPNIGSGVNGVTVVQSQN 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 NAALYDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 NAPLAEAAFINRASNVNAHVNYG-----DNSGTKDTOYGVG-----VEYFVPNSDF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKLLKVAA--FAAIVVSGSALAGVVPQWGGGGNH----NGGGNSS-GPDSTLSIYQYGSA 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 WKKLAIASALLSALAVSGAANA-YQAEVGGSYNYLDPDNGSSVSKFGVDGTYYFNPVQTR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 VVSGSALAGVVPQWGGGGNHNG------GGNSSGPDSTLSIYQYGSANAALYDQLVT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 273;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 TVGOYGGNNAALVNOTASDSSV--MVRQVGF 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : | | | : | | | : | | | | : | | | | : | | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
11.3%; Score 88; DB 4
Best Local Similarity 28.5%; Pred. No. 0.6;
Matches 43; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas aeruginosa
               393 ASGNGEHNYGIGNGN 407
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US-09-252-991A-26438
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                                                                                                                RESULT 10
US-09-328-352-6167
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COMPOTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 10.5%; Score 82; DB 3 Best Local Similarity 29.6%; Pred. No. 12; Matches 34; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STARE: New Jersey
COUNTRY: USA
                                                                                NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEFHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      600-1-230 CIP1
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 09/196,387
FILING DATE: ATGRANTION:
NAME: JACKSON ESC, DATA'S
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMULTATION INFORMATION:
TELEPHONE: 201-487-5800
FELEPHONE: 201-343-1684
                         09/095,225
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 949 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                  10:
                                                                                                                                                                     TELBEAK: 201.
TELERA: 13351
INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 949 amino acids
""DE: amino acid
""DE: amino acid
                     APPLICATION NUMBER: 09/0
FILING DATE: June 10, 19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-196-387-10
  PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQL--- 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 -VTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
CORRESPONDENCE: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.5%; Score 82; DB 4; Length 673; Best Local Similarity 29.6%; Pred. No. 7.4; Matches 34; Conservative 14; Mismatches 59; Indels
                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/841,835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMCPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         600-1-230 CIP1
                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/09196387
Patent No. 6277613
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 133521
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTBRISTICS:
LENGTH: 673 amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-09-841-835-8
                       STREET: 411 Hackens
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
                                                                                                                 07601
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99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSPSSPGSSLAESPEAA 157
                                                                                                                               6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQL--- 61
                                                                                                                                                                                                                                                          62 -VIRVVIHEMAHAGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                     158 GVSSTAPLGPGAÁGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
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Patent No. 6506587
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
NUMBER OF SEQUENCES: 12
10.5%; Score 82; DB 3; Length 949; 29.6%; Pred. No. 12;
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TOPOLOGY: linear

WOLECULE TYPE: protein
US-09-841-835-10

Query Match

Query Match

Watches 34; Conservative 14; Mismatches 59; Indels 6; Gaps 4;

Matches 34; Conservative 14; Mismatches 59; Indels 8; Gaps 4;

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Db 99 VAARVVFHEMAHAGYGNAPNPAGSGSNNSPSSSSPTSS-SSSSPESSFGSSLAESPEAA 157

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Db 158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNARDM 212

Search completed: August 2, 2004, 14:58:36

Job time: 13 secs
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us-09-543-407-26.rapb

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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US-10-437-963-11419	US-10-282-122A-6	US-09-820-843A-2	US-10-437-963-19306	US-10-437-963-16	US-10-233-553-23	US-10-233-55	US-10-282-122A-6457	US-10-282-122A-449	US-10-282-122A-6247	US-10-282-122A-6779	US-10-425-114-6775	US-10-185-990-1	US-10-185-990-1	US-10-408-765A-99	US-10-424-59	US-10-479-670-164	US-10-369-493-18	US-10-369-493-12	US-10-282-122A-6436	US-10-424-599-21	US-10-425-114-49960	US-09-810-264-28	US-10-437-963-14	US-10-479-670-80	US-10-437-963-10541	US-10-437-963-1529	US-10-437-963-12017	US-10-424-599-14844	US-10-425-114-5533
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1.8	1.8 1	1.8	1.8	1.7	1.7	1.7	1.6	1.6	1.6 1	1.6 6	1.3	1.3 1	1.3 1	1.3 1	1.2	1.2	1.2 1	1.1	1.1 2	1.0	6.0	6.0	6.0	8.0	7.0	0.7	0.7	10.7 3	7.0
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16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	6 E	40	41	42	43	44	45

ALIGNMENTS

US-UG-/44-8/48-4

US-UG-/44-8/48-4

Deblication NO. US2020081722A1

Sequence A. Application US/09741873B

Publication NO. US2020081722A1

GENERAL INFORMATION:

APPLICANT: Normark, Staffan

APPLICANT: Normark, Staffan

APPLICANT: Normark, Staffan

APPLICANT: Normark, Staffan

APPLICANT: Normark, Staffan

TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation

FILE REFERENCE: 012889-084

CURRENT FILING DATE: 1098-06-06

PRIOR FILING DATE: 1998-05-06

PRIOR FILING DATE: 1998-05-06

PRIOR FILING DATE: 1997-11-26

PRIOR PLICATION NUMBER: US 07/789,437

PRIOR APPLICATION NUMBER: US 07/789,437

PRIOR FILING DATE: 1992-11-06

PRIOR FILING DATE: 1992-11-03

PRIOR FILING DATE: 1994-10-05

PRIOR FILING DATE: 1994-10-05

SEQ ID NOS: 10

SEQ ID NO 4

LENGTH: 151

TAVE: DEATH: 151

TAVE: DEATH: 151 ò ó Length 151; Query Match
66.5%; Score 520; DB 12; Length 15
Best Local Similarity 68.2%; Pred. No. 2.2e-44;
Matches 103; Conservative 19; Mismatches 29; Indels ; TYPE: PRT ; ORGANISM: Escherichia coli US-09-741-873B-4

1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ 60

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DB 12;
PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR FILING DAFE: 1998-05-06
PRIOR FILING DATE: 1990-05-06
PRIOR FILING DATE: 1997-11-26
PRIOR PLING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR PILING DATE: 1999-05-04
PRIOR FILING DATE: 1999-11-06
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1994-11-03
PRIOR FILING DATE: 1994-11-03
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-01-28
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PRIOR FILING DATE: 1994-01-38
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 10
SEQ ID NOS: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09741873B Publication No. US20040096965A9 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Normark, Staffan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Escherichia coli
US-09-741-873B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 GFGNNATANOY 151
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Sequence 4, Application US/09741873B

Publication No. US2004009665A9

GENERAL INFORMATION:
APPLICANT: Olsen, Are
APPLICANT: Olsen, Are
CURRENT FLING DATE: US/09/741,873B

CURRENT PILING DATE: US/09/741,873B

CURRENT APPLICATION NUMBER: US/09/741,873B

CURRENT APPLICATION NUMBER: US/08/741,873B

PRIOR FILING DATE: 1998-05-06

PRIOR APPLICATION NUMBER: US 06/978,878

PRIOR FILING DATE: 1998-05-06

PRIOR APPLICATION NUMBER: US 07/347,189

PRIOR FILING DATE: 1991-11-06

PRIOR APPLICATION NUMBER: US 07/347,189

PRIOR FILING DATE: 1991-11-06

PRIOR PRILNG DATE: 1991-11-06

PRIOR FILING DATE: 1991-11-03

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-01-8

PRIOR FILING DATE: 1994-01-8

PRIOR FILING DATE: 1994-01-8

PRIOR FILING DATE: 1994-01-8

PRIOR FILING DATE: 1994-01-8

PRIOR FILING DATE: 1994-01-8

PRIOR FILING DATE: 1994-01-8

NUMBER OF SEQ ID NOS: 10

SOFTWARRE: Datentin version 3.0

SOFTWARRE: Datentin version 3.0
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APPLICANT: Normark, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
TITLE OF INVENTION WHERE: US/09/741,873B
CURRENT APPLICATION WHERE: 2003-04-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                           Sequence 2, Application US/09741873B Publication No. US20020081722A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
US-09-741-873B-2
                                                                                                                                                                                                                                                                                                                                                      RESULT 2
US-09-741-873B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-741-873B-4
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APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REPERENCE: 012899-084
CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT FILING DATE: 2003-04-04
FRIOR APPLICATION NUMBER: US 08/978,878
FRIOR FILING DATE: 1997-11-26
FRIOR FILING DATE: 1997-11-26
FRIOR PRIOR PRIDER: US/09/74/189
FRIOR FILING DATE: 1991-11-06
FRIOR FILING DATE: 1991-11-06
FRIOR FILING DATE: 1991-11-06
FRIOR FILING DATE: 1991-11-06
FRIOR FILING DATE: 1994-01-28
FRIOR FILING DATE: 1994-01-28
FRIOR FILING DATE: 1994-01-28
FRIOR FILING DATE: 1994-01-05
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 2
FRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 2
                                                                                                                                                                                                                                        81 VGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQV 140
                                                                                                                                                                                                                                                                          61 VGQGSDDSSIDLTQRGFGNSATLDQWNGRNSEMTVKQFGGGNGAAVDQTASNSSVNVTQV 120
                                                                                                                                                                              09
                                                                                                                        80
                                                                                                                     21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGNGAD
                                                                                                                                                                           1 GVVPQYGGGGNHGGGGNNSGNNSELNTYQYGGGNSALALQTDARNSDLTITQHGGGNGAD
                                                            Gaps
                                                            ö
                                                            28; Indels
      Length
Query Match

56.5%; Score 442; DB 12;
Best Local Similarity 64.9%; Pred. No. 1.3e-36;
Matches 85; Conservative 18; Mismatches 28;
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Length 131;

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387 GFGNAGDINTGFGNAGD--TNTGFGNAGFFNMGIGNAGNEDMGVGNGGSFNVGVGN--AG 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 338 LIGDNLVGIGALNSGIGN-LGFGNSG--NNNIGFFNSGNNNVGFFNS-----GNNNF 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 GYGNGADVGQGADNSTIELTQNGFRNNATIDQ--WNAKNSDITVGQYGGNNAALVNQTAS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GNNNIGFANTGNNNIGIGLSGDNQQGFNIASGWNS 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 VSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHA
                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: Description of Artificial Sequence:mTTC#3-His US-09-793-306-146
                                                                                                                                                                                                                                                                                                                                                                                             13.4%; Score 105; DB 9; Length 597; 29.0%; Pred. No. 0.065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.8%; Score 100; DB 9; Length 943; 26.0%; Pred. No. 0.37; ive 12; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 GYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGN-
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 571 GSGNIGVFNVGSGSLGNYNIGSGN-----LGIYNIGFGNVGDY
                                                                                                                                                                                                                                                                                                                                                                                                                                      18; Mismatches
  TITLE OF INVENTION: Of Tuberculosis
FILE REFERENCE: 0.14628-0.08740US
CURRENT APPLICATION NUMBER: US/09/793,306
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US 60/185,037
PRIOR PILING DATE: 2000-02-25
PRIOR PILING DATE: 2000-02-25
PRIOR FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 164
SOFTWARE: PATENT IN Ver. 2.1
SEQ ID NO 146
ILENGTH: 597
TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 131, Application US/09996634; Patent No. US20020172684A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 DSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              443 NQS-----VGFGNAGTLN 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 26.00
The 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                         40;
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                                                                                                                                                                                                                                                                                                                                                                             Sequence 20638, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater, Steven C.
APPLICANT: Glaman, Barry S.
APPLICANT: Glaman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20638
                                                                                                                                               VGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQV 140
                                                                                                                                                                        61 VGQGSDDSSIDLTQRGFGNSATLDQWNGRNSEMTVKQFGGGNGAAVDQTASNSSVNVTQV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 GSANAALYDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKN 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---IQGKQSGAGNSAAIFQEGTGSDVELQQTGTSNGAVPSGWNWTN 129
                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 146, Application US/09793366
Patent No. US20020098200A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Campos-Neto, Antonio
APPLICANT: Ovendale, Pamela
APPLICANT: Use, Shyian
APPLICANT: Use, Michael
APPLICANT: Lodes, Michael
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compounds and Methods for Diagnosis and Immunotherapy
                                                                                          21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGNGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 AAFAADSNTVYLNQTGNDQQANITQSGNGNSVGAFNGNSGFLQENGTLSGA-NLLTVKQS
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 DPGVFNKITQDSSSNGSKVSVIQDGKNVFSIKQGNTGNSTSVNQIG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---SDITVGQYGGNNAALVNQTASDSSVMVRQVG 141
  Pred. No. 1.3e-36;
3; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
14.9%; Score 116.5; DB 15;
Best Local Similarity 27.5%; Pred. No. 0.0032;
Matches 46; Conservative 20; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: unsure;
COCATION: (1)..(445)
COTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-20638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Rhodopseudomonas palustris
                    18;
64.98;
  Best Local Similarity 64.93
Matches 85; Conservative
                                                                                                                                                                                                                                                              121 GFGNNATAHQY 131
                                                                                                                                                                                                                                   141 GFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 GNSNSVGRD----
                                                                                                                                                                                                                                                                                                                                         RESULT 5
US-10-369-493-20638
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US-09-793-306-146
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---GNNNIGFANTGNNNIGIGLSGDNOOGFNIASGWNS 660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Romald C.
Hendrickson, RombonnDS AND METHODS FOR DIAGNOSIS OF
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                    50;
                                                                                   12.8%; Score 100; DB 10; Length 943; 26.0%; Pred. No. 0.37; ive 12; Mismatches 52; Indels 5(
                                                                                                                                                                                                                                                                             74 GYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGN---
                                                                                                                                                                                                                               571 GSGNIGVFNVGSGSLGNYNIGSGN-----LGIYNIGFGNVGDY----
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COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMERS: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                           122 ---NAALVNQTASDSSVM---VRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                            661 GTGNSGLFNSGTNNVGIFNAGTGNVGIANSGTGN 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 210121.417C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 199: US-10-193-002-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-997-181-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Campos-Neto, Antonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 199, Application US/10193002
Publication No. USCO303135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Skeiky, Yasir A.W.
Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (206) 622-49:
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGIH: 943 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                611 GFGNAGDFNOGFANT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                           Query Match
Best Local Similarity 26.09
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-193-002-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHA 73
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--NV 503 ----GNNNIGFANTGNNNIGIGLSGDNQQGFNIASGWNS 553 ---NV 629 -- 121 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHA 73 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHA IITLE OF INVENTION: Identification of Essential Genes in Microorganisms Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614

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57 LYDQLVTRVVTHEMAHAGYGNGADVG--QGADNST-IELTQNG-----FRNNAT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSS----GPDSTLSIYQYGSANAA 56
                                        PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/200, 727
PRIOR APPLICATION NUMBER: 60/200, 727
PRIOR PELING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-10-21
PRIOR PLING DATE: 2000-10-21
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-06
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PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 VDQINGYLSN-TAGTAQNVEVRLLNAQMQPINV---TIGANNDITIN 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 IDOWNAKNSDITVGOYGGNNAALVNQTASDSSVMVRQVGFGNNATAN 149
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29.3%; Pred. No. 0.12;
tive 18; Mismatches
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Publication No. US20030032772A1
GENERAL INFORMATION:
APPLICANT: HANSEN ERIC J.
APPLICANT: COPE, LEGLIE D.
APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CRGANISM: Moraxella catarrhalis
US-09-952-267-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.9%;
27.7%;
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Best Local Similarity
Matches 49; Conserv?
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Best Local Similarity
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US-10-282-122A-49412
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                                                                                                                                                                                                             RESULT 13
US-10-360-493-20619
US-10-360-493-20619
I US-10-360-493-20619
I US-10-360-493-20619
I Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Chor, Vongwei
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Chor, Xianteng
ITILE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
ITILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
ITILE OF INVENTION: USABLE 1203-02-28
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PLING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 SVVVAGTDYRDIVAGVLPSLGGVKKAYAIGDGSGPFAPFKDLASDTPFSAPEFGAADGF- 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 YDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVG- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 -----VIIHTAAVGGRPRGALISQG--NLLI-----AQSSLVDAWRLTEADVNLGM 188
630 GFGNAGDFNQGFANT-----GNNNIGFANTGNNNIGIGLSGDNQQGFNIASGWNS 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Forsyth, R. APPLICANT: Xu, H. TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 AIVVSGS----ALAGVVPQWGGGGNHNGGGNSSGP-----DSTLSIYQYGSANAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.6%; Score 98.5; DB 15; Length 486; 25.7%; Pred. No. 0.23; Live 22; Mismatches 50; Indels 35
                                                               122 ---NAALVNQTASDSSVM----VRQVGFGNNATAN 149
                                                                                                           680 GTGNSGLFNSGTNNVGIFNAGTGNVGIANSGTGN 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: unsure

COCATION: (1)..(486)

CTHER INFORMATION: unsure at all Xaa locations

US-10-369-493-20619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 ---- OYGGNNAALVNOTASDSSVM 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 LPLFHVTGLGLMLTLQQAGGASVI 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Rhodopseudomonas palustris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Tawick, John
APPLICANT: Farsylh, R.
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Best Local Similarity 25.73
Matches 37; Conservative
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US-10-282-122A-49412
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LENGTH: 486
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Sequence 14, Appl
Sequence 24, Appl
Sequence 20, Appl
Sequence 30, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 55, Appl
Sequence 5834, Ap
Sequence 5834, Ap
Sequence 5834, Ap
Sequence 5834, Ap
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 33, Appl
Sequence 33, Appl
Sequence 33, Appl
Sequence 5833, Ap
Sequence 5833, Ap
Sequence 5833, Ap
Sequence 5833, Ap
Sequence 5833, Ap
Sequence 6834, Ap
Sequence 6834, Ap
Sequence 146, Appl
Sequence 146, Appl
Sequence 146, App
Sequence 146, App
Sequence 146, App
Sequence 146, App
Sequence 146, App
Sequence 146, App
Sequence 146, App
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Sequence 5, Ap
Sequence 57, Ap
Sequence 18, P
Sequence 28, P
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Sequence 199
                                                                                         Sequence
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19 US-09-543-407-26
19 US-09-543-407-20
19 US-09-543-407-20
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19 US-09-543-407-18
19 US-09-543-407-14
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US-08-942-578-204
US-09-024-753-199
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      201:5
116:56
1116:57
1116:57
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201∴5
                                                                                                           2, 2004, 14:48:33 ; Search time 167.9 Seconds (without alignments) 877.809 Million cell updates/sec
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                                                                                                                                                                  US-09-543-407-26
782
1 MKLLKVAAFAAIVUSGSALA.......DSSVMVRQVGFGNNATANQY 151
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                    hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                        6019581 seqs, 976053577 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                 protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length DB
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Maximum DB
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; MOLECULE TYPE: protein US-08-233-642A-57
     CURRENT FILING DATE:
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                                                                                                                                                                                                                                                                                 61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELLQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 -----YDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSD 112
                                                                                                                                           1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ 60
                                                                                                                                                                                      1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ 60
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                                                                                                  Gaps
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GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Collinaon, S. Karen
APPLICANT: Collinaon, S. Karen
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REPERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA oTHER INFORMATION: sequence containing the replacement fragment oTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-20
                                                     Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.7%; Score 709; DB 19; Length 151; ilarity 89.9%; Pred. No. 1.3e-67; Conservative 0; Mismatches 0; Indels 1
                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 ITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
Collinson, S. Karen
APPLICANT:
Collinson, S. Karen
TITLE OF INVENTION:
PRESENTATION OF HETEROLOGOUS PER
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE:
NUMBER OF SEQ IO NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
                                             Query Match
100.0%; Score 782; DB 19;
Best Local Similarity 100.0%; Pred. No. 1.8e-75;
Matches 151; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                  121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                        121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
US-09-403-407-20
Sequence 20, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-543-407-26
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APPLICANT: Collinson, S. Karen
APPLICANT: Clouthier, Sharon C.
APPLICANT: Dron, James D.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: BASED VACCINES
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                               Query Match 88.5%; Score 692; DB 19; Length 1 Best Local Similarity 90.7%; Pred. No. 8.7e-66; Matches 137; Conservative 2; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATE: US/08/233,642A
FILING DATE: 26-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  920043.403C3
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US-08-233-642A-57
; Sequence 57, Application US/08233642A
; GENERAL INFORMATION:
; APPLICANT: Kay, William W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-6900
TELEFAX: (206) 682-6031
TELEFAX: 3723836 SEEDANBERRY
INFORMATION FOR SEO ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                            TYPE: PRT
, ORGANISM: Salmonella enteritidis
US-09-543-407-5
2000-04-05
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ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 151 amino acids
amino acid
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STATE: Washington
COUNTRY: U.S.A.
ZIP: 94104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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Gaps

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TYPE: PRT
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                                                                                         61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                       SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
                                1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESUMATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT FILING ADDRES: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FALSEQ for Windows Version 4.0
LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REPERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASESQ for Windows Version 4.0
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86.3%; Score 675; DB 19; Length 151;
Best Local Similarity 81.9%; Pred. No. 5.9e-64;
Matches 136; Conservative 0; Mismatches 0; Indels 30
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; Sequence 18, Application US/09543407
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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US-09-543-407-18
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LENGTH: 151
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61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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APPLICANT White, Aaron P.
APPLICANT Doran, James L.
APPLICANT Collinanon, S. Karen
APPLICANT Collinanon, S. Karen
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
TITLE REPERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
SOFTWARE: FASTESQ for Windows Version 4.0
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TYPE: PRT
CRGANISM: Artificial Sequence
CRGANISM: Artificial Sequence
CTATER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
CTHER INFORMATION: sequence containing the replacement fragment
CTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
US-09-543-407-28
                                                                                                                                                                                                   78.9%; Score 617; DB 19; Length 151; 73.6%; Pred. No. 1e-57; 1ive 0; Mismatches 0; Indels 46
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Pred. No. 2.2e-57;
6; Mismatches 23;
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
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US-09-543-407-12
Sequence 12, Application US/09543407
GENERAL INFORMATION:
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80.8%;
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Matches 128; Conservative
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Best Local Similarity
Matches 122; Conserv
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LENGTH: 151
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
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US-09-543-407-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
APPLICANT: Collinson, S. Karen
APPLICANT: KAY, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: White, Aaron P.
APPLICANT: Woran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REPERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.3%; Score 612; DB 19; Length 151; 81.5%; Pred. No. 3.6e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 77.9%; Score 609; DB 19; Length 151; Best Local Similarity 82.1%; Pred. No. 7.5e-57; Matches 124; Conservative 4; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 24, Application US/09543407; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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Matches 123; Conservative
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US-09-543-407-24
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OTHER INF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 VGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVWVRQV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GVVPQWGGGGNHNGGGRSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 22, Application US/09543407
| GRERAL INFORMATION:
| APPLICANT: White, Aaron P. |
| APPLICANT: Doran, James L. |
| APPLICANT: Collinson, S. Karen |
| APPLICANT: Collinson, S. Karen |
| APPLICANT: Collinson, S. Karen |
| APPLICANT: Collinson, S. Karen |
| APPLICANT: Collinson, S. Karen |
| APPLICANT: RESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES |
| TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES |
| TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES |
| CURRENT FILING DATE: 2000-04-05 |
| CURRENT FILING DATE: 2000-04-05 |
| NUMBER OF SEQ ID NOS: 59 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: RAy, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SEQ ID NO 31
LENGTH: 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 131;
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89.3%; Pred. No. 1.7e-56;
iive 2; Mismatches 12;
121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                       Sequence 31, Application US/09543407 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 117; Conservative
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61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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US-08-978-878-4
US-08-978-878-4
Sequence 4, Application US/08978878
SEQUENCE 4, Application US/08978878
SEQUENCE 4, APPLICANT NORMARK, Staffan
APPLICANT NORMARK, Staffan
TITLE 0F INVANTION FIRENOECTIN BINDING PROTEIN AS WELL AS ITS PREPARATION
FILE REFERENCE: 012889-081
CURRENT APPLICATION NUMBER: US/08/978,878
CURRENT PILING DATE: 1997-11-26
SALLIER APPLICATION NUMBER: SE 8801723-1
EARLIER FILING DATE: 1988-05-06
                                                                                                                                                                                                                                                                                                                          09
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                                                                                                                                                                                                                                                                                                                                                                                      61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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                                                                                                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
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APPLICANT COllinson, S. Karen
APPLICANT COllinson, S. Karen
APPLICANT COLLINSON, S. Karen
APPLICANT KAY, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REPERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILE SEQUENCE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FRASEO for Windows Version 4.0
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Recombinant Salmonella enteritidis 3b afgA sequence containing the replacement fragment encoding PT3 from GP63 of Leishmania major.
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                                                                                                                                                Length 151;
                                                                                                                                             73.8%; Score 577; DB 19; Length 15
80.8%; Pred. No. 2.1e-53;
ive 5; Mismatches 24; Indels
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68.9%; Pred. No. 1.4e-47;
iive 18; Mismatches 29;
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Best Local Similarity 68.9%
Matches 104; Conservative
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ORGANISM: Escherichia coli
                                                                                                                                                       Query Match
Best Local Similarity 80.8°
Matches 122; Conservative
         CTHER INFORMATION:
CTHER INFORMATION:
CTHER INFORMATION:
US-09-543-407-16
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EARLIER FILING DATE: 1989-05-04
EARLIER APPLICATION NUMBER: US 07/789,437
EARLIER APPLICATION NUMBER: US 07/970,846
EARLIER FILING DATE: 1991-11-06
EARLIER FILING DATE: 1992-11-03
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1995-06-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PARENTIN NUMBER: US 08/495,959
EARLIER FILING DATE: 1995-06-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PARENTIN NUMBER: US 08/495,959
EARLIER FILING DATE: 1995-06-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PARENTIN NET: 2.0
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                                                                                                                                                                                                                                                                                                                          TYPE: PRT
; ORGANISM: Escherichia coli
US-08-978-878-4
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US-99-44. EN JOHN CALLER JOHN CALLED TO SEQUENCE 4, Application US/09741873C

GENERAL INFORMATION:

APPLICANTE NORMATION:

TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation

TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation

TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation

TITLE OF INVENTION: PROPERTY OF 10269-084

CURRENT APPLICATION NUMBER: US 08/978,878

PRIOR FILING DATE: 1998-05-04

PRIOR APPLICATION NUMBER: US 07/347,189

PRIOR APPLICATION NUMBER: US 07/347,189

PRIOR PELING DATE: 1991-11-06

PRIOR FILING DATE: 1991-11-06

PRIOR PELING DATE: 1994-01-28

PRIOR APPLICATION NUMBER: US 07/789,437

PRIOR APPLICATION NUMBER: US 07/789,437

PRIOR PELING DATE: 1994-10-05

NUMBER OF:SEQ ID NOS: 11

NUMBER OF:SEQ ID NOS: 11

SOFTWARE: Patentin Version 3.0 Sequence 7905, Ap Sequence 7905, Ap Sequence 7906, Ap Sequence 7906, Ap Sequence 11109, A Sequence 219256, Sequence 2168, Ap Sequence 2168, Ap Sequence 2168, Ap Sequence 741, App Sequence 741, App Sequence 741, App Sequence 11, ö, 120 61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDOWNAKNSDITVGQYGG 120 9 9 61 TDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFCNSATLDQWNGXNSEMTVKQFGG 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ Sequence . 0 66.5%; Score 520; DB 5; Length 151; 68.2%; Pred. No. 5.5e-38; ive 19; Mismatches 29; Indels US-60-579-062-7907
US-10-425-115-300390
US-10-425-115-300390
US-60-565-632-7905
US-60-565-632-7906
US-60-579-062-7906
US-60-579-062-7906
US-60-579-062-7906
US-60-579-062-11109
US-60-565-632-11109
US-60-565-632-9168
US-10-170-2058-35751
US-60-565-632-9168
US-10-170-2058-741
US-10-170-2058-741
US-10-170-2058-741
US-10-170-2058-741
US-10-170-2058-741
US-10-170-2058-741 US-10-767-701-35342 121 NNAALVNOTASDSSVMVROVGFGNNATANOY 151 151 ALIGNMENTS GNGAAVDQTASNSSVNVTQVGFGNNATAHQY

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THILE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REPERENCE: 012889-084
CURRENT APPLICATION WUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
PRIOR PAPLICATION WUMBER: SE 8801723-1
PRIOR APPLICATION WUMBER: US 08/978,878
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1999-11-26
PRIOR FILING DATE: 1999-11-26
PRIOR FILING DATE: 1999-11-106
PRIOR FILING DATE: 1999-11-106
PRIOR PAPLICATION WUMBER: US 07/970,846
PRIOR PAPLICATION WUMBER: US 08/187,865
PRIOR PAPLICATION WUMBER: US 08/187,865
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-10-05
PRIOR FILING DATE: 1994-10-05
WUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Version 3.0
SEQ ID NO 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 VGOGADNSTIELTONGFRNNATIDOWNAKNSDITVGOYGGNNAALVNOTASDSSVMVROV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 VGQGSDDSSIDLTQRGFGNSATLDQWNGRNSEMTVKQFGGGNGAAVDQTASNSSVNVTQV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GVVPQYGGGGNHGGGGNNSGPNSELNTYQYGGGNSALALQTDARNSDLTITQHGGGNGAD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGNGAD 80
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APPLICANT: HANSEN, ERIC J.
APPLICANT: HANSEN, CHRISTOPH
APPLICANT: COPE, LESLIE D.
APPLICANT: COPE, LESLIE D.
APPLICANT: TESKE, MCHAEL J.
APPLICANT: FISKE, MCHAEL J.
APPLICANT: FRENDRBURG, ROSS A.
TITLE CONT: FRENDRBURG, ROSS A.
TITLE CONTENT APPLICATION UNDER: US/09/952,267B
CURRENT FILING DATE: 2001-09-12
PRIOR PILING DATE: 1999-06-21
PRIOR PILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PATENTIN VOR: 98
SOFTWARE: PATENTIN VOR: 98
SOFTWARE: PATENTIN VOR: 98
SOFTWARE: PATENTIN VOR: 98
TYPE: PRI
ORGANISM: MORAXEILA CATATHALIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.5%; Score 442; DB 5;
64.9%; Pred. No. 2.8e-31;
tive 18; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/09952267B GENERAL INFORMATION:
                                        Sequence 2, Application US/09741873C
GENERAL INFORMATION:
APPLICANT: Normark, Staffan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 64.99
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Escherichia coli
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US-09-952-267B-5
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RESULT 2
US-09-741-873C-2
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                                                                                                                                                                                                                                                    138 YSRAIGDSSTIGGGYYNQATGEXSTVAGGRNN----QATGNNSTVAGGSYNQATGNNSTV 193
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Sequence 5, Application US/10872768

GENERAL INFORMATION:
APPLICANT: HANSEN, ERIC J.
APPLICANT: AESTED D.
APPLICANT: PISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
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APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISHE, MICHAEL J.
APPLICANT: PREDBRING: ROSS A.
FILE REFERENCE: AMCY:024
CURRENT FILING DATE: 2004-06-21
FRIOR APPLICATION NUMBER: US/09/336,447
FRIOR PRIOR APPLICATION NUMBER: US/09/336,447
FRIOR FILING DATE: 1999-06-21
FRIOR FILING DATE: 1999-06-21
FRIOR APPLICATION OF: 2.1
FRIOR APPLICATION OF: 2.1
FRIOR APPLICATION OF: 2.1
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                                                                                                  28 GGGNHN-----GGGNSS---GPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGY
                                                                                                                                                      --TYSTIGGGY
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SENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HANSEN, ERLC J.
APPLICANT: COPE, LESTIE D.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
TILE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS FILE REFERENCE: AMCY:024
FILE REFERENCE: AMCY:024
CURRENT FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US/09/336,447
11.9%; Score 93; DB 5; Length 892; larity 27.7%; Pred. No. 5.7; Conservative 14; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6; Length 892; 5.7;
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                                                                                                                                                      89 GGGDYNEAKGNYSTVGGGSSNTAKGEKSTIGGGDTNDANG---
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11.9%; Score 93; DB 6
Best Local Similarity 27.7%; Pred. No. 5.7;
Matches 41; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 V----NQTASDSSVMVRQVGFGNNATAN 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Moraxella catarrhalis
                              Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
US-10-872-769-5
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US-10-872-768-5
          Query Match
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67 THEMAHAGYGNG----ADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDI-----TVGQ 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             776 ISAF-HSGVGNTDSQLAGFMRNAAGGT--LFNFGFANDGTLNLGNANLGDYNVGSGNVGS 832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.8%; Score 92; DB 6; Length 1459; larity 25.0%; Pred. No. 12; Conservative 20; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 574, Application US/60566425
GENERAL INFORMATION:
APPLICANT DOMON, BULLOO et al.
TITLE OF INVENTION: COLON DISEASE TARGETS AND USES THEREOF
FILE REFERENCE: CLO01522-PROV
CURRENT APPLICATION NUMBER: US/60/566,425
CURRENT PILING DATE: 2004-04-30
NUMBER OF SEQ ID NOS: 1422
SOFWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 YGGNNAALVNQTASDSSVMVRQVGFGNNATAN 149
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                                           CURRENT APPLICATION NUMBER: US/10/482,706
CURRENT FILING DATE: 2004-01-02
FRIOR APPLICATION NUMBER: PCT/GB02/03052
FRIOR PLLING DATE: 2002-07-04
FRIOR PLLING DATE: 2001-07-04
FRIOR PLLING DATE: 2001-07-04
FRIOR PLLING DATE: 2001-07-04
FRIOR PLLING DATE: 2001-05
FRIOR FLLING DATE: 2001-10-05
FRIOR FLLING DATE: 2001-10-05
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FRIOR FLLING DATE: 2001-10-05
FRIOR FLLING DATE: 2001-10-05
FRIOR FLLING DATE: 2001-10-05
FRIOR FLLING DATE: PRECENTING 129
FRIOR FLLING DATE: ACCOUNT 10-05
FRIOR FLLING DATE: ACCOUNT 10-05
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                                                           US/10/482,706
                                                                                                                           PCT/GB02/03052
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GENERAL INFORMATION:
APPLICANT: DOMON, Bruno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35; Conservative
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874 SQGGYGRNA 882
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Matches 38; Conserv
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Best Local Similarity
Matches 35; Conserv
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US-60-566-425-574
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US-60-576-812-606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 312468, Application US/10425115
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Sosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Can, Yongwei
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEG ID NOS: 369326
SEG ID NOS: 31468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89 GGGDYNEAKGNYSTVGGGSSNTAKGEKSTIGGGDTNDANG------TYSTIGGGY 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----GNGADVGQGADNSTI--ELTQNGFRNNATIDQWNAKNSDITVGQYG---GNNAAL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 YSRAIGDSSTIGGGYYNQATGEKSTVAGGRNN----QATGNNSTVAGGSYNQATGNNSTV 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGNHN------GGGNSS---GPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGY 75
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GENERAL INFORMATION:
APPLICANT: James, Brian William
APPLICANT: Marsh, Philip
APPLICANT: Hampshire, Tobias
TITLE OF INVENTION: Mycobacterial Antigens Expressed During Latency
                                                                                                                                                                                                                                                                                                                                           Query Match
11.9%; Score 93; DB 6; Length 892;
Best Local Similarity 27.7%; Pred. No. 5.7;
Matches 41; Conservative 14; Mismatches 49; Indels
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11.8%; Score 92; DB 6; Length 295;
Best Local Similarity 25.3%; Pred. No. 2;
Matches 37; Conservative 13; Mismatches 40; Indels
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US-10-425-115-312468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 V----NQTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 AGGSHNOATGEGSF---AAGVENKANAN 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 GNNAALVNQTASDSSVMVRQVGFGNN 145
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                                                                                                                                                                                           TYPE: PRT ORGANISM: Moraxella catarrhalis
PRIOR FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Zea mays
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US-60-566-425-571
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                   SEQ ID NO 571
LENGTH: 894
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                                                                                                                                                                                                                                                                                                                                                                                                                                            836 GSGGG----SYQGKQGGYSQS----NYNSPGS----GQ-----NYSGPPSSYQS 873
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                                                                                                                                                                                                                                                                                                                               27 GGGG------NHNGGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGN
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11.7%; Score 91.5; DB 7; Length 894;
Best Local Similarity 27.1%; Pred. No. 7.7;
Matches 35; Conservative 15; Mismatches 32; Indels 47
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11.7%; Score 91.5; DB 7; Length 891;
Best Local Similarity 27.1%; Pred. No. 7.7;
Matches 35; Conservative 15; Mismatches 32; Indels 4
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GENERAL INFORMATION:
APPLICANT: DOWON, Bruno et al.
TITLE OF INVENTION: COLON DISEASE TARGETS AND USES THEREOF
FILE REFERENCE: CL001522-PROV
CURRENT FILING DATE: 2004-04-30
NUMBER OF SEQ ID NOS: 1422
SOFTWARE: FastSEQ for Windows Version 4.0
ERGIN NO 570
LENGTH: 894
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; GENERAL INFORMATION:
; TITLE OF INVENTION: COLON DISEASE TARGETS AND USES THEREOF
; TITLE OF INVENTION: COLON DISEASE TARGETS AND USES THEREOF
; FILE REPERENCE: CL001522-PROV
; CURRENT PAPLICATION NUMBER: US/60/566,425
; CURRENT FILING DATE: 2004-04-30
; NUMBER OF SEQ ID NOS: 1422
TITLE OF INVENTION: COLON DISPASE TARGETS AND USES THEREOF FILE REFERENCE: CL001527PROV CURRENT APPLICATION NUMBER: US/60/576,812 CURRENT FILING DATE: 2004-06-04 NUMBER OF SEQ ID NOS: 1501 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 RQVGFGNNA 146
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877 SQGGYGRNA 885
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874 SQGGYGRNA 882
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CRGANISM: Homo sapiens
US-60-566-425-570
                                                                                                                                                                   TYPE: PRT
, ORGANISM: Homo sapiens
US-60-576-812-606
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US-60-566-425-570
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                                                                                                                                                                      11.7%; Score 91.5; DB 7; Length 894; 27.1%; Pred. No. 7.7; ive 15; Mismatches 32; Indels 47
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11.7%; Score 91.5; DB 7; Length 894;
Best Local Similarity 27.1%; Pred. No. 7.7;
Matches 35; Conservative 15; Mismatches 32; Indels 4
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GENERAL INFORMATION:
APPLICANT: DOMON, BILLOW DISPASE TARGETS AND USES THEREOF
TITLE OF INVENTION: COLON DISPASE TARGETS AND USES THEREOF
FILE REFERENCE: CL001522-PROV
CURRENT FELING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 575, Application US/60566425, GENERAL INFORMATION:
APPLICANT: DOMON, Bruno et al.
TITLE OF INVENTION: COLON DISEASE TARGETS AND USES THEREOF FILE REFERENCE: CLOOL522-RROV
CURRENT APPLICATION NUMBER: US/60/566,425
CURRENT FILING DATE: 2004-04-30
NUMBER OF SEQ ID NOS: 1422
SOFTWARE: FRACESQ for Windows Version 4.0
SEQ ID NO 575
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SOFTWARE: FastSEQ for Windows Version 4.0
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11.7
Best Local Similarity 27.1
Matches 35; Conservative
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US-60-566-425-575
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ORGANISM: Homo sapiens
                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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US-60-566-425-578
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US-60-566-425-575
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                                                                                                          27 GGGG------NHNGGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHENAHAGYGN 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
11.7%; Score 91.5; DB 7; Length 894;
Best Local Similarity 27.1%; Pred. No. 7.7;
Matches 35; Conservative 15; Mismatches 32; Indels 47; Gaps
                                                                              Gaps
                                                                              47;
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                                    11.7%; Score 91.5; DB 7; Length 894; 27.1%; Pred. No. 7.7; ive 15; Mismatches 32; Indels 4
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11.7%; Score 91.5; DB 7; Length 894;
Best Local Similarity 27.1%; Pred. No. 7.7;
Matches 35; Conservative 15; Mismatches 32; Indels 47
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 602, Application US/60576812
GENERAL INFORMATION:
APPLICANT DOWN, BIATON:
TITLE OF INVENTION: COLON DISEASE TARGETS AND USES THEREOF FILE REFERENCE: CLO01527PROV
CURRENT PELING DATE: 2004-06-04
NUMBER OF SEQ ID NOS: 1501
SOFTWARE: FastSEQ for Windows Version 4.0
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GENERAL INFORMATION:
APPLICANT DOWN, Bruno
TITLE OF INVENTION: COLON DISEASE TARGETS AND USES THEREOF
TILE REFERENCE: CL001527PROV
CURRENT PELING DATE: 2004-06-04
NUMBER OF SEQ ID NOS: 1501
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 894
                                  Query Match
Best Local Similarity 27.18
Matches 35; Conservative
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ORGANISM: Homo sapiens
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US-60-576-812-603
US-60-566-425-578
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US-60-576-812-602
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US-60-576-812-603
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        Qy
        27 GGGG------NHNGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGN 77

        Db
        795 GGGGSDYNYESKFNYSGSGGRSGGNS-----YGSGGASY------NPGSHGGYGG 838

        Qy
        78 GADVGCGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVNV 137

        Db
        839 GSGG----SSYQGRQGGYSQS----NYNSPGS----GQ------NYSGPPSSYQS 876

        Qy
        138 RQVGFGNNA 146

        Db
        877 SQGGYGNNA 885

        Db
        877 SQGGYGNNA 885

        Job time: 18.8 secs
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OM protein - protein search, using sw model

August 2, 2004, 14:39:53 ; Search time 9.4 Seconds (without alignments) 1545.204 Million cell updates/sec Run on:

US-09-543-407-26 782 1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Res

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121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151

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leishmanolysin (EC	hypothetical glyci		leishmanolysin (EC	probable PPE prote	PPE	probable PPE prote	PPE	ein	probable PPE prote	PPE	ice nucleation pro	probable PPE prote	hypothetical prote	trfA protein - sli	nuclear pore compl	
A44951	E70768	835327	C42049	B70524	B70987	B70663	B70520	842136	F70675	A70762	SNPSO	E70969	T26667	T14004	A54831	
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599	434	575	639	963	1053	354	1436	1748	582	678	1200	3716	586	1390	1317	
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30	31	32	33	34	35	36	3.7	38	33	40	41	42	43	44	45	

## ALIGNMENTS

 RESULT 1 JC6039 JC6039 JC6039 JC6039 JC6031 Potein agfA precursor - Salmonella enteritidis C;Species: Salmonella enteritidis C;Accession: JC6039; PC6015; A44898 C;Accession: JC6039; PC6015; A44898 R;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W. J. Bacteriol 178, 662-667, 1996 A;Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fimbriae. A;Reference number: JC6039; MUD:96146512; PMID:8550497 A;Accession: JC6039 A;Molecule type: DNA A;Residens: 1.51 cCOL> A;Residens: 1.51 cCOL> A;Residens: JC6039 A;Accession: PC6015
 A, Mosteria type: procein A, Residues: 21-52 < CCO2> A, Experimental source: strain 27655-3b A, Mote: the authors translated the codon ACG for residue 44 as 11e A, Note: the authors translated the codon ACG for residue 44 as 11e A, Colliano S. K.; Emody, L.; Muller, K.H.; Trust, T.J.; Kay, W.W. J. Bacteriol: 173, 4773-4781, 1991 A, Title: Purification and characterization of thin, aggregative fimbriae from Salmonell A, Reference number: A44898; MUID:91310586; PMID:1677357 A, Contents: 27655 A, Accession: A44898 A, Status: preliminary
 A; Moseiduses: 21-33 < CO3> A; Moseiduses: 21-33 < CO3> A; Mote: sequence extracted from NCBI backbone (NCBIP:45936) C; Genetics: A; Genetics: A; Cenetics: A; Description: major component of thin aggregative fimbriae A; Description: major component of thin aggregative fimbriae C; Keywords: fimbria F; 1-20/Domain: signal sequence #status predicted < SIG> F; 1-151/Product: fimbrin protein agfA #status experimental < MAT>
 Query Match         88.5%;         Score 692;         DB 2;         Length 151;           Best Local Similarity         90.7%;         Pred. No. 3.6e-51;         O. Gaps         0;           Matches 137;         Conservative 2;         Mismatches 12;         Indels 0;         Gaps 0;           Qy           MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ 60           Db           MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
Oy 61 LVTRVVTHEMAHAGYGNGADVGOGADNSTIELTONGFRNNATIDOWNAKNSDITVGGYGG 120 

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60 QLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG 119
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Best Local Similarity 67.1%
Matches 102; Conservative
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Best Local Similarity 68.9°
Matches 104, Conservative
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A;Map position: 23.15
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A;Molecule type: DNA
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NiAlternate names: csgA protein; major curlin protein
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change 01-Mar-2002
C;Accession: S70788; G64846; S31202; S34569; S34559
R;Hammar, M: Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S.
Mol: Microbiol. 18, 661-670, 1995
A;Atternce number: S70783; MUID:96414468; PMID:8817489
A;Accession: S70788
A;Accession: G70788
A;Accession: G7078
A;Accession: G70789
A;Accession: G70789
A;Accession: G70789
A;Accession: G70789
A;Cross-reference number: S70783; MUID:91147558; PIDN:ChA62282.1; PID:91147564
A;Cross-reference: EMBL:X90754; NID:91147558; PIDN:ChA62282.1; PID:91147564
A;Cross-reference: strain K12, substrain W3110
A;Accession: G48846
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Pred. No. 3.6e-51;
2; Mismatches 12;
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NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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Matches 137; Conservative
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A;Title: The RpoS sigma factor relieves H-NS-mediated transcriptional repression of csg.
A;Recession: S31202; MUID:93211294; PMID:8459772
A;Recession: S31202
A;Roldcule type: DNA
A;Residues: 1-6, VV, 8-151 < OLS1>
A;Roldcule type: DNA
A;Residues: BMBL:L04979
A;Rcoss-references: BMBL:L04979
A;Recession: S34560
A;Residues: 234560
A;Residues: 2142;44-50 < OLS2>
B;Olsen, A.N.; Armqvist, A.M.
Submitted to the EMBL Data Library, October 1992
A;Reference number: S34559
A;Recession: S34559
A;Residues: 1-133, RQRDSGWLW' < OLS3>
A;Residues: 1-133, RQRDSGWLW' < OLS3>
A;Residues: 1-133, RQRDSGWLW' < OLS3>
A;Residues: 1-133, RQRDSGWLW' < OLS3>
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Escherichia coli (strain O157:H7, substrain RIMD C.Species: Escherichia coli C.Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 #colores for the sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_change 18-Jul-2001 #text_c
                                   CSG
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A;Residues: 1-152 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34843.1; PID:g13360880; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs1420
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; Pred. No. 5.3e-37;
18; Mismatches 29
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QY 3 LLKVAAFAAIVYSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANA 55	Cy 116 GGYGGNNAALWNGTABDSSVWARDVGFGNNATANO 150  Db 97 GGFGSNHTTILTDDGNGNIAAGVGYGRGCSANVSO 131  RESULT 7  R	Oy 116 GQYGGNNAALVNQTASDSSVMVRQVGRGCRANVSQ 131  RESULT 8  B9565  Hypotherical glycine-rich protein [imported] - Sinothizobium meliloti (strain 1021) mag C;Species: Sinorhizobium meliloti C;Species: Sinorhizobiu
	PRESULT 5 Habsoft al protein csgA [imported] - Escherichia coli (strain 0157:H7, substrain EDL93 C,Species: Escherichia coli C,Species: Escherichia coli C,Species: Escherichia coli C,Species: Sastantichia sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C,Accession: Habsoft Hasquence_revision 16-Feb-2001 #text_change 14-Sep-2001 R,Perna, N. T.; Plunkett III, G, Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew Nature 409, 52-531, 2001 A,Itle: Genome sequence of enterchemorrhagic Escherichia coli 0157:H7. A,Reference number: A85480; MUID:21074935; PMID:11206551 A,Scatus preliminary A,Molecule type: DNA A; Residues: 1152 <870. A,Cessaion: H8566 A,Experimental source: strain 0157:H7, substrain EDL933 A,Cessaion: A,Molecule type: DNA A; Residues: 1152 <870. A,Cessaion: Muid:A,Molecule type: DNA A; Residues: 1152 <870. A,Cessaion: Matches 1057:H7, substrain EDL933 A,Cessaion:	RESULT 6 AD3143  CONSERVED Hypothetical protein Atu4768 [imported] - Agrobacterium tumefaciens (strain CS C, Species: Agrobacterium tumefaciens C, Species: Agrobacterium tumefaciens C, Species: Agrobacterium tumefaciens C, Species: Agrobacterium tumefaciens C, Species: Agrobacterium tumefaciens C, State 11.3m-2002 #sequence_revision 11.7m-2002 #text_change 18-Nov-2002 C, Accession: AD3143 R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, C; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S. Science 244, 2317-2323, 2001 A, Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CSB. A, Accession: AD3143 A, Reference number: AB2577; MUID:21608550; PMID:11743193 A, Reference number: AB2577; MUID:21608550; PMID:11743193 A, Reference number: AB2577; MUID:21608550; PMID:11743193 A, Reference number: SEBAE008689; PIDN:AAL45562.1; PID:g17743277; GSPDB:GN0187 A, Experimental source: strain CSB (Dupont) C, Genetics: A, Gene: Atu4768 A; Map position: linear chromosome Query Match Best Local Similarity 25.28; Pred. No. 0.0088; Matches 39; Conservative 26; Mismatches 59; Indels 31; Gaps 4;

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C,Accession: C90006
R,Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. R,Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. Basawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res 1.1-22, 2001
A,Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gend A,Reference number: A99629; MUID:21156231; PMID:11258796
A,Accession: C90806
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                                                                                                                      - Escherichia coli (strain O157:H7,
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ice nucleation protein inaA - Erwinia ananas
C.Species: Erwinia ananas
C.Spate: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 26-Aug-1999
                                                                                                                  minor curlin subunit precursor CsgB [imported] - Escherichia coli (strain O. C. Species: Escherichia coli
C. Species: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
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0.015;
ches 49;
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ilarity 29.8%; Pred. No. 0.015;
Conservative 17; Mismatches 4
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Best Local Similarity
Matches 34; Conserv
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nes 34; Conserv
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A,Gene: ECs1419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gurlin mucleator protein cagB precursor - Escherichia coli (strain K-12)

NyAlternace names: cagB protein; curlin nucleation component; minor curlin protein
Cipberes: Escherichia con Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling Coling C
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                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --- QGADNSTI--- ELTQNGFRNNATIDQWNAK---NSDITV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----GGYANTANVGFKGLTLTTQGSHAAGİVAQSVGGGGGTGGTASSYSAGIGFTASVAV 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86
                                                                                                                                                                                                                                                                                                                                             11 AIVVSGSALAGVVPQ--WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTH 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSANAALYDQLVT--RVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI AAAAGY DLANSEYNFAVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -NNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49; Indels 14;
                                                                                                                                                                                                                                                                             36;
                                                                                                                                                                                                     14.5%; Score 113; DB 2; Length 2174; 27.0%; Pred. No. 0.23; ive 21; Mismatches 51; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 151;
                                                                                                                                                                                                                                                                                                                                                                                        A,Reference number: A96039; MUID:21368234; PMID:11474104
A,Contents: annotation
C,Generics:
A,Gene: SMD21548
A,Genome: plasmid
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ilarity 29.8%; Pred. No. 0.015;
Conservative 17; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GQYGGNNAA--LVNQTASDSSVMVRQVG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMAHAGYGNGADVG----
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                40;
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                                                                                                                                                                                                                       Query Match
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Matches 4
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R; Parkhill, J; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar Nature 413, 848-852, 2001
A; Muthors: Parry, C.; Ouail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K. A; Reference number: AB0502; MUID:21534947; PMID:11677608
A; Reference number: AB0502; MUID:21534947; PMID:11677608
A; Residues: Preliminary
A; Molecule type: DNA
A; Residues: 1-151 < PAR>
A; Cross-references: GB:AL513382; PIDN:CAD08267.1; PID:g16502314; GSPDB:GN00176
C; Genetics: A; GB:AL513382; PIDN:CAD08267.1; PID:g16502314; GSPDB:GN00176
A; Gene: STX1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-1034 «NIC>
C;Comment: This protein consists of 52 repeats of closely related 16-amino acid motifs
C;Superfamily: ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ice nucleation active protein - Brwinia uredovora (strain KUIN-3)
C;Species: Brwinia uredovora
C;Species: Brwinia uredovora
C;Species: 30-699-1993 #sequence_revision 20-Aug-1994 #text_change 17-Mar-1999
C;Accession: JC2143
R;Michigami, Y: Watabe, S:; Abe, K.; Obata, H.; Arai, S.
Biosci. Biotechnol. Biochem: 58, 762-764, 1994
A;Title: Clohing and sequencing of an ice nucleation active gene of Brwinia uredovora.
A;Reference number: JC2143; MUID:94264407; PMID:7764866
A;Accession: JC2143.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              576 -----LTA-GYGSTQTAQE----NSDLTTG-YGSTSTAGYDSSLIAGYGSTQTAGYHSIL 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 GIATATNYDLARSEYNFAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISQEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 GGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGNGADVGQGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 RINNATIDQWNAKNSDIT-VGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
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Best Local Similarity 29.9%; Pred. No. 0.39;
Matches 40; Conservative 19; Mismatches 37; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.7%; Score 107; DB 2; Length 151; 30.4%; Pred. No. 0.039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 GSANAALYD--QLVTRVVTHEMAHAGYGNGADVGQ-GADNST----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2, 2004, 14:56:25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:|: ||:
T--AGYGSTQTAQE 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F,161-993/Region: R-domain
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e : 10.4 secs
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Best Local(Similarity
Matches 35, Conserv
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AP40635

nucleation component of curlin monomers [imported] - Salmonella enterica subsp. enterica
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AH0635
                                                                                                                     Sequence similarity to those
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cipate: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999 Cipate: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999 Cipate: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999 Cipate: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999 Cipate: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999 Cipate: 31-Dec-1996 #text_change 08-Oct-1999 Cipate: 31-Dec-1996 #text_change 08-Oct-1999 Cipate: 31-Dec-1996 #text_change 08-Oct-1999 Cipate: 31-Dec-1996 #text_change 08-Oct-1999 Cipate: 31-Dec-1996 #text_change 08-Oct-1999 Cipate: 31-Dec-1996 #text_change 08-Oct-1999 Cipate: 31-Dec-1996 #text_change 08-Oct-1999 Cipate: 31-Dec-1996 #text_change 08-Oct-1999 Cipate: 31-Dec-1996 #text_change 08-Oct-1999 Cipate: 31-Dec-1996 #text_change 08-Oct-1999 Cipate: 31-Dec-1996 #text_change 08-Oct-1999 Cipate: 31-Dec-1996 #text_change 08-Oct-1999 Cipate: 31-Dec-1996 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_change 08-Oct-1999 #text_
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A,Note: fimbriae bind to fibronectin, plasminogen, tissue plasminogen activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 QNGFRNNATIDQWNAKNSDITVGQYG----GNNAALV----NQTASDSSVMVRQVGFG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSANAALYD--QLVTRVVTHEMAHAGYGNGADVGQ-GADNST-----1ELTQNGF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 GGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELT 93
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                                             Fibb. K.; Watcabe, S.; Emori, Y.; Watcabe, M.; Arai, S.
Fibb. K.; Watcabe, S.; Emori, Y.; Watcabe, M.; Arai, S.
Fibb. Lett. 258, 297-300, 1989
A;Title: An ice nucleation active gene of Erwinia ananas. Sequence simila A;Reference number: 807053, MUID:90092494; PMID:2599095
A;Accession: 807053
A;Accession: 807053
A;Accession: 807053
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-132 AABBA
A;Cross-references: GB:X17316; NID:9296095; PIDN:CAA35194.1; PID:9296096
C;Superfamily: ice nucleation protein
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OM protein - protein search, using sw model

August 2, 2004, 14:36:12; Search time 5.3 Seconds (without alignments) 1483.508 Million cell updates/sec Run on:

US-09-543-407-26 782 1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151 Title: Perfect score: 7 Sequence:

Scoring table:

141681 segs, 52070155 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=S.enteritidis; STRAIN=27655-3B; MEDLINE=91310566; PubMed=1677357; Collinson S.K., Emocdy L., Mueller K.-M., Trust T.J., Kay W.W.; Purification and characterization of thin, aggregative fimbriae from Salmonella enteritidis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
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-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI AN COLLED SURRACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI. CAN BIND TO
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SPECIES=S.enteritidis; STRAIN=77655-3B;
MEDLINE=9401373; PubMed=8104955.
Doran J.L., Collinson S.K., Burian J., Sarlos G., Todd E.C.D.,
Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., Kay W W.;
"DNA-based diagnostic tests for Salmonella species targeting agfA,
the structural gene for thin, aggregative fimbriae.";
J. Clin. Microbiol. 31:2263-2273(1993).
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                                     Bacteriol. 185:2330-2337(2003)
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EMBL, AB008749, AAL20074.1; --
EMBL, AL627269, CAD08268.1; --
EMBL, AE016840; AA069399.1; --
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StyGene, SG10608; csgA.
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MEDLINE=91310586; PubMed=1677357;

Collinean S.K., Emcedy L., Trust T.J., Kay W.W.;

Collinean S.K., Emcedy L., Trust T.J., Kay W.W.;

Purification and characterization of thin, aggregative fimbriae from Salmonella enteritidis.";

J. Bacteriol. 173:4773-4781(1991).

-!- FUNCTION: CURLIN 1S THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURPACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hammar M., Arngvist A., Bian Z., Olsen A., Normark S.,
"Expression of two csg operons is required for production of
fibronectin- and congo red-binding curli polymers in Escherichia coli
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Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
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"A 718-kb DNA sequence of the Escherichia coli K-12 genome
Corresponding to the 12.7-28.0 min region on the linkage map.";
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STRAIN=12 / W1110;
MEDLINE=93211294; PubMed=8459772;
Olsen A., Arnqvist A.;
"The RpoS sigma factor relieves H-NS-mediated transcriptional
repression of csgA, the subunit gene of fibronectin-binding curli
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STRAIN-RIZ / MGG1655,
MEDIJNE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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MEDLINE=93023873; PubMed=1357528;
Arnqvist A., Olsen A., Pfeifer J., Russell D.G., Normark S.;
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                                                        01-DEC-1992 (Rel. 24, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
   151 AA.
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                                                                                                                                                           Major curlin subunit precursor.
CSGA OR B1042.
Escherichia coli.
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Science 277:1453-1474(1997),
STANDARD;
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PSOURCE FROM N.A.

RX MEDLINE=21156231; PubMed=11258796;

RX MEDLINE=21156231; PubMed=11258796;

RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Rhara S., Shiba T., Hattori M., Shinagawa H.;

RA Lida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Rhara S., Shiba T., Hattori M., Shinagawa H.;

RA C., Takami H., Honda T., Sasakawa G., Ogasawara N., Yasunaga T., Rhara S., Shiba T., Hattori M., Shinagawa H.;

RA C., Takami H., Honda T., Sasakawa H.;

RA C., Takami H., Honda T., Sasakawa H.;

RA C., Takami H., Honda T., Sasakawa H.;

RA C., Takami H., Honda T., Sasakawa H.;

RA C., Takami H., Honda T., Takami K., Tokami K., Tokami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami K., Takami 
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STRAIN=X12 / MC4100;
MEDLINE=96414468; PubMed=8817489;
Hammar M., Arnqvist A., Bian Z., Olsen A., Normark S.;
Hammar M., Arnqvist A., Bian Z., Exprisesion of two csg operons is required for production of fibronectin- and congo red-binding curli polymers in Bscherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEE-1995 (Rel. 31, Created)
01-CT-1996 (Rel. 34, Last sequence update)
01-CCT-1996 (Rel. 34, Last sequence update)
Minor curlin subunit precursor.
CSGB OR B1041 OR 21675 OR ECS1419.
Escherichia coli ol57:H7.
Bacteria, Proteobacteria, Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64.1%; Score 501.5; DB 1; Length 67.1%; Pred. No. 2.6e-35; ive 19; Mismatches 30; Indels
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MAJOR CURLIN SUBUNIT.
; EE2D2D94DDE91243 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fimbria; Signal; Complete proteome SIGNAL 1 20 BY SI
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NCBI_TaxID=562, 83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AR275733, AAK53212.1; -... EMBL, AE005315; AAG55788.1; -... EMBL, AP002584; BAB34843.1; -... PIR, D90806; D90806.
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21 152 MA
152 AA; 15099 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 67.1
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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P39828;
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                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its web yn ono-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
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STRAIN=0157:H7 / ATCC 43895;
MEDLINE=212.8556; PubMed=11319125;
Uhlich G.A., Keen J.E., Elder R.O.;
"Mutations in the csgD promoter associated with variations in certain strains of Escherichia coli 0157:H7.";
Appl. Environ. Microbiol. 67:2367-2370(2001).
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STRAIN=O157:H7 / EDD933 / ATCC 700927;
STRAIN=O157:H7 / EDD933 / ATCC 700927;
PEDIJNES-21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Grosta D.J., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Melon R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.9%; Score 523; DB 1; Length 151; 68.9%; Pred. No. 4.1e-37; ive 18; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAJOR CURLIN SUBUNIT.
A -> E (IN REF. 1).
C003470D208D395F CRC64;
               SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Major curlin subunit precursor.
ESCAR OR 21676 OR ESCS1420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                               EMBL; L04979; AAA23616.1; -.
EMBL; X90764; CAA62282.1; -.
EMBL; AE000205; AAC74126.1; -.
EMBL; D90741; BAA35832.1; -.
EMBL; D90742; BAA35840.1; -.
PIR; S70788; S70788.
ECOGONE; EG11489; CSGA.
SIGNAL; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 AA; 15049 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 68.998
Matches 104; Conservative
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Q93U24;
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RESULT 3 CSGA\_ECO57

Query Match

à Оp à g

à Dp 9

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EMBL, AE000205, AAC74125.1; -...
EMBL, D90741; BAA35831.1; -...
EMBL, AE005315, AAG55787.1; -...
EMBL, AP002554; BAB34842.1; -...
PIR, C90806, C90806.
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                                                                                                                                                                                                                                                                                                                                                              Conservative
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HSSP; P06620; 1INA.
                                                                                                                                                                                                                                                                 151 AA;
                                                                                                                                                                                                                                                                                                            Query Match.
Best Local Similarity
Matches 34; Conserv
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P20469;
                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=0157:H7 / RIMD 0509952;
SEQUENCE FROM N.A.
STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Maxino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arngvist A., Olsen A., Normark S.;
"Sigma S-dependent growth-phase induction of the csgBA promoter in
"Sigma S-dependent growth-phase induction of the csgBA promoter in
Escherichia coli can be achieved in vivo by sigma 70 in the absence
of the nucleoid-associated protein H-NS.";
Mol. Microbiol. 13:1021-1032(1994).
-:- PUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE
COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH
TEMPERATURES BELOW 37 DEGREES CELGIUS. CURLI CAN BIND TO
FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                              STRAIN=K12;

MEDLINE=97061202; PubMed=8905232;

MEDLINE=97061202.

NEDLINE=97061202; PubMed=8905232;

IXemoro K., Inada H., Baba T., Fujita K., Hayashi K., Honjo A.,

IXemoro K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,

Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,

Mori H., Moromura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,

Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,

Yano M., Horiuchi T.;

"A 718-kb DNA sequence of the Escherichia coli K-12 genome

Corresponding to the 12.7-28.0 min region on the linkage map.";
                                                                                                               MEDLINE=97426617; PubMed=9278503; Battner F.R., Plunkett G. HII, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [4]
SCHUBNCE FROM N.A.
STRAIN=O157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Perna N.T., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
"Melch R.A., Blattner F.R.;
"Genome sequence of entrerhagic Escherichia coli 0157:H7.",
Nature 409:529-533(2001).
                                                                                                                                                                                                               Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95157246; PubMed=7854117;
                    Mol. Microbiol. 18:661-670(1995)
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                                                                                             / MG1655;
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                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Gregor J., La.-
Shao Y.;
                                                                 SEQUENCE FROM N.A.
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MEDIINE=90092494; PubMed=2599095;
Abe K., Watabe S., Emori Y., Watanabe M., Arai S.;
"An ice nucleation active gene of Erwinia ananas. Sequence similarity to those of Pseudomonas species and regions required for ice nucleation activity.";
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 SNRAKIDQTGDYNL-AYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 -NNATIDOWNAKNSDITVGQYGGNNAALVNQTASDSSVWVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FERST LECT. 288:297-300 (1989).

-!- FUNCTION: Ice nucleation proteins enable bacteria to nucleate crystallization in supercooled water.

-:- SUBCELLULAR LOCATION: Outer membrane (By similarity).

-:- DOMAIN: CONTAINS MANY IMPEREET REPEATS OF THE CONSENSUS OCTABEPTIDE A AG-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.

-:- SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pantoea ananas (Erwinia uredovora).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
                                                                                                                                                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                                                                                 Length 151;
                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                    151 MINOR CURLIN SUBUNIT.
15882 MW; B18D266B964014B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interproving PR000258; Ice_nucleatn.
Pfam, PF00818; Ice_nucleation; 69.
PRINTS; PR00327; ICENUCLEATION; 49.
PROSITE; PS00314; ICE_NUCLEATION; 49.
Ice_nucleation; Repeat; Outer_membrane.
DOMAIN 162 1281 OCTAPEPTIDE PERIODICITY.
                                                                                                                                                                                                                                                                                                                                                   49;
                                                                                                                                                                                                                                                                                                           0.0083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ice nucleation protein inaA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1322 AA
                                                                                                                                                                                                                                                                             14.3%; Score 112; DB
29.8%; Pred. No. 0.00
:ive 17; Mismatches
                                                                                                                                      POTENTIAL.
PIR; G85655; COTST.
PIR; S70787.
PIR; S70787.
PIMPIA; S10781; CSGB.
Fimbria; Signal; Complete proteome.
PIMPIA; POTENT
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Fimbria; Signal; Complete proteome SIGNAL 1 21 POTEN
                                                                                                                                                                                                                                                                      CSGB_SALTY
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                                                                                                                                                           QNGFRNNATIDQWNAKNSDITVGQYG-----GNNAALV----NQTASDSSVMVRQVGFG 143
                                                                                     93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CT18;
MEDLINE-21534947; PubMed=11677608;
MEDLINE-21534947; PubMed=11677608;
MEDLINE-21534947; PubMed=11677608;
MEDLINE-21534947; PubMed=11677608;
MIDLINE-21534947; PubMed=11677608;
Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Baker S., Davies R., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Whitehead S., Barrell B.G.;
"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Bacteriol. 185:2330-2337(2003).
-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COILED SURPACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECURNCE FROM N.A.
STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
MEDLINE=22531367; PubMed=1664504;
MEDLINE=22531367; PubMed=1264504;
Burland V., Lodoy Lannin V., Schwartz D.C., Blattner F.R.,
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18";
                                                                                   34 GGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELT
                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
                               DB 1; Length 1322;
                                                                                                      Indels
  1322 AA; 131094 MW; 89B0EE24AA837039 CRC64;
                                                        21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
110-0CT-2003 (Rel. 42, Last annotation update)
Indoor curlin subunit precursor.
CSGB OR STY1180 OR F1777.
                             n
Similarity (29.9%; Pred. No. 0.22;
38; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                    151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL627269; CAD08267.1; -. EMBL; AE016840; AA069400.1; -.
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                                                                                                                                                                                                                               1014 SSQTARE 1020
                                                                                                                                                                                                 144 NNATANO 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=601;
                                                          38;
                                                                                                                                                                                                                                                                                                    SALTI
                                                                                                                                             94
     SEQUENCE
                               Query Match
                                              Local
                                                                                                                                                                                                                                                                                      CSGB_SALTI
                                                           Matches
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                                                                                                                                                                                                                                                                          97
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J. Baccériol. 178:662-667(1996).

J. Baccériol. 178:662-667(1996).

O. BACCÉRIOL. THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF CURLIN MONOMERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SPECIESÉS. Lyphimurium, STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINEŽ21534948; PubMed=11677609;
MEDLINEŽ21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.,
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                      GSANAALYD--QLVTRVVTHEMAHAGYGNGADVGQ-GADNST------IBLTQNGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES-S.typhimurium; STRAIN=SR-11;
MEDLINE=98117058; PubMed=9457880;
Roming U., Bian Z., Hammar M., Sierralta W.D., Normark S.;
"Curli fibers are highly conserved between Salmonella typhimurium and
Escherichia coli with respect to operon structure and regulation.";
J. Bacteriol. 180:722-731(1998).
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      RNNATIDOWNAKNSDIT-VGOYGGNNAALVNOTASDSSVMVRQVGFGNNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 NNRAKVDQ--AGNYNFAYIEQTGNANDASISQSAYGNSAAIIQKGSGNKANITQY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=27655-3B;
SPECIES=S.enteritidis; STRAIN=27655-3B;
MEDLINE=96146512; PubMed=8550497;
Collinson S.K., Clouthler S.C., Doran J.L., Banser P.A., Kay W.W.;
"Salmonella enteritidis agfabc operon encoding thin, aggregative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS5226 Annual Simulator, Fri, 131 Annual PS5236 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Minor curlin subunit, precursor (Fimbrin SEF17 minor subunit).
CSGB OR AGFE OR STM143.
Salmonella typhimurium, and
Salmonella typhimurium, and
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                           16;
                                                                                                                                        1; Length 151;
                                                                                                                                                                                                           47; Indels
21 POTENTIAL.
151 MINOR CURLIN SUBUNIT.
16254 MW; 161C54326E573495 CRC64;
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                                                                                                                                     13.7%; Score 107; DB 1, 30.4%; Pred. No. 0.022;
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                                                                                                                                                                                                               17; Mismatches
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                                                                                                                                                                                                                  Conservative
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                                        151
                                                                         151 AA;
                                                                                                                                                                          Local Similarity
les 35; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                          86
                                                                         SEQUENCE
                                                                                                                                            Query Match
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51 GSANAALYD--QLVTRVVTHEMAHAGYGNGADVGQ-GADNST------IELTQNGF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76
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-! FUNCTION: Ice nucleation proteins enable bacteria to nucleate crystallization in supercooled water.

-! SUBCELLULAR LOCATION: Outer membrane.

-! SUBCELLULAR LOCATION: Outer membrane.

-! DOMAIN: CONTAINS IMPERECT REPEATS OF A CONSENSUS OCTAPEPTIDE A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.

-! MISCELLANGOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.

-! SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 NNRAKVDQ---AGNYNFAYIEQTGNANDASISQSAYGNSAAIIQKGSGNKANITQY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98 RNNATIDOWNAKNSDIT-VGOYGGNNAALVNOTASDSSVMVRQVGFGNNATANQY 151
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Michigami Y., Watabe S., Abe K., Obata H., Arai S.;
"Cloning and sequencing of an ice nucleation active gene of Erwinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pantoea ananas (Erwinia uredovora).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            576 ----LTA-GYGSTQTAQE----NSDLTTG-YGSTSTAGYDSSLIAGYGSTQTAGYHSIL 624
                                                                                                                                                                                                                                                                                                                                                                                                                                             531 GYGSTSTAGANSS------LİAGYGSTQTASYNSVLT------AGYGSTQTAREGSD 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87 NSTIELTQNGFRNNATIDQWNAKNSDITVGQYG----GNNAALV----NQTASDSSVM 136
                                                                                                                                                                                                                                                                                                                                                   86
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"The consensus sequence of ice nucleation proteins from Erwinia herbicola, pseudomonas fluorescens and Pseudomonas syringae.";
Gene 85:239-242(1989).
-! FUNCTION: Los nucleation proteins enable bacteria to nucleate
crystallization in supercooled water.
-! SUBCELLULAR LOCATION: Outer membrane.
-! SUBCELLULAR LOCATION: Outer membrane.
-! PRIODICITY IS SUPERIMPOSED.
-! PERIODICITY IS SUPERIMPOSED.
-! MISCELLANGOUS. A STRUCTURAL MOBEL IS SUGGESTED IN WHICH THE ICE
NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
-! SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                   27 GGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGNGADVGQGAD
                                                                                                                                                                                                                                              38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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REMBL, M26322, AAA24823.1; -.
RIR; JOO188; JOO289, ILNA.
REMS, PRO6020, ILNA.
REMS, PRO60315; ICE_MUCLEATIO.
REMS, PRO60317; ICEMUCLEATIO.
REMS, PRO60314; ICE_MUCLEATIO.
REMS, PRO60314; ICE_MUCLEATIO.
REMS, PRO60314; ICE_MUCLEATIO.
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REMS, PRO60314; ICE_MUCLEATIO.
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REMS, PROF0314; ICE_MUCLEATIO.
REMS, PROF0314; IC
                                                                                                                                               Length 1034;
                                                                                                                                                                                                                                              Indels
162 993 OCTAPEPTIDE PERIODICITY.
1034 AA; 103378 MW; FA222523D333EADD CRC64;
                                                                                                                                               Query Match
13.6%; Score 106; DB 1; Lo
Best Local Similarity 29.9%; Pred. No. 0.22;
Matches 40; Conservative 19; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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MEDLINE=90152370; PubMed=2515997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 VRQVGFGNNATANO 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterobacteriaceae; Pantoea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      625 T--AGYGSTQTÁQE 636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Srwinia herbicola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI TaxID=549;
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                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P16239
     DOMAIN
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ICEN ERWHE
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DB 1; Length 1258;

13.4%; Score 104.5; DE 29.5%; Pred. No. 0.36;

Best Local Similarity

Query Match

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1105 TGTAGADSSLIAGYGSTQTAGYGSTQTAREDSSLTAG-YGSTSTAGHDSSLI 1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 33-1649 FROM N.A.
STRAIN=Indian tick typhus, and Malish 7;
STRAIN=20393643; PubMed=10939649;
ROLN V.; RROULL D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AF008659, AAL03623.1, -.
EMBL, AF123721, AAR34124.1; -.
EMBL, AF123726, AAR34129.1; -.
EMBL, AF149110, AAD39533.1, -.
FIR; E97835, E97835, InterPro, IPR006315, Autotransport.
InterPro, IPR00546, Autotransporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 353-1655 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                   Rickettšia conorii.
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                                                                                773 GSTSTAGADSSL-IAGYGSTQTÄGYHSILT-----AGYGSTQTAQERSDLTTGYGS 822
                                                                                                                                               79
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                                                                                                                        DVGQGADNSTIE---LTQN-GFRNNATI----DQWNAKNSDITVGQYG-----GNNAALV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 GGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGN-----GADV----
    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xanthomonas campestris (pv. translucens).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
      45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 1567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhao J., Orser C.S.; "Conserved repetition in the ice nucleation gene inaX from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INCEPPO, IDRO02258; ICe_nucleatn.
Pfam; PF00818; ICe_nucleation; 81.
PRINTS; PR00327; ICENUCLEATIN.
PROSITE; PS00314; ICE_NUCLEATION; 57.
ICE nucleation; Repeat; Outer membrane.
SEQUENCE 1567 AA; 152548 MW; C8B451D959ECAD63 CRC64;
      Indels
                                          34 GGGNSSGPDSTLSIYQYGSANAALYDQLVTRVVTHEMAHAGYGN-
  37;
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(Rel. 16, Last sequence update)
(Rel. 40, Last annotation update)
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    Mismatches
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MEDLINE=91080859; PubMed=2259339;
  23;
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Best Local Similarity
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01-NOV-1990 (
16-OCT-2001 (
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P18127;
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The rickettsial outer membrane protein A and B genes of Rickettsia
australis, the most divergent rickettsia of the spotted fever group.",
Submitted (MAY-1999) to the EMEL/Genbank/DDBJ databases.
-I. FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
VIRULANCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (By
similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (By similarity).
-!- SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a S-
layer with hexagonal symmetry (By similarity).
-!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                           OMPB RICCN STANDARD; PRT; 1655 AA.

OFFA63; OFFA63; OFFA64;

OFFA63; OFFA63; OFFA64;

16-CCT-2001 (Rel. 40, Last sequence update)

16-CCT-2001 (Rel. 40, Last sequence update)

28-FBE-2003 (Rel. 41, Last annotation update)

Outer membrane protein B precursor (168 kDa surface-layer protein)

(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)

(TOMPB D) (Contains: 120 kDa surface-exposed protein (Surface protein

OMPB OR; RC1085.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
Science 293:2093-2098(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Malish 7;
MEDLINE=21442074; PubMed=11557893;
Ogata H;, Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M., Raoult D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales;
Rickettsiaceae; Rickettsiaae, Rickettsia.
NCBI_TaxID=781;
                                                                                1164 AGYGSTÓTÁGYNSILT--TGYGSTQTÁQE 1190
----NQTASDSSVMVRQVGFGNNATANQ 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 -----GGNGYINCGGVG-GPNNS---LDGNNLINPASVSNYNESNSKFHNHHHHHHPQH 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 LONAAAAYIMSAGSG------GGGCTGNGGGGASGPGGGPSANSGGGGGGG----
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                                                                                                                                                                                                                                                                                             PIR; A56038; A56038.

TRANSFAC; PO7244; ZADR.

TRANSFAC; PO6669; -

FlyBase; FBGN003028; ovo.

FlyBase; PFGN003028; zar C2H2.

PFANSTITE; PS00028; zar C2H2; 4.

PROSITE; PS00028; zar CZH2; 4.

Zinc-finger; Metal-binding; DNA-binding; Repeat; Nuclear protein;
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D7068BB2BC0F6F77 CRC64;
PRESENCE IN THE GERM LINE PRECURSOR POLE CELLS.
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12; Mismatches
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C2H2-TYPE 1.
C2H2-TYPE 2.
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C2H2-TYPE 4.
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EMBL; X59772; CAB36921.1; ALT_SEQ.
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43; Conserve
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"Multiple products from the shavenbaby-ovo gene region of Drosophila melanogaster: relationship to genetic complexity.";
Mol. Cell. Biol. 14:6809-6818(1994).
                                                                                                                  TYPHUS).
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TYPHUS).
TYPHUS).
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Bukoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Bphydroidea, Drosophilidae, Drosophila.
                     TIGREAMS; TIGRO1414; autotrans barl; 2.
Antigen; S-layer; Cell wall; Complete proteome.
CHAIN 1 1334 120 kDa SURFACE-EXPOSED PROTEIN.
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                                                                                            32 kDa BETA PEPTIDE
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2003 (Rel. 42, Last annotation update)
0vo protein (Shaven baby protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.1%; Score 102.5; DE 26.8%; Pred. No. 0.73; ive 18; Mismatches
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TISSUE=Ovary;
MEDLINE=95021209; PubMed=7935398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 26.8
nes 38; Conservative
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P51521; Q9XZU4;
01-OCT-1996 (Rel
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the FNBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Outer membrane protein B precursor (168 kDa surface-layer protein) (Surface protein antigen) (Cell surface antigen S) (Grass) (TompB) (TompB) (Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
-!- FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
                                                                                                                                                                                                                                                                                                     Inchivama T.,
Uchiyama T.,
"Sequencing of the gene encoding the protein rOmp B of Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 34.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (By similarity).
--- SUBSELLULAR LOCATION: Cell wall. This bacterium is covered layer with hexagonal symmetry.
--- SIMILARITY: BELGONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35;
                                                                                                                                                                                                                                                                                                                                                               japonica.";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETISIAL
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (By
                                                                                                                 Ricketralaceae, Rickettsleae, Rickettslales, NCB Taxides, NCB Taxides, Rickettsleae, Rickettsla
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32 kDa BETA PEPTIDE.
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InterPro, IPR005315, Autotransport.
InterPro, IPR00546, Autotransporter.
Ffan, PP03797, Autotransporter, 1.
TIGRFAMS; TIGR01414; autotrans_bar1; 2.
Antigen; S-layer; Cell wall.
CHAIN 1339 1656 32 kDa BETA E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55;
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SEC-1998 (Rel. 37, Last sequence update)
OCT-2001 (Rel. 40, Last annotation update)
nucleation protein.
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Last annotation update)
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i, Mismatches
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  PRT; 1196 AA
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Pfam; PF00818; Ice_nucleation; 61.
PRINTS; PR00327; ICENUCLEAIN.
PROSITE; PS00314; ICE NUCLEATION; 42.
Ice_nucleation; Repeat; Outer membrane.
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=INAS;
MEDLINE=97462815; PubMed=9323042;
Schmid D., Pridmore D., Capitani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24;
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  STANDARD;
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                                                                                                                                                                                 Pseudomonas syringae
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30-MAY-2000
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006653;
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Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania

Leishmania chagasi

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                                                                                                                                                                                                                                                                                  Ramamoorthy R., Donelson J.E., Paetz K.E., Maybodi M., Roberts S.C.,
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ZINC (CATALYTIC) (BY SIMILARITY).
                                                                          SEQUENCE FROM N.A.
MEDLINE=90205976; PubMed=2320059;
Miller R.A., Reed S.G., Parsons M.;
"Leishmania gp63 nolecule implicated in cellular adhesion lacks an Arg-Gly-Asp sequence.";
Mol. Biochem. Parasitol. 39:267-274(1990).
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HSSP, P08148; LLML.

HSSP, P08148; LLML.

HRENDS, M08.001; -..

InterPro; IPR001577; Peptidase_M8.

PRINTS, PR00457; Peptidase M8; 1.

PRINTS, PR001579; LSHMANOLYSIN.

PROSITE; PS00142; ZINC PROTEASE; 1.

Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc; Zymogen; Signal; Cell adhesion; GPI-anchor; Lipoprotein.

SIGNAL

PROPEP 40 97 ACTIVATION PEPTIDE.
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Best Local Similarity
                     Eukaryota, Euglenc
NCBI_TaxID=44271;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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## Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SPTREMBL\_25:\* 1: sp\_archea:\* 2: sp\_bacteria:\* 3: sp\_fungi:\* 5: sp\_invertebrate:\* 6: sp\_mamman:\* 7: sp\_mho:\* 8: sp\_phage:\* 9: sp\_phage:\* 10: sp\_plant:\* 11: sp\_rodent:\* 12: sp\_virus:\* 13: sp\_virus:\* 14: sp\_unclassified:\* 15: sp\_virus:\* 16: sp\_virus:\* 17: sp\_virus:\* 18: sp\_virus

	Description	O33802 salmonella	Q7x243 citrobacter	Q7x240 citrobacter	Q8cw63 escherichia	Q7x237 enterobacte	Q54069 salmonella	Q983j5 escherichia	Q8eih4 shewanella	Q8u6n9 agrobacteri	Q92uu8 rhizobium m	Q7uczl shigella fl	Q8cw64 escherichia	Q83ru7 shigella fl	Q7x244 citrobacter	Q8pd38 xanthomonas	Q8efu3 shewanella
SUMMARIES	ID	033802	Q7X243	Q7X240	QBCW63	Q7X237	Q54069	Q9S3J5	Q8EIH4	6N9D80			Q8CW64		Q7X244	Q8PD38	Q8EFU3
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	% Query Match	87.3	74.2	68.0	65.0	56.6	38.9	15.6	15.5	14.6	14.5	14.3	14.3	14.3	14.1	13.9	13.7
	Score	683	580.5	532	508.5	442.5	304	122	121	114.5	113	112	112	112	110	108.5	107
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## ALIGNMENTS

Database :

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1 MKLLKVAAFAAIVVSGSALAGVVPQW--GGNHHGGGSNYGPDSSLSIYQYGSNNSANALQ
                                    61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
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Enterobacteriaceae; Enterobacter.
NCBI_TaxID=28141;
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67.8%; Pred. No. 4.8e-34;
iive 18; Mismatches 30; Indels
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Major curlin subunit precursor.
csGA OR C1306.
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002)
EMBL; AE016759; AAN79779.1; -.
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Zogaj X., Bokranz W., Nimtz M., Romling U.;
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SEQUENCE FROM N.A.
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01-MAR-2003
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Production of Cellulose and Curli Fimbriae by Members of the Family
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 72-1131-4158 (2003).
EMBL, AJS15700; CADS6672-1; -.
SEQUENCE 150 AA, 15016 MW; 1D7141B8D6973DC6 CRC64;
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                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
NCBI_TaxID=213763;
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
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01-OCT-2003 (TremBLre
01-OCT-2003 (TremBLre
Curlin-csgA protein.
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STRAIN=Fec2;
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ch 15.6%;
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26; Conservative
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TIGR; S00865; -.
Hypothetical protein; Comple
SEQUENCE 502 AA; 52441 MW
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Enterobacteriaceae Isolated from the Human Gastrointestinal Tract."; Infect. Immun. 72:4151-4158(2003).
EMBL; AJS15702; CADS6678.1; -. SEQUENCE 150 AA; 15112 MW; 5D8BB2D872DF15F3 CRC64;
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Enterobacteriaceae, Salmonella,
NCBI_TaxID=592;
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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COX J.M., Eglezos S., Woolcock J.B.;
wirdlence of Salmonella enteritidis in chickens correlates with colony morphology and expression of SEF17 fimbriae.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, US3207; AAA98671.1;
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Pred. No. 1e-17;
2; Mismatches 13; Indels
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Last annotation update)
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Last annotation update)
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larity 80.3%;
Conservative
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SEF17 fimbrin (Fragment)
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76 AA;
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Q983J5;
01-MAY-2000 (
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                                                                                                                        Query Match
Best Local S
Matches 91
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Q54069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TRANSPOSON=Insertion sequence IS1;
MEDLINE=99314153; Pubmed=10386375;
MEDLINE=99314153; Pubmed=10386375;
MODLINE=99314153; Pubmed=10386375;
Non-outliation of Bscherichia coli 078:K80 isolates associated with
IS1 inserti on in csgB and reduced persistence in poultry infection.";
FEMS Microbiol. Lett. 175:247-253(1999).
NON_TER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINE=2297686; PubMed=12368813; MEDINE=2297686; PubMed=12368813; MeDINE=2297886; PubMed=12368813; Medine=2.597686; PubMed=1.T., Nelson K.E., Gaidos E.J., Nelson W.C., Heidelberg J.F., Paulsen I.T., Nelson M., Brinkac L., Daupton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daupherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., "Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; "Genome sequence of the dissimilatory metal ion-reducing bacterium
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                       Score 122, DB 2, Length 29;
Pred. No. 0.0022;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 121; DB 16; Length Su
Pred. No. 0.086;
Transtrhes 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteome.
D08CA23D6C46B62D CRC64;
                                                                                                                                                                                                                                                                         E290DFC07ABBB243 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKLLKVAAFAAIVVSGSALAGVVPQWGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nat. Biotechnol. 20:1118-1123(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conserved hypothetical protein.
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502 AA; 52441 MW;
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56 ALYDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITV 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                      "The genome of the natural genetic engineer Agrobacterium tumefaciens \mathbb{C}58.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21608551; PubMed=11743194; Goddner B., Hinkle G., Gattung S., Miller N., Blanchard M., Gordoner B., Targen S., Miller N., Blanchard M., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.; hand C., Compander S., Lomo C., Sear C., Strub G., Gelo C., Slater S.; hand Dathogen and biotechnology agent Agrobacterium tumefaciens CSB.",
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                                                                                                                                                                                                                                          MEDLINE-21669550; PubMed=11743193; Monks D.E., Kitajima J.P., Nocd D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.P. Jr., Woo L., Chen Y., Paulsen I.T., Elsen J.A., Karp P.D., Bovee D. Sr., Kutyavin T., Levy R., Li W.-J., McClelland E., Palmieri A., Karp V. Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D. Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 16; Length 145;
                                                                                                                       ATU4768 OR AGR L 228.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; Complete proteome.
15 AA; 14984 MW; DEDC870E1713D51A CRC64;
                                                01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Atu4768.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical glycine-rich protein SMb21548.
RB0989 OR SMB21548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.6%; Score 114.5; DB 16; 25.2%; Pred. No. 0.064; ive 26; Mismatches 59;
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                     145 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AE009405; AAL45562.1; -.
EMBL, AAE008209; AAK88682.1; -.
PIR, AD3143; AD3143.
PIR, H98144; H98144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 294:2317-2323(2001).
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Matches 39; Conservative
                   PRELIMINARY;
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                                                                                                                                                                                                NCBI TaxID=176299;
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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SEQUENCE 14
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Q92UU8
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Q8U6N9
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738 ----GGYANTANVGFKGLTLTTQGSHAAGIVAQSVGGGGGTGGTGSSYSAGIGFTASVAV 793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 EMAHAGYGNGADVG------QGADNSTI--ELTQNGFRNNATIDQWNAK---NSDITV
                                                                                                                                                              Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P., Vorhoelter F.J., Herrandez-Lucas I., Becker A., Cowie A., Gouzy J., Golding B., Puchler A., "The complete sequence of the 1,683-kp psymB megaplasmid from the N2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
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STRAIN=245T / ATCC 700930 / Serotype 2a;
MEDLINE=22590274; PubMed=12704152;
Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
Pournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A
Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
Schwartz D.C., Blattner F.R.,
"Complete genome sequence and comparative genomics of Shigella
flexneri serotype 2a strain 2457F.";
Infect. Immun. 71:2775-2786(2003).
Endel: ARe016981; ARe16542.1;
EMBL: ARe016981; ARe16542.1;
SEQUENCE 151 AA; 15868 WW; 5D5D2668964014A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.5%; Score 113; DB 16; Length 2174; 27.0%; Pred. No. 2.3;
Plasmid pSymB (megaplasmid 2).
Bacteria, Proteobacteria, Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            693 AIATAGAGAVGILAQSIGGGGGN---GGNATGGDAGFGSFQIGGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                              PEGM; PF03797; Autotransporter; 1.
PROSITE; PS00435; PEROXIDASE 1; 1.
PROSITE; PS00583; PFWE KINASES 1; 2.
PROSITE; Hypothetical protein; Complete proteome.
SEQUENCE 2174 AA; 203314 MM; 006EB68297B44182 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                      GO; GO:0046821; C:extrachromosomal DNA; IEA.
GO; GO:0004601; F:peroxidase activity; IEA.
GO; GO:0006979; P:response to oxidative stress; IEA.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51;
                                                                                                                                                                                                                                  fixing endosymbiont Sinorhizobium meliloti.";
Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001)
EMBL; AL603645; CAC49389.1; --
PIX; E95965; E95965.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Mismatches
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                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR005546; Autotransporter.
InterPro; IPR002016; Peroxidase.
InterPro; IPR002173; PfkB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                STRAIN=1021;
MEDLINE=21396508; PubMed=11481431;
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25,
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Best Local Similarity 27.0
Matches 40; Conservative
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                                                                                                           SEQUENCE FROM N.A.
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Q7UCZ1;
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us-09-543-407-26.rspt

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Yu J.;
"Genome sequence of Shigella flexneri 2a: insights into pathogenicity
"Genome comparison with genomes of Escherichia coli K12 and O157.";
Nucleic Acids Res. 30:4432-4441(2002).
EMBL; AE015131; AAN42658.1;
Complete processes.
                                                                                                                                                                                                                                                                                                                                                      26 GIAAAAGYDLANSEYNFAVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oggaj X., Bokranz W., Nimtz M., Romling U.;
"Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract."; Infect.:Immun. 72:4151-4156(2003).
EMBL, AJS15700; CAD566711.; -.
SEQUENCE 151 AA, 16158 MW; BD00AF57E1400704 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 -NNATIDOWNAKNSDITVGOYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                           86 SNRAKIDOTGDYNL-AYIDOAGSANDASISOGAYGNTAMIIOKGSGNKANITOY
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Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou
                                                                                                                                                                                                                                                                                                                         GSANAALYDOLVT--RVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.1%; Score 110; DB 2; Length 151; larity 27.2%; Pred. No. 0.16; Conservative 22; Mismatches 47; Indels
                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                    160 AA; 16919 MW; 50269F5268D2A32F CRC64;
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Last sequence update)
Last annotation update)
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25, Last seq
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Bacteria, Proteobacteria, Gammag
Enterobacteriaceae, Citrobacter
NCBI_TaxID=213763,
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(TrEMBLrel. 24,
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STRAIN=301 / Serotype 2a;
STRAIN=301 / Serotype 2a;
MEDLINE=2222406; PubMed=12384590;
Min Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
                                                                                                                                    GIAAAAGYDLANSEYNFAVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-OS:HI / CTT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coll.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
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                                                                                                                                                                                            99 -NNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                       SNRAKIDOTGDYNL-AYIDOAGSANDASISOGAYGNTAMIIOKGSGNKANITOY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli O6.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNRAKIDOTGDYNL-AYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQY
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                                                                                                     GSANAALYDOLVT - - RVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFR - - -
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         Length 151;
                                                       Indels
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Minor curlin subunit precursor, similar ro CsgA.
CSGB OR SF1035.
                                                                                                                                                                                                                                                                                                                                                                                          01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Minor curlin subunit precursor.
CSGB OR C1305.
                                                         49;
            DB 16;
         ; Score 112; DB 1
; Pred. No. 0.11;
17; Mismatches
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            14.3%; 29.8%;
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                                                         Conservative
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SEQUENCE 160 AA;
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            Query Match
Best Local Simil
Matches 34; C
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QBCW64
CBCW64
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                                                                                                                                                                      Nature 417:459-463(2002).

BMBL, AR012148, AAM3923.1. -.

GO, GO:0009279; C:external outer membrane (sensu Gram-negativ. ..; IBA. InterPro; IPR000258; Ice_nucleatn.

Pfam; PF00318; Ice_nucleatin, 68.

PRINTS; PR00317; ICENUCLEATIN, 40.
                                                                                                                                                                                                                                                                                                                                                                         105 -QWNARUSDITVGQYGGNNAAL-----VNQTASDSSVMVRQVGFGNNATA 148
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                                                                                                                                                                                                                                                                           29;
                                                                                                                                                                                                                                                          DB 16; Length 1333;
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13.9%; Score 108.5; DB 16; Length
Best Local Similarity 26.3%; Pred. No. 3;
Matches 46; Conservative 22; Mismatches 48; Indels
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SEQUENCE 1333 AP
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E. coli N

Abr82649 E. coll.
Aab36323 Salmone
Aab36328 Salmone
Aab36328 Salmone
Aab36329 Solmone
Abb2329 Proteir
Aaw32312 leishme
Abr82642 E. coll
Abr82647 E. coll
Abc3520 Mycobac
Abc3520 Mycobac
Abc3520 Mycobac
Abc3527 Arabido
Abg69842 Human p
Abb69842 Human p

Salmonell Salmonell Salmonell Protein e Leishmani

E. coli V Salmonell Salmonell

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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a recombinant agfh gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antiqen. Also described are: (1) use of thin aggregative fimbriae (SEFI/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-honologue fimbrin subunits, respectively; (2) directing recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmoneila; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AgfA::PT3#9 amino acid sequence SEQ ID NO:28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kay WW;
                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
AAB36340
AAB36324
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AAB36336
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ABR826989727
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 Salmonella enteritidis.
Escherichia coli.
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N-PSDB; AAC64630.
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 Synthetic
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Aab36351 AgfA::PT3
                                                                                                    August 2, 2004, 14:35:42 ; Search time 44.9 Seconds (without alignments) 950.215 Million cell updates/sec
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1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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11: geneseqp1980s:*
2: geneseqp1990s:*
4: geneseqp2001s:*
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Match 1
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Result

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compy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant Agfa protein containing a replacement segment or segments of foreign amino acid sequence or sequence segment on a Salmonella, E. coli or large acid sequence or sequences grown on a Salmonella, E. coli or but only the sequence of a conjunction with a carrier or diluent. (I) is useful for the expression of recombinant Agfa protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogens, which may be important for directing an immune response in mannogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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Best Local Similarity 100.0%; Pr
Matches 151; Conservative 0;
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The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative finbriae (SEPI)/TARF) mucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, cspA and AgfA, homologue fimbrin shunits. respectively, (2) directing recombination of a recombinant gene into the chromosome of the homologue species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment of segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful celliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/Cell), the hybrid fimbrin protein possesses both the immunication properties relevant for an efficient live
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine, the carrier fimbrial subunit proteins are usually strong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 151;
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91.9%; Score 712; DB 3; Length 15:
Best Local Similarity 91.1%; Pred. No. 3.3e-61;
Matches 144; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SDARKSETTITOSGYGNGADVGQGADNYDOLVTRVVTHEMAHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR74625 standard; protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94WO-IB000207.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AgfA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUN-1995
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(KING/)
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assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae (or the production of fimbriae comprising recombinant of Enterobacteriaceae (or the production of fimbriae comprising recombinant of a recombination of a recombinant gene into the chromosome of the homologous species, replacing the native compositions species, (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer response in an animal, protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. Coli or acid sequence or sequences grown on a Salmonella, E. Coli or acid sequence or sequences grown on a Salmonella, E. Coli or acid sequence or sequences grown on a salmonella, E. Coli or acid sequence or sequences grown on a salmonella, E. Coli or acid sequence of the confinent of the manual. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and abhesion properties relevant for an efficient live vaccine, the carrier fimbrial submit proteins are usually strong immunogens, which may be important for directing an immune response in manual in expensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 683; DB 3;
Pred. No. 2.2e-58;
1; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NNAALVNOTASDSSVWVRQVGFGNNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Encoded by GCC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella enteritidis 27655-3b agfA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Doran JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW23570 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.1%;
90.1%;
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Matches 136; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmoneíla enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
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29-SEP-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW23570;
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          Dp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SDARKSETTITOSGYGNGADVGOGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
                                                                                                                                                                                             The Salmonella AgfA protein and DNA are used in vaccine and genetic immunization compositions, respectively, to elicit an immune response to Alamonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                       1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                        MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are:
                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella enteritidis AgfA amino acid sequence SEQ 1D NO:5.
                                                                                                                                                                                                                                                                                                                         Score 683; DB 2; Length 151;
Pred. No. 2.2e-58;
1; Mismatches 14; Indels
          Doran JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
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        Clouthier SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 135; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB36341 standard; protein; 151 AA
                                                                                                                                                           Disclosure, Fig 7B; 95pp; English.
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                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 90.1%;
Matches 136; Conservative
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      Collinson SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella enteritidis
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                                            WPI; 1994-358275/44.
N-PSDB; AAQ87467.
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                                                                                                                                                                                                                                                                                        Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200060102-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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Gaps

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AAB36353 standard; protein; 151
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Matches 136; Conserv
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                                                                                Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-2001
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\mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}^{\frac{1}{2}} \mathbb{R}
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                                                                                                                                                                                                                                                                                                                                              The present sequence represents agfA encoded by the full agfA gene derived from Salmonsela enteritidis 27655-3b. The mucleic acid can be used to provide diagnostic associated Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic 25-WAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDARKSETIITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                   Isolated Salmonella gene agfA - used for diagnosis of Salmonella or enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 678; DB 2; Length 151;
Pred. No. 6.6e-58;
1; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AgfA::PT3#5 amino acid sequence SEQ ID NO:20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNAALVNQTASDSSVMVRQVGFGNNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 NNPALVNQTASDSSVMVRQVGFGNNATANOY 151
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                                                                                                                                                                                                                                                                  Example 2; Fig 7; 85pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 89.4°
Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                 WPI; 1997-309886/28.
                                                                                                                                              Isolated Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-672631/65.
                                                              N-PSDB; AAT74142
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 151 AA;
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RESULT 6 AAB36350

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA consequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEPI7/TAF) nucleation depended assembly system of strains of Salmontella, Escherichia coli and consequence to the production of fimbriae comprising recombinant of a recombinant gene into the chromosome of the composous species; (3) directing recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, copy of that gene; and (4) eliciting an immune response in an animal. Comprising separating an amino acid polymer comprising separating an amino acid polymer comprising separating a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, B. coli or Enterobacteriaceae host cell, from the host cell and introducing the correct constitution an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to copies/cell), the hybrid fimbrim protein possesses both the carrier fimbrial subunit proteins are usually strong munuogens, which may be important for directing an immune response in an animal in construction with a carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response community the hybrid fimbria are usually strong immunogens, which may be important for directing an immune response construction of the presented of immunogens in an immune response in an efficient live the animal may be important for directing an immune response consequence of immunogence is given in the horsely and abased and hybrid fimbriae are easy and interved epitemporation of the presented epitemporation of the presented epitemporation of the presented epitemporation of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella, agfA, chromosomal gene replacement, fimbrin, epitope, vaccine, immune response, immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.4%; Score 662; DB 3; Length 151;
81.9%; Pred. No. 2.4e-56;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inexpensive to purify in large amount. The purie exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AgfA::PT3#8 amino acid sequence SEQ ID NO:26.
                                                                                Page 137; 139pp; English
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05-APR-2000; 2000WO-CA000356.

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are:

(1) use of thin aggregative finbriae (SERIA/TAPA) mucleation depended assembly system of strains of Salmonella Escherichia coli and cassembly system of strains of Salmonella Escherichia coli and directing recombination of finbriae comprising recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of the native copy of that gene; and (4) eliciting an immune response in an animal, copy of that gene; and (4) eliciting an immune response in an animal, comprising separating a replacement segment or segments of foreign amino cortaining a replacement segment or segments of foreign amino cortaining a replacement segment or segments of foreign amino cortaining a replacement segment or segments of foreign amino cortaining a replacement segment or segments of foreign amino cortaining an amino acid polywer or segments of foreign amino cortaining an amino containing a replacement segment or segments of foreign amino cortain and the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which may be important for an efficient live vaccine, the darrier fimbrial submult protein sare usually strong immunogens, which may be important for directing an immune response conceptive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                             Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 138; 139pp; English
                                                                                                    Collison SK,
99US-0127888P
                                              (UYVI-) UNIV VICTORIA.
                                                                                                    White AP, Doran JL,
                                                                                                                                                        WPI; 2000-672631/65.
N-PSDB; AAC64629.
05-APR-1999;
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Seguence 151 AA;

1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGNHNGGGNSSGPDSTLSIYQYGSANAAL--- 57 97 97 61 SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHA------F 58 ------YDQLVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGF Gaps 98 RNNATIDOWNAKNSDITVGOYGGNNAALVNOTASDSSVMVRQVGFGNNATANQY 151 Score 617, DB 3, Length 151; Pred. No. 5.7e-52; 0, Mismatches 0; Indels 46; Query Match 79.6%; Best Local Similarity 73.6%; Matches 128; Conservative ( g ò g ð DP

AgfA::PT3#10 amino acid sequence SEQ ID NO:30. AAB36355 standard; protein; 151 AA (first entry) 26-FEB-2001 AAB36355; RESULT 8 AAB36355 

Salmonella enteritidis. Escherichia coli. Synthetic.

WO200060102-A2 

Kay WW;

05-APR-2000; 2000WO-CA000356

12-CCT-2000.

99US-0127888P

(UYVI-) UNIV VICTORIA

Kay WW; Collison SK, White AP, Doran JL,

WPI; 2000-672631/65 N-PSDB; AAC64631 Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

English. Disclosure; Page 139; 139pp;

The present invention describes a recombinant agfA gene (1) where a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA segment the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) uses of thin aggregative fimbriae (SETI)/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant of a recombinant gene into the chromosome of the homologous species, respectively; (2) directing recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement esgment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or comprising separating an amino acid polymer comprising a recombinant polymer coll or comprising sequences not cell, from the host cell and introducing the protein containing a replacement esgment or segments of foreign amino consequence or sequences grown on a Salmonella, E. coli or succeived from the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to 500,000 copies/Cell), the hybrid fimbrina protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogenicity and adhesion properties relevant for an efficient live companient the inserted epicope, and hybrid dimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention

Sequence 151 AA;

SDARKSETTITQSGYGNGAD------YDQLVTRVVTHEMAHAFR MKILKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 79.1%; Score 613; DB 3; Length 151; larity 74.6%; Pred. No. 1.4e-51; Conservative 0; Mismatches 0; Indels 44; Gaps 99 NNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151 Query Match Best Local Similarity Matches 129; Conserv 61

엄 à d ò RESULT 9

Salmonella, agfA, chromosomal gene replacement, fimbrin, epitope, vaccine, immune response, immunogen.

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are:

(1) use of thin aggregative fimbriae (SEF1/TAR) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant depended affA. CsgA and AgfA. Homologue fimbrin subunits, respectively; (2) directing recombinant denomologues species; (3) directing recombinant gene homologous species; (3) directing recombinant gene are compliant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising are combinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and inroducing the protein containing a replacement segment of recombinant AgfA protein which the animal in conjunction with a carrier or dilutent. (I) is useful for the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant AgfA protein high numbers (up to 500,000 copies/cell), the hybrid fimbrian protein possesses both the system the carrier fimbrial submit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                        Salmonella, agfA, chromosomal gene replacement, fimbrin, epitope, vaccine, immune response; immunogen.
                                                                                                                                                    AgfA::PT3#1 amino acid sequence SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kay WW;
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                      AAB36346 standard; protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-2000; 2000WO-CA000356
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                                                                                                         (first entry)
                                                                                                                                                                                                                                                         Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           White AP, Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-672631/65.
                                                                                                                                                                                                                                                                                  Escherichia coli
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                                                                                                                                                                                                                                                                                                                                          WO200060102-A2.
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                                                                                                           26-FEB-2001
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                                                                                                                                                                                                                                                                                                    Synthetic.
AAB36346
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEPI)/TAP) nucleation depended assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant C AgFA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) directing recombinant gene into the chromosome of the homologue species, replacing the native composition species, (3) directing recombinant gene into the chromosome of the homologue species, replacing the native corp. of that gene, and (4) eliciting an immune response in an animal, comprising separating a replacement segment or segments of foreign amino protein containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino protein containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment of segment or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or segments or seg
SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120
                                        61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella, agfA; chromosomal gene replacement; fimbrin; epitope;
vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                          AgfA::PT3#2 amino acid sequence SEQ ID NO:14.
                                                                                                                            Kay WW;
                                                                                           NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Page 136; 139pp, English.
                                                                                                                                                                                                                                                                AA.
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Escherichia coli.
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Gaps

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Length 151;

78.1%; Score 605; DB 3; Length 151 80.1%; Pred. No. 8.3e-51; ive 5; Mismatches 25; Indels

Matches 121; Conservative

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Best Local Similarity

Query Match

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Sequence 151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                         Gaps
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                                                 Length 151;
                                                                        Indels
                                              Score 603; DB 3; L
Pred. No. 1.3e-50;
; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                    AgfA::PT3#4 amino acid sequence SEQ ID NO:18.
the exemplification of the present invention
                                                                                                                                                                                                                     121 LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
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                                                77.8%;
80.8%;
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                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli
                         Sequence 151 AA;
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Matches 122; (
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Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) useful for the expression of recombinant AgfA protein which is useful eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copiess/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and haspensive to purify in large amount. The present sequence is given it the exemplification of the present invention
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Pred. No. 2e-50,
4, Mismatches 25, Indels
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Escherichia coli.
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N-PSDB; AAC64628.
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assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant by GIAA, CSGA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombinant gene into the chromosome of the homologous species, replacing enemblacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a finbrial presentation system the heterologous antigens are presented in high numbers (up to 10,000 copies/cell), the hybrid fimbrin protein possesses both the immunogens, which may be important for directing an immune response in an immune response in an immune response in an immune response in manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual manual m
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Pred. No. 2.5e-50;
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81.5%;
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Best Local Similarity
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SPRIJ/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enerotacteriaceae for the production of fimbriae comprising recombinant of Enerotacteriaceae for the production of fimbriae comprising recombinant of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a recombinant of the native comprising separating an amino acid polymer comprising a recombinant of the comprising separating an amino acid polymer comprising a recombinant of corein containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the hererologous antigens are presented in high numbers (up to system the hererologous antigens are presented in high numbers (up to vaccine, the carrier fimbrial submit proteins are usually strong immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial submit proteins are usually strong immunogens, which may be important for directing an immune response consequence in singerted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention present sequence is given i
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                                             Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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N-PSDB; AAC64624.
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Best Local Simi:
Matches 121,
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                                                                                                                                                                                                                                                                                                                           Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                               Collison SK,
05-APR-2000; 2000WO-CA000356
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65.7%; Score 509; DB 3; Length 151; 68.2%; Pred. No. 1.8e-41; ive 15; Mismatches 33; Indels
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                Best Local Similarity 58.23
Matches 103, Conservative
              Local Similarity
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  Query Match
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2, 2004, 14:48:29

completed: August

Search completed: Aug Job time: 45.9 secs

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E. coli CsgA subunit 15 kDa protein.
                ABR82651 standard; protein; 151
                                                   (first entry)
                                                   04-DEC-2003
                                  ABR82651;
RESULT 15
         ABR82651
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SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120
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Plasma protein; immune response; antibacterial; vaccine; gene therapy.
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Matches 102; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-646136/61.
                                                      Escherichia coli.
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                                                                               Sequence 42
                                                                                           Sequence
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                                         Sequence
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                              Sequence
                                                                                                                                                                                                                                                                                                                                                                DEPLICANT: COLLINGO, Sames L. APPLICANT: Collingon, Karen S. APPLICANT: Collingon, Karen S. APPLICANT: Clouthier, Sharon C. TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF SALMONELLA NUMBER OF SEQUENCES: 610 CORRESPONDENCE ADDRESS: ADDRESSES: 8eed and Berry STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle STATES: washington COUNTRY: U.S.A. ZIP: 99104-7092
COUNTRY: U.S.A. ZIP: 99104-7092
COMPUTER: READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: DETECTION OF COMPUTER: DATE OF COMPATIBLE COMPATIBLE COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: C-LOSYMS-LOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT, APPLICATION DATA:
APPLICATION NUMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET VUMBER: 35,570
REFERENCE/DOCKET VUMBER: 35,570
REFERENCE/DOCKET VUMBER: 35,570
TELEPRAS: (206) 622-4900
TELEPRAS: (206) 622-4900
TELEPRAS: (206) 622-4901
TELEPRAS: (206) 622-4001
TELEPRAS: (206) 622-4001
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US-08-899-575-34
US-08-383-619-16
US-08-129-591-16
US-09-129-597-16
PCT-US93-08364-16
PCT-US93-08364-16
US-09-495-880A-22
US-08-553-497A-22
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US-09-219-019-4
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US-09-219-019-4
US-09-219-019-6
US-09-218-018-6
US-09-463-666A-6
US-09-463-668A-1
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Pred. No. 4e-61;
1; Mismatches
                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                              Sequence 59, Application US/08233788A Patent No. 5635617 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 151 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 89.4°
Matches 135; Conservative
  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                  US-08-233-788A-59
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Sequence 4764, App
Sequence 3, Appli
Sequence 109, Appli
Sequence 119, App
Sequence 204, Appli
Sequence 204, Appli
Sequence 204, Appli
Sequence 204, Appli
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32096, A
11, Appli
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Sequence 6
Sequence 2
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Sequence 2
Sequence 2
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Sequence
Sequence
                                                                                                                                            US-09-543-407-28
775
1 MKLLKVAAFAAIVVSGSALA..........DSSVMVRQVGFGNNATANQY
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2. /cgn2 = /ptodata/2/iaa/5B_COMB.pep:*

3. /cgn2 = 6/ptodata/2/iaa/6A_COMB.pep:*

4. /cgn2 = 6/ptodata/2/iaa/6B_COMB.pep:*

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5. /cgn2 = 6/ptodata/2/iaa/PCTUS COMB.pep:*

6. /cgn2 = 6/ptodata/2/iaa/PCTUS COMB.pep:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-233-788A-59

US-09-233-788A-57

US-09-234-788A-57

US-09-26-55-204

US-09-072-596-139

US-09-477-135A-131

US-09-477-135A-131

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US-09-336-44A-5

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US-08-1336-44A-13

US-08-1336-44A-13

US-08-1336-44A-13

US-08-1338-438-11-16

US-08-1338-11-16

US-08-1338-11-16
                                                                                                                                                                                                                                                               hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                  - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 2000000000
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918
415
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Match 1
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77.5
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Maximum DB
                                                                   OM protein
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RESULT 4
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                                                                            61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                    SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120
MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGFDSTLSIYQYGSANAALALQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Doran, James L.
APPLICANT: Ray, William W.
APPLICANT: Collinson, Karen S.
APPLICANT: Collinson, Karen S.
APPLICANT: Collinson, Karen S.
APPLICANT: Collinson, Karen S.
APPLICANT: Collinson, Karen S.
APPLICANT: Collinson, Karen S.
ALTILE OF INVENTION: OF SALMONELLA.
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 498; DB 1; Length 120;
Pred. No. 4.6e-43;
1; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Searchie
COUNTRY: U.S.A.

ZTATE: Washington
COUNTRY: U.S.A.

ZERPAGEE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: THE PC COMPATIBLE
COMPUTER: THE PC COMPATIBLE
COMPUTER: PATCHIN Release #1.0, Version #1.25
CONFARE: PatchII Release #1.0, Version #1.25
CONFARE: PatcHII Release #1.0, Version #1.25
CONFARE: PatcHII Release #1.0, Version #1.25
CONFARE: PatcHII Release #1.0, Version #1.25
CONFARE: PatcHII Release #1.0, Version #1.25
CONFARE: PatcHII Release #1.0, Version #1.25
CONFARE: DatcHII Release #1.0, Version #1.25
CONFARE: DatcHII Release #1.0, Version #1.25
ATTORNEY AGENT INFORMATION:
NAME: King, Joshue
REGISTRATION NUMBER: 92.043.403C2
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: CACHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 main a cids
                                                                                                                                                                                     NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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Patent No. 6562958
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                 Sequence 57, Application US/08233788A Patent No. 5635617 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 86.6%;
Matches 97; Conservative 1
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amino acid
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STATE: Washingt
COUNTRY: U.S.A.
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US-09-328-352-4764
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APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4764
LENGTH: 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
TITLE OF INVENTION: TO SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
TITLE OF INVENTION: TO SAID POLYPEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
STREEP
STREEP
STREEP
                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 ALALQSDARKSETTI-----TQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                354 APTITSNIVNDNDIIDNGNSGGIGSGSGNGSG-DCLLNGAASGNGEH----NYGIGNGNG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 AGNGIA-----SGNGEHNYGIGNGNGDDVDITAPITGVLNISGNSFTLIGNSSSSSVNT 353
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       42;
                                                                                                                                                                                                                                                                                                                                              11.0%; Score 85; DB 4; Length 975; 25.3%; Pred. No. 4.2; cive 18; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: Microsoft Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 SGSALAGVVPQWGGGGNHNGG-GNSSGPDSTLSIYQYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/864,038A FILING DATE: May 28, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: D8-184459
FILING DATE: 15-July-1996
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F-5610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08864038A
Patent No. 6001592
GENERAL INFORMATION:
APPLICANT: Kunio NAKASHIMA et al.
                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: C. Bruce Hamburg
REGISTRATION NUMBER: 22,389
REBERDIGE/DOCKET UMBER: F-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)986-2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/8
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                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 25.33
Matches 38; Conservative
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CITY: Tsu-city
STATE: Mie-prefecture
COUNTRY: JAPAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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3Y: linear
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us-09-543-407-28.rai

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TUBERCULOSIS
504 GFGNAGDFNQ------GFANTGNNNIGFANTGNNNIGIGLSGDNQQGFNIASGWNS 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                504 GFGNAGDFNQ------GPANTGNNNIGFANTGNNNIGIGLSGDNQQFNIASGWNS 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                                                                                                 APPLICANT: Campos Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Midhael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 GYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      464 GSGNIGVFNVGSGSLGNYNIGSGN-----LGIYNIGFGNVG----
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIA
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 ---NAALVNQTASDSSVM---VRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          554 GTGNSGLFNSGTNNVGIFNAGTGNVGIANSGTGN 587
                                          122 ---NAALVNQTASDSSVM----VRQVGFGNNATAN
                                                                                   554 GTGNSGLFNSGTNNVGIFNAGTGNVGIANSGTGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
10.8%; Score 84; DB 4
Best Local Similarity 24.7%; Pred. No. 5.1;
Matches 38; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210121.41709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, CURRENT'APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 198104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                     Sequence 199, Application US/09072596; Patent No. 6458366; GENERAL INFORMATION: APPLICANT: Reed, Steven G. APPLICANT: Skeiky, Yasir A.W.
                                                                                                                                                                                                                                                    Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 199:
SEQUENCE CHARACTERISTICS:
LENGTH: 943 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 0
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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US-09-477-135A-131
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US-09-072-596-199
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                                                                                                                                                                                                                                                                                                                      419 LLKSSASASASASASAG-----GGGGGGNGGGNGGGG-------GGGAGALA---- 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .--- 121
                                                                                                                                                                                                                                                                             3 LLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQS
                                                                                                                                                                                                                                  Indels 23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 204, Application US/09056556

Patent No. 6350456

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
ATITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGN----
                                                                                                                                                                                            Length 738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIRICATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.457
TELEPHONE: (206) 622-4900:
                                                                                                                                                                                     Score 84.5; DB 3;
Pred. No. 3.3;
4; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.8%; Score c., 24.7%; Pred. No. 5.1;
                                                                                                     LOCATION: From 1 to 738
; IDENTIFICATION METHOD: E (by experiment)
US-08-864-038A-3
           ORGANISM: Pinctada fucata
CELL TYPE: mantle epithelial cell
FEATURE:
                                                                                                                                                                                                                                  4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 204:
SEQUENCE CHARACTERISTICS:
LENGTH: 943 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                      -----AALAAAĞAĞĞĞ 471
                                                                                                                                                                                        Query Match
Best Local Similarity 35.5%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                63 ARKSETTITQSGYGNG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 24.7%
Matches 38, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 6300
CITY: Seattle
                                                                                   NAME/KEY: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
  ORIGINAL SOURCE
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US-09-056-556-204
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MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
STREET: 115
CITY: New )
                                                                                                                                                                                                                                                                                                                    US-09-072-967-204
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Sequence 131, Application US/09477135A

Patent No. 6572865

GENERAL INFORMATION:
APPLICANT: Nano, Francis
TITLE OF INVENTION: immunostimulatory Peptides
TITLE OF INVENTION: immunostimulatory Peptides
TITLE OF INVENTION: immunostimulatory Peptides
TITLE OF INVENTION: immunostimulatory Peptides
TITLE OF INVENTION: immunostimulatory Peptides
TITLE OF INVENTION: immunostimulatory Peptides
CURRENT APPLICATION NUMBER: US/09/477,135A
CURRENT FILING DATE: 1099-12-15
PRIOR PLILOR DATE: 1997-12-15
PRIOR PLILOR DATE: 1995-06-14
PRIOR PLILOR DATE: 1995-06-15
NUMBER OF SEQ ID NOS: 169
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 131
LENGTH: 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 GSALAGVVPQWGGG-GNHN-GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Reed, Steven G,
APPLICANT: Reid, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Gumpos-Neto, Antonio
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardzik, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Hendrickson, Ronald C.
ITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
ITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
NUMBER OF SEGUENCES: 355
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.8%; Score 84; DB 4; Length 943; 24.7%; Pred. No. 5.1; tive 12; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 GYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER: ERADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 05-MAY-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 ---NAALVNQTASDSSVM----VRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              661 GTGNSGLFNSGTNNVGIFNAGTGNVGIANSGTGN 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 204, Application US/09072967
Patent No. 6592877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38; Conservative
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Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: SEEL STREET: 6300 CCCITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-477-135A-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-072-967-204
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PRESIDENTIAL PROCRASTORS

MANNEL MAKE, David J.

MANNEL MAKE, David J.

MANNEL MAKERS. 2011411C9

MERCHARCH/COCKET NUMBER: 2011411C9

MERCHARCH/COCKET NUMBER: 201141C9

MERCHARCH/COCKET NUMBER: 20114

MERCHARCH/COCKET NUMBER: 20116

MERCHARCH/COCKET NUMBER: 20116

MERCHARCH/COCKET NUMBER: 20116

MERCHARCH/COCKET NUMBER: 20116

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RESULT 12
US-09489-039A-11518
US-09489-039A-11518
Sequence 11518
Sequence 11518
Sequence 11518
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
ATTLE OF INVENTION:
PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT RILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
                        9
                                                                                                                                                               58 ALQSDARKSETTITQSGYGNGA-DYDQLVTRVVTHEMAHAFRN---NATIDQWNAKNSDI 113
                                                                                                                                                                                                         -----TSVLQSGYGNTLNNYSNPNTASLSNSANNVSGNLGVNVAAGNFNQQXNDL 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---VTHEMAHAFRNNATIDQWNAKNSDITVGQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               482 GPVMÓSQPAYNHNQFSGAIANGAESMISTFSLGSTLASGVSSAQALQSQKSEAFQSTLGR 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        542 GFSDGVSQDQAYSRLSNIGRNVSSQNTAQSQLINQQAKNFMDKFQVDD---SHSDAVKGA 598
                                                                                                  5 KVAAFAAIVVSGSALAGVVPQWGG-----GGNHNGGGNSSGPDSTLSIYQYGSANAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 GVVPQWGGGGNHN--GGGNSSGPDSTLSIYQYGS----ANAALALQSDARKSETTITQS
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                        28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 10.3%; Score 80; DB 4; Length 1207; Best Local Similarity 23.5%; Pred. No. 18; Matches 36; Conservative 23; Mismatches 66; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT Weltzin, Richard A.
APPLICANT Guy, Bruno
APPLICANTON IL AND GAS ABAINST Helicobacter Infection
TILE OF INVENTION: Methods Against Helicobacter Infection
FILE REFERENCE: 0613/05502
CURRENT APPLICATION NUMBER: US/09/336,115C
CURRENT FILING DATE: 1999-06-18
PRIOR PALLING DATE: 1998-06-19
PRIOR PLILING DATE: 1998-06-19
                      61; Indels
                                                                                                                                                                                                                                                                                     114 TV----GQYGGNNAALVNQTASDSSVMVRQVGFG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 YG--GNNAALVNQTASDSSVMVRQVGFGNNATA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  599 FAMQATGTLDVDQAASMLMPMVGKARAAMKAAA 631
  20.1%; Pred. No. 3.3;
sive 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   // Sequence 6/ Application US/09336115C
// Patent No. 6576244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 GYGNGADYDQLVTRV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Helicobacter pylori
  Best Local Similarity 20.1% Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-489-039A-11518
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US-09-336-115C-6
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LENGTH: 745
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                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERBNCE: 107196.136

CURRENT PAPLICATION NUMBER: US, 60/094,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PLING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

ERROTH: 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parente 32096, Application US/09252991A
Patent No. 651793
GENERAL INFORMATION:
APPLICANT: MAIC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ALD AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ALD AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT PEPLICATION NUMBER: US/09/252,991A
PRIOR PALICATION NUMBER: US 60/074,788
PRIOR PLILING DATE: 1999-02-18
PRIOR PLILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32096
LENGTH: 339
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                                                                                                                                                                                                                               LALQSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVG 116
                                                                                                                                                                                                                                                            1 MKLLKVAAFAAIVV----SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAA 56
                                                                                                                                                                    16 GSALAGV-----VPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTI 70
                                                                                             Gaps
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                                                                                          34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.5%; Score 81.5; DB 4; Length 558; 30.7%; Pred. No. 4.5; ive 11; Mismatches 39; Indels 11
                                         10.6%; Score 82; DB 3; Length 2123; 25.8%; Pred. No. 24; tive 17; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 339;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 TOSGYGNGADYDQLVTRVVTHEMAHAFR 98
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                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-09-252-991A-30983
; Sequence 30983, Application US/09252991A
; Parent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Pseudomonas aeruginosa
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                                                                                          31; Conservative
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                                         Query Match
Best Local Similarity
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Matches 27; Conserv
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US-09-252-991A-30983
US-08-968-685A-10
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US-09-222-991A-26438

Sequence 26438, Application US/09252991A

Sequence 26438, Application US/09252991A

Sequence 26438, Application US/09252991A

SEQUENCE 26438, Application US/09252991A

SEQUENCE 26438

TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

WOMBER OF SEQ ID NOS: 33142

LENGTH: 1415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        930 ADFAISGO-LKDHASHYGAGGLVGRNRGGLIRSSGSQGTLSLSGGGMNLGGLVGYSSAGG 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 -RKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAXNSDITVGQYGGN- 121
                                                                                                                                                                                                                                                                                                                           102 AYQAVFLAINAAVGL---WNTIGYAVMCGNGNGTESGPGSVIFNDQPGQDSTQITCNRFE 158
                                                                                                                                                                                                                                                                                                                                                                          38 SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 AAIVVSGSALAGVVPQWGGGG--NHNGGG--NSSGPDSTLSIYQYGSANAALALQSDA-- 63
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 RNNATIDOW-NAKNSDITVGOYGGNNAALVNOTASDSSVMVRQVGFGNNAT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 DINGGVYQFCKAKNGSSSSSNGGNGSSTQTTATTTQDGVIITTTYNNNKAI 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
                                                                                                                                                                                                                                          39;
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                                                                                                                                                                                           10.3%; Score 79.5; DB 4; Length 745; 20.5%; Pred. No. 11; tive 27; Mismatches 70; Indels 39
                                                                                                                                                                                                                                                                                      -- GGGGNHNGGGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 NAALVNQTA-SDSSVMV-RQVG--FGNNATAN 149
                                                                                                             ; LOCATION: 721
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-336-115C-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Pseudomonas aeruginosa US-09-252-991A-26438
                                                                                                                                                                                                                                                                                      8 AFAAIVVSGSALAGVVPQW-
                                                                                                                                                                                                Query Match
Best Local Similarity 20.55
Matches 35; Conservative
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(20)
FEATURE:
NAME/KEY: VARIANT
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US-09-841-786-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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Sequence 4, Application US/09841786
Patent No. 6669940
GENERAL INFORMATION:
APPLICANT: NGGRADA, T. G.
APPLICANT: STEWART, GEORGE C.
APPLICANT: NARAYANAN, SANJEEV K.

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-TIITQSGYGNGADY---DQLVTRVVTHEMAHAFRNNAT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 VTSSDSTFVGA---WGGSAALOWNHIGSGNSNISAGLAGAAAVNNIQSKTSALVKNSDIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 IVVSGSALAGVVPQWGGGG----NHNGGGW---SSGPDSTLSIYQYGSANAALALQSDAR
APPLICANT: CHENGAPPA, M. M.

TITLE OF INVENTION: RECOMBINANT FUSOBACTERIUM NECROPHORUM LEUKOTOXIN

TITLE OF INVENTION: VACCINE AND PREPARATION THEREOF

FILE REPERENCE: 30296

CURRENT APPLICATION NUMBER: US/09/841,786

CURRENT FILING DATE: 2001-04-24

PRIOR FILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PALENTIN Ver. 2.1

SEQ ID NO 4

LENGTH: 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33;
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
10.1%; Score 78.5; DB 4; Length 714;
Best Local Similarity 22.8%; Pred. No. 13;
Matches 31; Conservative 16; Mismatches 56; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: August 2, 2004, 14:58:36 Job time : 12 secs
                                                                                                                                                                                                                                                                                                           ; TYPE: PRT ; ORGANISM: Fusobacterium necrophorum US-09-841-786-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 IDQWNAKNSDITVGQY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : : | | |
151 AGESESQKMDVDVTAY 166
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

August 2, 2004, 14:54:48; Search time 36.8 Seconds (without alignments) 1287.123 Million cell updates/sec US-09-543-407-28 775 1 MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151 1291235 Total number of hits satisfying chosen parameters: 1291235 seqs, 313682936 residues Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM protein - protein search, using sw model BLOSUM62 Gapop 10.0 , Gapext 0.5 length: 0 length: 2000000000 sed sed Perfect score: Scoring table: Minimum DB Maximum DB Sequence: Searched: Database Run on:

Published Applications AA:\*

1: /cgn2\_6/prodata/2/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/prodata/2/pubpaa/PCT\_NBW\_PUB.pep:\*

3: /cgn2\_6/prodata/2/pubpaa/PCT\_NBW\_PUB.pep:\*

4: /cgn2\_6/prodata/2/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/prodata/2/pubpaa/US07\_NBW\_PUB.pep:\*

6: /cgn2\_6/prodata/2/pubpaa/US08\_PUBCOMB.pep:\*

7: /cgn2\_6/prodata/2/pubpaa/US08\_PUBCOMB.pep:\*

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11: /cgn2\_6/prodata/2/pubpaa/US09\_PUBCOMB.pep:\*

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16: /cgn2\_6/prodata/2/pubpaa/US08\_PUBCOMB.pep:\*

17: /cgn2\_6/prodata/2/pubpaa/US08\_PUBCOMB.pep:\*

18: /cgn2\_6/prodata/2/pubpaa/US08\_PUBCOMB.pep:\*

18: /cgn2\_6/prodata/2/pubpaa/US06\_PUBCOMB.pep:\*

18: /cgn2\_6/prodata/2/pubpaa/US06\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 905, App	'n	ņ	m	equence 1	equence 1	ednence	3	equence 6	equence 1	equ	eg	equ	equ	Sequence 32, Appl	ਰੂ	Sequence 4, Appli	P.	eg	Sequence 275468,	Sequence 57763, A	Sequence 9, Appli	Sequence 54094, A	Seguence 4894, Ap	Sequence 246651,	Sequence 108981,	Sequence 9134, Ap	Sequence 187064,	ed ਰ	Sequence 1847, Ap
US-10-293-418-905	US-10-282-122A-	US-10-282-122A-5437	US-09-996-634-131	US-09-997-182-13	US-09-997-181-13	US-10-1	US-10-084-843-20	US-10-282-122A-	US-10-437-963-1622	US-10-424-599-2	US-10-282-122A-	US-10-282-122A-	US-10-437-963-1	US-10-244-596-3:	US-10-244-596-3	US-10-647-057-4	US-10-282-122A-	. US-10-425-114-5604	US-10-4	US-10-425-114-5776	-813-214A-9	US-10-282-122A-5	9-738-626-4894	US-10-424-599-24665	US-10-437-963-1089	US-10-369-493-913	US-10-437-963-18706	US-10-282-122A-5	US-09-880-748-184
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## VII GNMEN

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RESULT 1

US-09-741-973B-4

i Sequence 4, Application US/09741873B

i Publication No. US20020081722A1

i Sequence 4, Application US/09741873B

i Publication No. US20020081722A1

i Sequence 6, Application No. US20020081722A1

i Sequence 6, Application No. US20020081722A1

i PERIOR PERENCE: 012889-06

i TILLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation

i TILLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation

i TILLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation

CURRENT APPLICATION NUMBER: US 003-04-04

i PRIOR PILING DATE: 1996-11-26

i PRIOR PILING DATE: 1997-11-26

i PRIOR APPLICATION NUMBER: US 07/397, 487

i PRIOR APPLICATION NUMBER: US 07/789, 437

i PRIOR PILING DATE: 1992-11-06

i PRIOR PILING DATE: 1994-10-06

i PRIOR PILING DATE: 1994-10-05

i PRIOR PILING DATE: 1994-10-05

i PRIOR PILING DATE: 1994-10-05

i SOFTWARE: Patentin Version 3.0

i SEQ ID NO 4

i LENGTH: 151

i TYPE: PAT

i CRANISM: Escherichia coli

US-09-741-873B-4

ORGANISM: Escherichia coli

US-09-741-873B-4

ORGANISM: Escherichia coli

US-09-741-873B-4

ORGANISM: Escherichia coli

US-09-741-873B-4

ORGANISM: Escherichia coli

US-09-741-873B-4

ORGANISM: Secherichia coli

ORCHYMENTA CONSENTATION (57.5%; Matches 33; indels 0; Gaps 0;
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGFDSTLSIYQYGSANAALALQ 60

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APPLICATION NUMBER:
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Sequence 4, Application US/09741873B

Publication No. US20040096965A9

GENERAL INPORMATION:
APPLICANT: Olsen, Are
APPLICANT: Olsen, Are
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084

CURRENT APPLICATION NUMBER: US/09/741,873B

CURRENT APPLICATION NUMBER: US 08/974,1873B

CURRENT APPLICATION NUMBER: S 8801723-1

PRIOR APPLICATION NUMBER: US 08/978,878

PRIOR FILING DATE: 1998-05-04

PRIOR PELING DATE: 1999-11-26

PRIOR PELING DATE: 1999-11-26

PRIOR PELING DATE: 1991-11-06

PRIOR PELING DATE: 1991-11-06

PRIOR PELING DATE: 1991-11-06

PRIOR PELING DATE: 1994-01-28

PRIOR PELING DATE: 1994-01-28

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                                                                                             SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                               61 IDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG 120
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APPLICANT: Normark, Staffan
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084
CURRENT APPLICATION NUMBER: US/09/741,873B
9
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                                                                                                                                                                                                                                                121 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
                                                                                                                                                                                                              121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Escherichia coli
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Best Local Similarity 67.5
Matches 102; Conservative
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US-09-741-873B-4
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US-09-741-873B-2
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81 YDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQV 140
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APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012895-084
CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT FILING DATE: 2003-04-04
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PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1989-05-04
PRIOR FILING DATE: 1989-05-04
PRIOR FILING DATE: 1989-105-04
PRIOR FILING DATE: 1991-11-06
PRIOR PLING DATE: 1991-11-06
PRIOR PLING DATE: 1991-11-03
PRIOR PILING DATE: 1992-11-03
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-00-28
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 2
LENGTH: 131
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PRIOR APPLICATION NUMBER: SE 8801723-1

PRIOR FILING DATE: 1958-05-06

PRIOR FILING DATE: 1958-05-06

PRIOR FILING DATE: 1997-11-26

PRIOR PILING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: US 07/347,189

PRIOR PILING DATE: 1999-05-04

PRIOR FILING DATE: 1992-11-06

PRIOR FILING DATE: 1992-11-03

PRIOR FILING DATE: 1992-11-03

PRIOR FILING DATE: 1992-11-03

PRIOR PILING DATE: 1992-11-03

PRIOR PILING DATE: 1994-01-28

PRIOR PILING DATE: 1994-01-28

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Escherichia coli
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DB 12; Length 131;

55.2%; Score 428;

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Sequence 21, Application US/09820843A

Publication No. US2030303963A1

GENERAL INFORMATION:
A COMPUTATION OF Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTE
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REPERENCE: 063915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin version 3.0
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PRIOR APPLICATION NUMBER: 60/191,078

PRIOR PELING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR PRIOR FILING DATE: 2000-05-26

PRIOR PRIOR PRIOR NUMBER: 60/230,335

PRIOR PRIOR PRIOR OF STATE 2000-09-09

PRIOR PRIOR DATE: 2000-09-09

PRIOR PRIOR DATE: 2000-09-09

PRIOR PRIOR DATE: 2000-10-23

PRIOR PRIOR DATE: 2000-10-23

PRIOR PRIOR DATE: 2000-11-22

PRIOR PRIOR DATE: 2000-11-22

PRIOR PRIOR DATE: 2000-11-22

PRIOR PRIOR DATE: 2000-11-2-22

PRIOR PRIOR DATE: 2000-12-22

PRIOR PRIOR DATE: 2000-10-20

PRIOR PRIOR DATE: 2000-10-20

PRIOR PRIOR DATE: 2001-02-16

PRIOR PRIOR DATE: 2001-02-16

PRIOR PRIOR DATE: 2001-02-16

PRIOR PRIOR PRIOR DATE: 2001-02-16

PRIOR PRIOR PRIOR DATE: 2001-02-16

PRIOR PRIOR PRIOR PRIOR NUMBER: 60/267,636

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PRIOR PRIOR PRIOR PRIOR PRIOR SECOND NUMBER: 60/267,636

PRIOR PRIOR PRIOR PRIOR PRIOR SECOND NOS: 76614

SECOND NO NUMBER: 2001-02-16

SECOND NO NOS: 76614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQ
                                                                                         APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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Best Local Similarity 28.1%; Pred. No. 3.5;
Matches 39; Conservative 21; Mismatches
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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LENGTH: 354
TYPE: PRT
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 186417
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                                                                                                                                                                                                                                        61 VGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGGGNGAAVDQTASNSSVNVTQV 120
                                                                                                                                                                                                            81 YDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQV 140
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                                                                                            21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD 80
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12.3%; Score 95; DB 16; Length 400;
Best Local Similarity 23.6%; Pred. No. 0.52;
Matches 37; Conservative 20; Mismatches 62; Indels
                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT4530_83218C.1.pep
US-10-437-963-186417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 VGQYGGNNAALVNQTASDSSVMVRQVGF--GNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 SAVYGGATA----TAFDLDLMVESCGMFCGGGGAGN 391
         Pred. No. 1.1e-34;
                                  15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 50616, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:
APPLICANT: Wang, Liangeu
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Chisen, Kari
APPLICANT: Cyskind, Undith
APPLICANT: Zyskind, Undith
APPLICANT: Tawick, John

APPLICANT: Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 186417, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252 MNGSSSSSSMEQLGGGGGMSSNGNGS
         64.1%;
         Best Local Similarity 64.1%
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                              GEGNNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                121 GEGNNATAHOY 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 GYGNGADYDQLV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-282-122A-50616
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT FILING NAMER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-22
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20638
LENGTH: 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 GSANAA----LALQSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQW 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 AAFAA-----IVVSGSALAGVVPQWGGGG-----GNSSGPDSTLSIYQY 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---STLSIYQYGSANAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 AAFAADSNTVYLNQTGNDQQANITQSGNGNSVGAFNGNSGFLQENGTLSGA-NLLTVKQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31; Gaps
                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: A polypeptide encoded by an open reading frame of OTHER INFORMATION: SEQ ID NO:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 NWTNDPGVFNKITQDSSSNGSKVSVIQDGKNNVFSIKQGNTGNSTSVNQIG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -SDITVGQYGGNNAALVNQTASDSSVMVRQVG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 LLISGATSLETGVPSRFSGSGSGKDYTLSITSLQTEDVA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 ALOSDARKSETTITO--SGYGNGADYDOLVTRVVTHEMA 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32;
                                                                                                                                                                                                                                                                                                                                                                                                                         DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 15;
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; OTHER INFORMATION: unsure at all Xaa locations US-10-369-493-20638
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 87.5; DE Pred. No. 1.6; 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.3%; Score 87.5; DE 26.3%; Pred. No. 3.3; tive 18; Mismatches
                       PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: PCT/US99/12512
PRIOR FILING DATE: 1999-06-04
PRIOR PILING DATE: 1999-06-04
PRIOR FILING DATE: 1998-06-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20638, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Rhodopseudomonas palustris
       PRIOR APPLICATION NUMBER: 09/730,374
                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 27.3%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 GGGGNHNGGGNSSGPD
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les 45; Conserve
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NAME/KEY: unsure
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US-10-369-493-20638
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Best Local S:
Matches 45,
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Publication No. US20040141982A1
CENERAL INFORMATION:
APPLICANT: Lust, John A.
TITLE OF INVENTION: USE OF GENETICALLY ENGINEERED ANTIBODIES TO CD38 TO TREAT MULTIPL
FILE REFERENCE: 150.188US2
CURRENT APPLICATION NUMBER: US/10/704,206
CURRENT FILING DATE: 2003-11-07
                                                                                                                                                                                                                                                                                                                                                      200 AGDVNSGVGNAGDVNTGLGNSGNINTGGFNPGTLNTGFFSAMTQAGPNS--GFFNAGTGN 257
                                                                                                                                                                                                                                                                                                                       AALALQSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDIT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 GGGGGGGGGGGGGGDIELTQSPSSFSVSLGDRVTITCKASEDIYNRLAWYQQKPGNAPR 185
                                                                                                                                                                                                                        -- NSSGPDSTLSIYQYGSAN 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---STLSIYQYGSANAAL 57
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: A polypeptide encoded by an open reading frame of CTHER INFORMATION: SEQ ID NO:1
US-09-730-374-3
                                                                                                                                                                            40;
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US-05-730-374-3
Sequence 3, Application US/09730374
Fatent No. USZ0010031261A1
Fatent No. USZ0010031261A1
Fatent No. USZ0010031261A1
Fatent No. USZ0010031261A1
FAPELICANT: LUST, JOHN A.
APPLICANT: LUST, JOHN A.
TITLE OF INVENTION: USE OF GENETICALLY ENGINEERED ANTIBODIES
TITLE OF INVENTION: USE OF GENETICALLY ENGINEERED ANTIBODIES
TITLE OF INVENTION: USE OF GENETICALLY ENGINEERED ANTIBODIES
TITLE OF INVENTION: USE OF GENETICALLY
FILE APPLICATION NUMBER: US 009/730,374
CURRENT FILING DATE: 1996-06-04
FRIOR APPLICATION NUMBER: 60/088,277
FRIOR PILING DATE: 1996-08-05
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 249;
                                                                                                                        DB 10; Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32; Indels
                                                                                                                                                                         63; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 TG-YG--NSGFYNAAVNNTGIFVTGVMSSGFFNFGTGN 335
                                                                                                                                                                                                                                                                                                                                                                                                                   115 VGOYGGNNAALVNQTASDSSVMVRQV---GFGNNATAN 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 11.3%; Score 87.5; DB 9; 1 Similarity 27.3%; Pred. No. 1.6; 27; Conservative 9; Mismatches 32;
                                                                                                                        ch 11.5%; Score 89; DB Similarity 24.1%; Pred. No. 1.7; 38; Conservative 17; Mismatches
                                                                                                                                                                                                                     10 AAIVVSGSALAG-VVPQWGGGGNHNGGG-
                                                                                                                                                                                                                                                                                                                                                                258 SGFGHNDPAGSGNSGIONSGFGNS---
CTHER INFORMATION: PPE

"NAME/FET" misc feature

"OTHER INFORMATION: gi|1781260

US-09-820-843A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 GGGGNHNGGGNSSGPD--
                                                                                                                        Query Match
Best Local Similarity
Matches 38; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 249
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358 FGNSGNNNIGFFNSG-NNNVGFFNSGNNNFGFGNAGD-----INTGFGNAGDINT-- 406
                                                                                                                                                                                                                                                                                                                               TRVVTHEMAHAFRNNATIDQ--WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFG 143
                                                                                                                                                                                                                                                                                                                                                                                                               -----GFGNAGFFNMGIGNAGNEDMGVGNGGSFNVGVGN--AGNQS-----VGFG 449
                                                                                                                                                                     26 WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADYDQLV 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --SANA 55
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CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT PILING DATE: 2003-02-20

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR PILING DATE: 2000-10-23

PRIOR PELING DATE: 2000-11-22

PRIOR PILING DATE: 2000-11-22

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

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PRIOR PILING DATE: 2001-02-06

PRIOR PILING DATE: 2001-02-06

PRIOR PILING DATE: 2001-02-16

PRIOR PILING DATE: 2001-02-16

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PRIOR PILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42;
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        DB 9; Length 597;
                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                             47;
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11.1%; Score 86; DB 1
Best Local Similarity 26.0%; Pred. No. 12;
Matches 39; Conservative 17; Mismatches
            111.2%; Score 87; DB 9 27.0%; Pred. No. 5.3; ive 15; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang, Liangsu
Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zyskiná, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
Query Match
Best Local Similarity 27.0%
Marches 34, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 NNATAN 149
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Sequence 146, Application US/09793306

Sequence 146, Application US/09793306

Sequence 146, Application US/09793306

GENERAL INFORMATION:

APPLICANT: Skeiky, Yasir

APPLICANT: Ovendale, Famela

APPLICANT: Lodes, Michael

APPLICANT: Corixa Corporation

APPLICANT: Corixa Corporation

APPLICANT: Corixa Corporation

TITLE OF INVENTION: of Tuberculosis

TITLE OF INVENTION: of Tuberculosis

TITLE OF INVENTION: of Tuberculosis

CURRENT APPLICATION NUMBER: US/09/793,306

CURRENT FILING DATE: 2000-02-25

PRIOR APPLICATION NUMBER: US 60/185,037

PRIOR FILING DATE: 2000-02-25

PRIOR APPLICATION NUMBER: US 60/223,828

PRIOR APPLICATION NUMBER: US 60/223,828

PRIOR FILING DATE: 2000-08-08

NUMBER: O SEQ ID NOS: 164

SEQ ID NO 146

LENGTH: 597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 TITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGNNAALVNQ 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             633 --MOEGWGSGGD-----EM-----NLSTSOWEDEEGDV-----WINAASOES 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 AAIVVSGSALAGVVPQWGGG-GNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSET 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 35; Gaps
                                                                                                              Sequence 998, Application US/10408765A
Publication No. U220040101874A1
Generation No. U220040101874A1
Generation No. U220040101874A1
GENERAL INPORMATION:
APPLICANT: Generation S.
APPLICANT: Charg, Edin D.
APPLICANT: Glason, Bradford W.
APPLICANT: Glason, Bradford W.
APPLICANT: Glason, Bradford W.
APPLICANT: Glason, Bradford W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: DENTIFIED IN THE MITOCHONDRIAL PROTEOME
ITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REPERENCE: 660088.465
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SEQ ID NO 998
LENGTH: A48
TABLE ABELS THE SERVENCE CONTINUENCE OF WINGOWS Version 4.0
BENTH: PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS TO THE PARTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 16; Length 1448;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 28.6*
Matches 36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 TASDSS 134
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                                                               SULT 11
-10-408-765A-998
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1886 GGVNIGGNNIGIANTGIFDIGLANLGSYNIGLANLGD-----DNLGFGNAGSYNIGF 1937
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299 AGNGIA-----SGNGEHNYGIGNGNGDDVDITAPITGVLNISGNSFTLIGNSSSSSVNT 352
                                                                                                                                    56 ALALQSDARKSETTI-----TQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNA 108
                                                                                                                                                                                                   353 APTTTSNIVNDNDTIDNGNSGGTGSGSGNGGG-DGLLNGAASGNGEH----NYGIGNGNG 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 TRVVTHEMAHAFRNNATIDOWNAKNSDITVG-------OYGGNNAALVNQTASDS 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 31; Gaps
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                                                                                                                                                                                                                                                                                                                         109 KNSDIT----VGQYGGNNAALVNQTASDS 133
                                                                                                                                                                                                                                                                                                                                                                                             408 DDVDITAPITGVFNFSGNSFSLIGNSSSSS 437
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25.0%; Pred. No. 38;
ive 15; Mismatches
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Sequence 64364, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Obleen, Kari
APPLICANT: Zyskind, Undith
APPLICANT: Tynick, John
APPLICANT: Trawick, John
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US-10-282-122A-64364
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Yamamoto, Robert
Forsyth, R.
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Matches 34; Conservative
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ORGANISM:
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104 ILIGYYMGSAFDQWGRGTMVTVSSGGGGSGGGGSGGGSALEIVMTQSPGTLSLSPGERA 163
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                                                                                                                                 US-09-880-748-905

US-09-880-748-905

Sequence 905, Application US/09880748

Publication No. US20030059937A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REPERENCE: PFF23

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR APPLICATION NUMBER: 60/216,248

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-25

NUMBER OF SEQ ID NOS: 3239

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 905
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11.0%; Score 85; DB 10; Length 25.
Best Local Similarity 23.0%; Pred. No. 2.9;
Matches 29; Conservative 11; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 VVSGSALAGVVPQWG------GGGNHNGGGNSSGPDSTLSI-
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                               1997 -----IGFFNSGTGN 2006
134 SVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-905
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Job time : 36.8 secs
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Sequence 5833, Ap
Sequence 18734, A
Sequence 18734, A
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Sequence 20, 7
Sequence 26, 7
Sequence 30, 7
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Sequence 14, P
Sequence 18, P
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GENERAL INFORMATION:
APPLICANT White, Aaron P.
APPLICANT Collinson, S. Karen
APPLICANT CALINSON, S. Karen
APPLICANT COLINSON, S. Karen
APPLICANT COLINSON, S. Karen
APPLICANT COLINSON, S. Karen
APPLICANT COLINSON, S. Karen
APPLICANT COLINSON, S. Karen
APPLICANT COLINSON SACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION BACTERIAL FIMBRIAL SYSTEM FOR
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543.407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASELSEQ for Windows Version 4.0
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19 US-09-543-407-28
19 US-09-543-407-22
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19 US-09-543-407-12
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LENGTH: 151
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            August 2, 2004, 14:48:33; Search time 167.9 Seconds (without alignments) 877.809 Million cell updates/sec
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775
1 MKLLKVAAFAAIVVSGSALA........DSSVMVRQVGFGNNATANQY 151
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1: /cgn2 6/ptodata/2/paa/USO6 COMB.pep:*
2: /cgn2 6/ptodata/2/paa/USO6 COMB.pep:*
3: /cgn2 6/ptodata/2/paa/USO7 COMB.pep:*
4: /cgn2 6/ptodata/2/paa/USO8 COMB.pep:*
6: /cgn2 6/ptodata/2/paa/USO8 1 COMB.pep:*
6: /cgn2 6/ptodata/2/paa/USO8 2 COMB.pep:*
7: /cgn2 6/ptodata/2/paa/USO8 4 COMB.pep:*
7: /cgn2 6/ptodata/2/paa/USO8 5 COMB.pep:*
7: /cgn2 6/ptodata/2/paa/USO8 5 COMB.pep:*
7: /cgn2 6/ptodata/2/paa/USO8 7 COMB.pep:*
7: /cgn2 6/ptodata/2/paa/USO8 7 COMB.pep:*
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                                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Searched:

Minimum DB Maximum DB

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18735, A 6, Appli 41783, A 108562,

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                                                                                                                                                     1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNFNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 22, Application US/09543407

Sequence 22, Application US/09543407

GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

TITLE OF INVENTION: BRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

TITLE OF INVENTION: UNMER: US/09/543,407

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 22

LENGTH: 151
                                                                                                      Gaps
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US-09-543-407-5
Sequence 5, Application US/09543407
Sequence 5, Application US/09543407
Septence 7, Application US/09543407
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
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                                               Query Match 100.0%; Score 775; DB 19; Length 151; Best Local Similarity 100.0%; Pred. No. 1.2e-74; Matches 151; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
91.9%; Score 712; DB 19; Length 151;
Best Local Similarity 91.1%; Pred. No. 7.2e-68;
Matches 144; Conservative 0; Mismatches 0; Indels 1.
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                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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US-09-543-407-22
US-09-543-407-28
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APPLICANT: Kay, William W.
APPLICANT: Collinson, S. Karen
APPLICANT: Clouthier, Sharon C.
APPLICANT: Doran, James L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: BASED VACCINES
NUMBER OF SEQUENCES: 58
NUMBER OF SEQUENCES: -
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                         Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.5%; Score 678; DB 6; Length 151;
89.4%; Pred. No. 3.3e-64;
iive 1; Mismatches 15; Indels
                                                                                                                                                                                                                       Query Match 88.1%; Score 683; DB 19; Length 1 Best Local Similarity 90.1%; Pred. No. 9.5e-65; Matches 136; Conservative 1; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: 930 COLUMNIA CENTER, 701 FILLIN AVENUE
STATE: Washington
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORFUTER: IBM PC compatible
CORFUTER: BACATION PC SOFTWARE:
SAFELICATION DATA:
APPLICATION NUMBER: US/08/233,642A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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CLASSIFICATION: 424
ATTORNEY/ABORT INFORMATION:
NAVE: King, Joshua
REGISTRATION NUMBER: 35,570
REFRENCE/DOCKET NUMBER: 920043.403C3
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SSCTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 57, Application US/08233642A GENERAL INFORMATION:
                                                                                           ; LENGTH: 151
; TYPE: PRT
; ORGANISM: Salmonella enteritidis
US-09-543-407-5
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TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 89.4
Matches 135; Conservative
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US-09-543-407-26
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                                                                                                                        SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                          1 MYCLIKVAAFAAIUVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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US-09-543-407-26
US-09-543-407-26
Sequence 26. Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                        SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG
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APPLICANT: Whie, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REPERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85.4%; Score 662; DB 19; Length 151; larity 81.9%; Pred. No. 1.7e-62; Conservative 0; Mismatches 0; Indels 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                               121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
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US-09-543-407-20
Sequence 20, Application US/09543407
; GENERAL INFORMATION:
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Best Local Simi
Matches 136;
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ENGTH: 151
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61 SDARKSETTITQSGYGNGADVGQGADNSTIBLTQNGFRNNATYDQLVTRVVTHEMAHA-- 118
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                                                                             OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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                                                                                                                                                                                                                      Length 151;
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                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                      Query Match
Pest Local Similarity 73.6%; Pred. No. 1.2e-57;
Matches 128; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.1%; Score 613; DB 19; 74.6%; Pred. No. 3.2e-57; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT White, Aaron P.
APPLICANT Doran, James L.
APPLICANT Collinson, S. Karen
APPLICANT Collinson, S. Karen
APPLICANT (Alliason, S. Karen
APPLICANT (Alliason, S. Karen
APPLICANT KAY, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REPERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 151
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US-09-543-407-12
; Sequence 12, Application US/09543407
; GENERAL INFORMATION:
APPLICANT: White, Aaron P.
; APPLICANT: Doran, James L.
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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Matches 129, Conservative
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121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
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                                                                                                                                            RESULT 10
US-09-543-407-18
Sequence 18, Application US/09543407;
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGNSSGPDSTLSIYQYGSANAALALQ 60
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GENERAL INFORMATION:

APPLICANT: White, Aaron F.

APPLICANT: Origina W.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

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TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION OF HETEROLOGOUS PEPTIDE SEQUENCES

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 151
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APPLICANT: Collinson, S. Karen
APPLICANT: KAY, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT PELLING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 151
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                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CRGANISM: Artificial Sequence
CRGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
CHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
US-09-543-407-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.1%; Score 605; DB 19; Length 151; 80.1%; Pred. No. 2.3e-56; ive 5; Mismatches 25; Indels (
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Matches 121; Conservative
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US-09-543-407-14
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SEQUENCE 24, Application US/09543407

SEQUENCE 24, Application US/09543407

SEQUENCE 24, Application US/09543407

APPLICANT: Wilte, Aaron P.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

TITLE OF INVENTION: BRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

FILE REFERENCE: 920043.406

CURRENT APPLICATION WHERE: US/09/543.407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE REALSEQ for Windows Version 4.0

SEQ ID NO 24
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                                                                                                                                                                                                                                                                                                APPLICANT: Dozah, James L. APPLICANT: Collinson, S. Karen APPLICANT: Collinson, S. Karen APPLICANT: Kay, William W. TITLE OF INVENTION: BACTERIAL FIMERIAL SYSTEM FOR TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES FILE REPERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SEQ ID NO 18
LENGTH: 151
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80.8%; Pred. No. 6.3e-56;
iive 4; Mismatches 25;
121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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DB 19; Length 151;

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121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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Best Local Similarity 68.23
Matches 103, Conservative
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US-09-543-407-7
                                                                              US-09-543-407-16
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                                                                                                                                        SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                      SDARKSETTITQSGYGNGADVGQGADNSTIBLTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
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                                                                                      1 MKLIKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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                                                                                                                                                                                                                                                                                                            US-09-543-407-31
US-09-543-407-31
Sequence 31, Application US/09543407
SERERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: REPRESENCE: 920043-406
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
TITLE OF INVENTION UNMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FARSEE for Windows Version 4.0
SEQ ID NOS: 31
                                                         1 MKLLKVAAFPAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                      Gaps
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGGUS PEPTIDE SEQUENCES
FILE REPERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ. ID NOS: 59
SOFTWARE: FRASEQ for Windows Version 4.0
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Pred. No. 8.1e-56;
; Mismatches 25; Indels
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Pred. No. 1.8e-55;
1; Mismatches 14;
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US-09-543-407-16
Sequence 16, Application US/09543407
GENERAL INFORMATION:
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; ORGANISM: Salmonella enteritidis
US-09-543-407-31
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88.5%;
81.5%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 88.5'
Matches 116; Conservative
                      Matches 123; Conservative
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  Best Local Similarity
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US-08-978-878-4
Sequence 4; Application US/08978878
Sequence 10 Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Comparison of Compar
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APPLICANT While, Aaron P.
APPLICANT Collinson, S. Karen
APPLICANT Collinson, S. Karen
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
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OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                         Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 151,
                                                                                                                                                                                                                                                                                                                                                                                                             26; Indels
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                                                                                                                                                                                                                                                                                   Query Match
73.3%; Score 568; DB 19;
Best Local Similarity 80.1%; Pred. No. 2.2e-52;
Matches 121; Conservative 4; Mismatches 26;
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Best Local Similarity 67.5%; Pred. No. 1e-45;
Matches 102; Conservative 16; Mismatches 33; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 NNAALVNOTASDSSVMVRQVGFGNNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: US 07/347,189
EARLIER PILING DATE: 1989-05-04
EARLIER APPLICATION NUMBER: US 07/789,437
EARLIER FILING DATE: 1991-11-06
EARLIER FILING DATE: 1991-11-06
EARLIER FILING DATE: 1997-11-03
EARLIER FILING DATE: 1997-01-8
EARLIER APPLICATION NUMBER: US 08/187,865
EARLIER APPLICATION NUMBER: US 08/187,865
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1995-06-28
NUMBER OF SEQ ID NOS: 10
SCOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 4
LENGTH: 151
TYPE: PRT
TYPE: PRT
TYPE: PRT
TYPE: PRT
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TYPE: PRT
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

2, 2004, 14:49:38 ; Search time 17.8 Seconds (without alignments) 888.146 Million cell updates/sec August Run on:

US-09-543-407-28 775 1 MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Sequence:

Scoring table:

601315 segs, 104695340 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pending Patents AA New:\*
(cgn2\_6/ptodata/2/paa/VCG\_NEW\_COMB.pep:\*
(cgn2\_6/ptodata/2/paa/USO6\_NEW\_COMB.pep:\*
(cgn2\_6/ptodata/2/paa/USO7\_NEW\_COMB.pep:\*
(cgn2\_6/ptodata/2/paa/USO8\_NEW\_COMB.pep:\*
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(cgn2\_6/ptodata/2/paa/USO8\_NEW\_COMB.pep:\*
(cgn2\_6/ptodata/2/paa/USO8\_NEW\_COMB.pep:\* 1064506 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

4 4 5 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	Description	nce 4, Appl	equence 2, Appl	equence 1730	Sequence 38, Appl	Sequence 9, Appli	Sequence 45603, A	equen	Sequence 339993,	eguen	eguen	equen	Sequence 458, App	edneu	equen	eguen	eguen	equen	Sequence 5, Appli	eguen	Sequence 280, App	ednen	Sequence 2, Appli	ednen	Sequence 3429, Ap	Sequence 1222, Ap	Sequence 15216, A
OUMINISK I ES		-09-741-873C-	-09-741-873C-	A-1	F-US04-10229-38	US04-09388-	-10-767-701-4560	10-425-115-32095	0-425-115-339	-10-425-115-19320	-10-805-394-489	9-248-796A-26	804-21492-4	0-170-205E-166	10-425-115-31246	I-US04-21492-40	-09-952-267	-10-872-768-	-10-872-769	10-854-439-5	-324-28	38-2	-603-150-	-115-351	E-342	-439-12	US-09-248-796A-15216
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~	13, App	13,	Sequence 72, Appl	2740		34383	22147	Sequence 11388, A	Sequence 12224, A	Seguence 287789,	Seguence 1245, Ap	13,	14,	20,	14,	Sequence 15, Appl	591	340
US-09-952-267B-13	US-10-872-768-13	US-10-872-769-13	US-10-796-907-72	US-10-425-115-274032	US-10-425-115-309662	US-10-425-115-343835	US-10-425-115-221471	US-60-581-351-11388	US-60-581-351-12224	US-10-425-115-287789	US-60-556-841-1245	US-10-490-953-13	US-10-490-953-14	US-10-490-953-20	US-10-723-981-14	US-10-723-981-15	US-10-045-674A-591	US-10-425-115-340009
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## ALIGNMENTS

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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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67.5%; Pred. No. 6.1e-38;
iive 16; Mismatches 33; Indels
US-09-741-873C-4; Sequence 4; Application US/09741873C
Sequence 4; Application US/09741873C
SENERAL INFORMATION:
APPLICANT Normark, Staffan
                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 67.58
Matches 102; Conservative
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61 SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQMNAKNSDITVGQYGG 120 61 TDARNSDLTITOHGGNGADVGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGG 120 9 1 MKLLKVAALAAIVFSGSAVAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ ð QQ 셤  $\delta$ 

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                                                   132 GNQNVGSNSYSPDT-----YGSAIGTLGVQEKTAPAVTGİHSKĞIĞ-AAAYPELT--- 180
                                                                                                                                                               ---NAGNTGLAKGTAPASTSATYGESPSADYSKSGATGVVPATYLN 223
30 GNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADYDQLVTRVV 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTALAAAVALMAGTSAFAAAT----GGFSTTDGGNVSGARSFTASTYQQINTIIANAKLD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --YTGN 93
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APPLICANT: McCann, Ryan
APPLICANT: McCann, Ryan
APPLICANT: Gerendash, Joel
APPLICANT: Janssen, Giselle
APPLICANT: Janssen, Giselle
APPLICANT: Dandod, Samun
TITLE OF INVENTION: THEM AND METHODS FOR MAKING AND USING THEM
FILE REFERENCE: 564462009440
CURRENT APPLICATION WUMBER: PCT/US04/10229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.3%; Score 87.5; DB 1; Length 619; 26.9%; Pred. No. 9.4; tive 10; Mismatches 43; Indels 4
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                                                                                                               90 THEMAHAFRNNATIDOWNAKNSDITVGOYGGNNAALVNQTAS
                                                                                                                                                                                                                                                        224 TSGAPTGSLNTAGVVGGAGFGDNSNTSSY 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/460,842
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-04-04
PRIOR FILING DATE: 2003-07-03
NUMBER OF SEQ ID NOS: 134
SOFTWARE: PESESEQ for Windows Version 4.0
SEQ ID NO 38
LENGTH: 619
                                                                                                                                                                                                                         132 -----DSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 38, Application PC/TUS0410229 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (36)...(387)
; OTHER INFORMATION: Catalytic domain PCT-US04-10229-38
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; Sequence 9, Application PC/TUS0409388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Diversa Corporation
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Best Local Similarity 26.9%
Matches 36; Conservative
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Solbak, Arne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1)...(35) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Unknown
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: DOMAIN
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NAME/KEY: SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                        PCT-US04-10229-38
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Sequence 17306, Application US/09248796A
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
SEQ ID NOS: 28208
SEQ ID NO 17306
LENGTH: 388
                      Sequence 2 Application US/09741873C

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
Normark, Staffan
APPLICANT:
APPLICANT:
Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REPREBENCE:
OLS899-084
CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
FRICA REPLICATION NUMBER: US 08/978,878
FRICA REPLICATION NUMBER: US 08/978,878
FRICA REPLICATION NUMBER: US 07/347,189
FRICA RELING DATE: 1993-05-04
FRICA REPLICATION NUMBER: US 07/347,189
FRICA RELING DATE: 1991-11-06
FRICA RELING DATE: 1991-11-06
FRICA RELING DATE: 1991-11-06
FRICA RELING DATE: 1991-11-06
FRICA RELING DATE: 1991-11-06
FRICA REPLICATION NUMBER: US 07/970,846
FRICA RELING DATE: 1991-11-03
FRICA RELING DATE: 1994-01-28
FRICA RELING DATE: 1994-01-28
FRICA RELING DATE: 1994-01-28
FRICA RELING DATE: 1994-01-28
FRICA RELING DATE: PARENTEN US 08/18/519
FRICA RELING DATE: PARENTEN US 08/318,519
FRICA RELING DATE: PARENTEN US 08/318,519
FRICA RELING DATE: PARENTEN US 08/318,519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 VGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGGGNGAAVDQTASNSSVNVTQV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GVVPQYGGGGNHGGGGNNSGPNSELNTYQYGGGGNSALALQTDARNSDLTITQHGGGNGAD 60
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11.5%; Score 89.5; DB 5; Length 388;
Best Local Similarity 22.1%; Pred. No. 3.6;
Matches 33; Conservative 17; Mismatches 44; Indels 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5; Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 55.2%; Score 428; DB 5; Length 13 Best Local Similarity 64.1%; Pred. No. 5e-31; Matches 84; Conservative 15; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 GFGNNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GFGNNATAHOY 131
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US-09-248-796A-17306
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ORGANISM:
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Sequence 320950, Application US/10425115
GENERAL INFORMATION:
APPLICANT La Rosa, Thomas J.
APPLICANT Zhou, Yihua
APPLICANT Zhou, Yihua
APPLICANT Zhou, Yongwei
APPLICANT Shou, Yongwei
APPLICANT Shou, Yongwei
APPLICANT Shou, Yongwei
APPLICANT Shou, Yongwei
APPLICANT Shou, Yongwei
APPLICANT Should Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPREBENCE: 38-21(2322)B
CURRENT APPLICATION NUMBER: 2003-04-28
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 320950
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133 IRLLEERAQEAILASCRDVLRASGFRFEDAWAKVIPGSDEGVYAWVAANYALGRLGGDPN 192
                                                                                                                                                                                                                                                                                                                                                                                         61 GXYGEAGGSGXAYAQGGGGGGGGGQYGGSG-------SGYGSGSGYG 102
                                                                                                                                                                                                                                                            88 VVTHEMAH---AFRNNATID----QWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----RKSETTITQ-----SGYGNGADYDQLVTR 87
                                                                                                                                                                                                                                                                                                                                    ----QYGSANAALALQSDARKSETTITQSGYGNGADYD
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                                                                                                                                                                65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.9%; Score 84.5; DB 6; Length 511; 23.3%; Pred. No. 14; ive 22; Mismatches 64; Indels 5
                                                                                                           Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 ---HEMLRSRGSFKNGTLADPCAPRGYSRNEEMMLRMSGASRSTLENQ---
                                                                                                                                                                Indels
                                                                                                                                                                                                                      1 MKLLKVAAFAAIVV--SGSALAGVVPQW---GGGGGNHNGGGN----
           , OTHER INFORMATION: Clone ID: SORBI-28MAY03-C82834_1.pep
US-10-767-701-45603
                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 QLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGNNA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q-----AGGSGSNGGAYAQGGAQGGGGGGQQYGGSGS 134
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US-10-425-115-320950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE: .
NAME/KEY: unsure
LOATION: (1)..(511)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                        Query Match
Best Local Similarity 24.2%; Pred. No. 5.5;
Matches 39; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 339993, Application US/10425115; GENERAL INFORMATION: APPLICANT: La Rosa, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 STLSIYQYGSANAALALQSDA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local, Similarity 23.3
Matches 44, Conservative
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ORGANISM; Zea mays
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US-10-425-115-339993
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FEATURE:
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     APPLICANT: INCYTE CORPORATION; MARQUIS, Joseph P.;
APPLICANT: TRAW, Uyen K.; YANG, Yonghong G.;
APPLICANT: TRAW, Uyen K.; YANG, Yonghong G.;
APPLICANT: TRAW, Trami, CHAMLA, Narindar K.;
APPLICANT: TRAGE Jaji; WANG, Jonathan T.;
APPLICANT: ELIOTT, Vicki S.; CHIEN, David;
APPLICANT: SILIOTT, Vicki S.; CHIEN, David;
APPLICANT: SILIOTT, Vicki S.; CHIEN, David;
APPLICANT: SILIOTT, Vicki S.; CHIEN, David;
APPLICANT: FAUREO, Kristin D.; RICHARDSON, Thomas W.,
APPLICANT: FAUREO, Kristin D.; RICHARDSON, Mariah R.,
APPLICANT: FAUREO, Kristin D.; RICHARDSON, Mariah R.,
APPLICANT: PROFILING APPLIAL J.A.; BAUGHN, Mariah R.,
APPLICANT: PROFILING PROFILIS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND D.; FILE OF INVENTION: PROFILE CT/USO4/09388
CURRENT PRILING DATE: 2004-04-01
PRIOR APPLICATION NUMBER: US 60/455,568
PRIOR PELING DATE: 2003-03-24
PRIOR PELING DATE: 2003-06-04
PRIOR PELING DATE: 2003-06-04
PRIOR PELING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 40
SOFTHARE: PERL PROFILM
SOFTHARE: PERL PROFILM
SOFTHARE: PERL PROFILM
SOFTHARE: PERL PROFILM
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GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: APPLICANT: Actional Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38-21535318 and Uses Thereof For Plant Improvement FILE REFERENCE: 2004-01-29
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 45603
LENGTH: 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1082 --MOEGWGSGGD------MISTSOWEDERGDV-----WINDASOES 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1031 STLVDNGTAAWGKPPSSGSGWGDHPA-----EPPVAFGRAGAPVAASALCKPASKS-- 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 TITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGNNAALVNQ 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 AAIVVSGSALAGVVPQWGGG-GNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSET 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.3%; Score 87.5; DB 1; Length 1905; 28.6%; Pred. No. 35; tive 16; Mismatches 39; Indels 35
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LOCATION: (1)..(234)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 7525307CD1
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Matches 36; Conservative
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ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1117 TSSCSS 1122
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US-10-767-701-45603
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DB 6; Length 224;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFPLICANI: CALLA, ANDO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT PELICATION NUMBER: US/10/805,394
CURRENT FILING DATE: 2004-03-22
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PACENTIN VERSE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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Best Local Similarity 24.6%; Pred. No. 3 Matches 35; Conservative 19; Mismatch
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                                                                                                                                                                                                                                                                                      Sequence 4894, Application US/10805394 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Corynebacterium glutamicum
US-10-805-394-4894
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ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 OSGYGNGADYDOLV-
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
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us-09-5

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF SINCENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF SINCENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF SINCENTION: Nucleic Acid Molecules and Other Molecules Associated With
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GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Con, Yonguic
APPLICANT: Con, Yonguic
APPLICANT: Con, Yonguic
APPLICANT: Con, Yonguic
APPLICANT: Shou, Yihua
APPLICANT: Con, Yonguic
APPLICANT: Shou, Yonguic
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 193207
LENGTH: 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 ETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGGNNAALV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---FSAPRNGVAIPNANGO-----VPTYNGNTGIPL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 IVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTIT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 AAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 AQIPASATIGAAVAATNPOPGGSGTGGGVVGAGGPDAPLELYMHD----ILGGSSPTARP 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 OSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.5%; Score 81; DB 6; Length 147; 24.6%; Pred. No. 6.6; cive 18; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 6; Length 276;
11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 EDGRG-----SNADVRAHTFGKVADL----SNADVAVDQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; CTHER INFORMATION: Clone ID: MRT4577_107790C.1.pep
US-10-425-115-193207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_73240C.1.pep
US-10-425-115-339993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1)..(276)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 10.6%; Score 82; DB 6 Best Local Similarity 27.1%; Pred. No. 11; Matches 29; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 ITGLLGNIYNGQVPFARPIG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 DTGLSRAGFL--OPGTGN 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 NQTASDSSVMVRQVGFGN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 24.6%
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: unsure
LOCATION: (1)..(
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TITLE OF INVENTION: Weinstock et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS TITLE OF INVENTION: 10146.123 CURRENT APPLICATION NUMBER: US/09/248,796A CURRENT APPLICATION NUMBER: US/09/248,796A CURRENT FILING DATE: 1999-02-12 PRIOR APPLICATION NUMBER: US 60/074,725 PRIOR APPLICATION NUMBER: US 60/096,409 PRIOR FILING DATE: 1998-09-13 NUMBER OF SEQ ID NOS: 28208 SEQ ID NOS: 28208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
9
                                                                                               45 GTAIAGVLTKGGATVEHIGSADSDIATINGDVVILAVPYPAVESIIASHKDALAGKTVID 104
                                                                                                                                                                                                                                    105 ITNPLNFETFDSLVVPVGSSATAEIQAQLPTSRVLKAFNTNFAATLATGKVGDITTTVLV 164
                                                      16 GSALAGVVPQWGGGGNHNGGGNSS----GPDSTLSIYQYGSANAALALQSDARKSETTIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.5%; Score 81; DB 5; Length 457; 25.0%; Pred. No. 25; tive 19; Mismatches 69; Indels
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40; Conservative
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Best Local Similarity
Matches 40; Conserv
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Sequence 16659, Application US/10170205E
GENERAL INFORMATION:
APPLICANT' ADAMS, MATK
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, THEREOF
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
FILE REPERRICES: CLOO1381
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40112
SEQ TEM NOW 16659
LENGTH: 1627
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APPLICANT LA ROSA, Thomas J.
APPLICANT LOVORWATION:
APPLICANT LOVORWATION:
APPLICANT LOVORWATION:
APPLICANT LOVORWATION:
APPLICANT CAO, Yongwei
APPLICANT CAO, Yongwei
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APPLICANT CAO, YONGWEI
APPLICANT CAO, YONGWEI
APPLICANT CAO, YONGWEI
COTTEN CAO, YONGWEI
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEC ID NOS: 369326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 YQYGSANAALALQSDARKS----ETTIT-QSGYGNGADYDQLVTRVVTHEMAHAFRN-N 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 TRVVTHEMAHAFRNNATIDOWNAKNSDITVGOYGGNNAALVNOTASDSSVMVRQVGFGNN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62] AAAAKSGHAWSGAANQEDKSPTWGEPPKPKSQHWGDGQRSNPAWSAGGGDWADSSSVLGH 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----TNTKANPGTNWG 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADYDQLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --- MGGGGNHN-----GGGNSSGPDSTLSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   48;
                                                                                                                                                                                                                                                                                                                                                                                                Length 1627;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                51; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   681 LGDGKKNGS-GWDADSNRSGSGWNDTTRSGNSGWGNS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 ATI-----DQWNAKNSDITVGQYGGNNAALVNQTAS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     729 ETLKPGPQQNWASKPQDNNVSNWGG--AASVKQTGT 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; CTHER INFORMATION: Clone ID: MRT4577_48027C.1.pep
US-10-425-115-312468
                                                                                                                                                                                                                                                                                                                                                                                                      Score 80; DB 6;
Pred. No. 1.4e+02;
5; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.2%; Score 79; DB 6; 25.4%; Pred. No. 23; iive 13; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 AAIVVSGSALAGVVPQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                      10.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 25.4%
Matches 32, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                Query Match 10.33
Best Local Similarity 26.33
Matches 41, Conservative
                                                                                                                                                                                                                                                                                                        TYPE: PRT
CRGANISM: Homo sapiens
US-10-170-205E-16659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYPNPY 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-425-115-312468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 312468
LENGTH: 295
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APPLICANT: Healey, Shaun
APPLICANT: Healey, Shaun
APPLICANT: Healey, Shaun
APPLICANT: Healey, Shaun
APPLICANT: Healey, Shaun
APPLICANT: Pullian, Derrick
TITLE OF INVENTION: GLUCANASES, NUCLEIC ACIDS ENCODING THEM AND METHODS FOR MAKING AN
TITLE OF INVENTION: THEM
THIS PEPRICALION NUMBER: PCT/US04/21492
CURRENT APPLICATION NUMBER: PCT/US04/21492
PRIOR APPLICATION NUMBER: 60/484,725
PRIOR APPLICATION NUMBER: 60/484,725
NUMBER OF SEQ ID NOS: 518
SOFTWARE: Patent in version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSTASGDGN-CEY----IVSNEWNTGFTGAIRITNEGSSAINGWNVSWSYSDGTSVTS 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITQSGYGNGADYDQLVTRVVTHEMAHAF-----RNNATIDQWNAK------ 109
                                                       289 SSEFLASLINGLGSGGGGGGGSNINSYKNHSTTSTTSKYFNSSSTATKLSSSKSIYSNS 348
                                                                                                                                                              349 TTSRSSLSVSSSSTDGGGGANLFGLLLNSVAAVSRTLAAESTLSTGTTTTSDSANSNTKD 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---GGGNSSGPDSTLSIYQYGSANAALALQSDARKSET 68
                                                                                                                   TITQSGY------GNGADYDQL-----VTRVVTHEMAHAFRNNATIDQWNAKNSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
10.5%; Score 81; DB 1; Length 568;
Best Local Similarity 20.7%; Pred. No. 32;
Matches 35; Conservative 22; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
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NAME/REY: DOMAIN
LOCATION: (46)...(307)
OTHER INFORMATION: Cellulase (glycosyl hydrolase family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: DOMAIN

DOCATION: (385)...(413)

COTATION: Cellulose or protein binding domain

PCT-US04-21492-458
                                                                                                                                                                                                                                                    YS--SYSGTITSFPSTTGSLS------GDGNKLIGGNKY 439
                                                                                                                                                                                                              113 ITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNAT-ANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE: OTHER INFORMATION: Obtained from environmental sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE: NAME/KEY: DOMAIN LOCATION: (470) ... (567) OTHER INFORMATION: Cellulose binding domain
                                                                                                                                                                                                                                                                                                                                                                          Sequence 458, Application PC/TUS0421492 GENERAL INFORMATION:
                         SGSALAGVVPQWGGGGNHNGGGNSS-
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Diversa Corporation APPLICANT: Steer, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WGGGGNHN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: SIGNAL
                                                                                                                                                                                                                                                                                                                                  RESULT 12
PCT-US04-21492-458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 458
LENGIH: 568
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RESULT 13

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Sequence 402 Application PC/TUS0421492

| Sequence 402 Application PC/TUS0421492
| Sequence 402 Application PC/TUS0421492
| GENERAL INFORMATION:
| APPLICANT: Diversa Corporation | APPLICANT: Steer. Brian | APPLICANT: Callen, Walter | APPLICANT: Callen, Walter | APPLICANT: Pulliam, Derrick | TITLE OF INVENTION: GLUCANASES, NUCLEIC ACIDS ENCODING THEM AND METHODS FOR MAKING AN TITLE OF INVENTION: GLUCANASES, NUCLEIC ACIDS ENCODING THEM AND METHODS FOR MAKING | TITLE OF INVENTION: GLUCANASE: 2004-07-20 | FILE REFERENCE: 56446200540 | CURRENT APPLICATION NUMBER: 60/484,725 | PRIOR FILING DATE: 2003-07-02 | PRIOR FILING DATE: 2003-07-02 | PRIOR FILING DATE: 2003-07-02 | PRIOR FILING DATE: 2003-07-02 | PRIOR FILING DATE: 2003-07-02 | PRIOR FILING DATE: 2003-07-02 | PRIOR FILING DATE: 2003-07-02 | PRIOR FILING DATE: 2003-07-02 | PRIOR FILING DATE: 2003-07-02 | PRIOR FILING DATE: 2003-07-02 | PRIOR FILING DATE: 2003-07-02 | PRIOR FILING DATE: 2003-07-02 | PRIOR FILING DATE: 2003-07-02 | PRIOR FILING DATE: 2003-07-02 | PRIOR FILING DATE: 2003-07-02 | PRIOR FILING DATE: 2003-07-03 | PRIOR FILING DATE: 2003-07-03 | PRIOR FILING DATE: 2003-07-03 | PRIOR FILING DATE: 2003-07-03 | PRIOR FILING DATE: 2003-07-03 | PRIOR FILING DATE: 2003-07-03 | PRIOR FILING DATE: 2003-07-03 | PRIOR FILING DATE: 2003-07-03 | PRIOR FILING DATE: 2003-07-03 | PRIOR FILING DATE: 2003-07-03 | PRIOR FILING DATE: 2003-07-03 | PRIOR FILING DATE: 2003-07-03 | PRIOR FILING DATE: 2003-07-03 | PRIOR FILING DATE: 2003-07-03 | PRIOR FILING DATE: 2003-07-03 | PRIOR FILING DATE: 2003-07-03 | PRIOR FILING DATE: 2003-07-03 | PRIOR FILING DATE: 2003-07-03 | PRIOR FILING DATE: 2003-07-03 | PRIOR FILING DATE: 2003-07-03 | PRIOR FILING DATE: 2003-07-03 | PRIOR FILING DATE: 2003-07-03 | PRIOR FILING DATE: 2003-07-03 | PRIOR FILING DATE: 2003-07-03 | PRIOR FILING DATE: 2003-07-03 | PRIOR FILING DATE: 2003-07-03 | PRIOR FILING DATE: 2003-07-03 | PRIOR FILING DATE: 2003-07-03 | PRIOR FILING DATE: 2003-07-03 | PRIOR FILING DATE: 2003-07-03 | PRIOR FILING DATE: 2003-07-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 TITQSGYGN-----GADY-----GADY-----GADY------DQLVTRVVTHEMAHAFRNNATIDQW 106
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-----YQNSLYRANW 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: DOMAIN
COCATION: (39)...(300)
OTHER INFORMATION: Cellulase (glycosyl hydrolase family 5)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (493)...(521)
; OTHER INFORMATION: Cellulose or protein binding domain PCT-US04-21492-402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : : | | | : : | 368 SGGSTGGGNNVYPNWTARDWSGGAYNHANAGDQMV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 ---NAKNSD---ITVGQYGGNNAALVNQTASDSS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : | | : : | | | 417 YINSVPGSDASWISLGACGGNGSTISSSSSSSS 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: DOMAIN
LOCATION: (393)...(428)
OTHER INFORMATION: Carbohydrate binding domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: DOMAIN
LOCATION: (610)...(959)
OTHER INFORMATION: Glycosyl hydrolases family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: August 2, 2004, 15:29:55 Job time: 17.8 secs
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NAME/KEY: DOMAIN
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August 2, 2004, 14:39:53 ; Search time 9.4 Seconds (without alignments) 1545.204 Million cell updates/sec
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775
1 MKLLKVAAPAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                              283366 seqs, 96191526 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	fimbrin protein ag	major curlin chain	curlin protein csg	upn	rot	hypothetical glyci	e)	п	probable PPE prote	Œ	prot	probable PPE prote	curlin nucleator p	minor curlin subun	curlin minor chain	ice nucleation pro	ion pr	E prot	l D	sease	ucleation	ncleation pr	PE prot	conserved hypothet	hypothetical prote	nucleation compone	leishmanolysin (EC	probable PPE prote	probable PPE prote
SUMMARIES	CI			S70788																								562	98	7052
	DB	2	N	N	N	2	N	N	0	~	Н	7	7	7	N	~1	~	7	~	7	N	7	7	~	~1	~	N	Н	~	7
	Length	151	10	151	10	ın	~	74	IO.	<b>117</b>	$\circ$	$\sim$	$\mathbf{H}$	10	٠n	ഥ	C/I	56	un.	0	4	m	25	O.	4	4	u	ŲΥ	U)	20
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121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151

leishmanolysin (EC leishmanolysin (EC hemolysin A - Serr probable PPE prote probable PPE prote hypothetical cell hypothetical prote related to C2H2 zi protein F39DB.Lb hypothetical prote hypothetical prote	842049 844951 844951 828185 700575 87136075 8713621 751024 721998 721998	0000000000	48 88 88 88 88 88 88 88 88 88 88 88 88 8	000.000.000.0000.000000000000000000000	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	ろ 3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
related to C2H2 zi	21	~	770	10.6	0	43
hypothetical prote	LU	~	343	10.7	83	42
	AB1390	7	277	10.7	83	41
	F70675	~	582	10.8	ω.	40
	D70575	7	3300	10.8	84	33
hemolysin A - Serr	A28182	~	1608	10.8	84	38
leishmanolysin (EC	A44951	~	599	10.8	84	37
leishmanolysin (EC	B42049	~	599	10.8	84	36
hypothetical prote	T26667		586	10.8	84	35
probable lipoprote	D81411		978	10.9	4	34
probable lipoprote	C81265		928	10.9	84.5	33
leishmanolysin (EC	S19916		646	10.9	4.	32
hypothetical prote	H98323	N	1341	11.0	82	31
conserved hypothet	AF2959	(1)	1052	11.0	82	30

	RESULT 1	
	otein agfA p	
	C;Species: Salmonella entericidis C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999	
	an, J.L.; Ba	
	thin, ac	
	12, PMID:8550497	
	A; Molecule type: DNA	
	A, Cross-references: GB:U43280; NID:g1184712; PIDN:AAC43599.1; PID:g1184714	
	A; Molecule type: protein	
	A;Note: the authors translated the codon ACG for residue 44 as 11e R:Collinson, S.K.; Emody, L.; Muller, K.H.; Trust, T.J.; Kay, W.W.	
	J. Bacteriol, 173, 4773-4781, 1991	Ē
	MID:1677357	2
	A;Contents: 27655	
	A; Accession: Afrogo A; Status: preliminary	
	A; Molecule type: protein	
	. w	
	A; Gene: agfA. C: Braction:	
	A) Description: major component of thin aggregative fimbriae	
	nasminogen, tissue piasminogen	
	C./reywolver increments sequence #status predicted <sig> F;1-20/Domain: signal sequence #status predicted <mat> F;21-151/Product: fimbrin protein agfA #status experimental <mat></mat></mat></sig>	
	Query Match Best Local Similarity 90.1%; Pred. No. 1.4e-51;	
	vative 1	
	Qy 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGFDSTLSIYQYGSANAALALQ 60	
	Db 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSGPDSTLSIYQYGSANAALALQ 60	
	Qy 61 SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRINATIDQMNAKNSDITVGQYGG 120	
	DD 61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120	
· · · - <del>-</del>	Qy 121 NWAALVNQTASDSSVMVRQVGFGNNATANQY 151	

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A; Description: major component of wild-type curli; interaction between CsgA and CsgB tri
A;Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli that
and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers
F;1-20,Domain: signal sequence #stætus predicted <SIG>
F;21-151/Product: curlin #stætus experimental <AMT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H-NS-mediated transcriptional repression
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A;Cross-references: GB:BA000007; PIDN:BAB34843.1; PID:g13360880; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 OSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIDN:AAA23616.1; PID:g290425 W3110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKLLKVAAFAAIVVSGSALAGVVPQW-GGGGNHNGGGNSSGPDSTLSIYQYGSANAALAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
A;Title: The RpoS sigma factor relieves H-NS-mediated to A;Reference number: S31202; MUID:93211294; PMID:8459772 A;Accession: S31202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 62.9%; Score 487.5; DB 2; Best Local Similarity 66.4%; Pred. No. 7.6e-35; Matches 101; Conservative 16; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 68.2%; Pred. No. 1.1e-36;
Matches 103; Conservative 15; Mismatches 33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                 October 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Accession: S34559
A;Molecule type: DNA
A,Residues: 1-133, *RQRDGWLW' < OLS3>
A,Cross-references: EMBL:L04979; NID:9290424;
A,Experimental source: strain K-12, substrain
                                                                                                                                                                                                                                                                                         A,Molecule type: protein
A,Residues: 21-42;44-50
R;Olsen, A.N.; Arnqvist, A.M.
submitted to the EMBL Data Library,
A,Reference number: S34559
                                                                                                                           A Molecule type: DNA
A Residues: 1-6,'V',8-151 <OLS1>
A; Cross-references: EMBL:L04979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: csgA
A; Map position: 23.15
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                       A; Accession: S34560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Gene: ECs1420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics:
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N.Alternate names: csgA procein; major curlin protein
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change 01-Mar-2002
C;Cacession: 870788; 646486; 531202; 834569; 834559

R;Hammar, M.; Arngvist, A.; Bian, Z.; Olsen, A.; Normark, S.

Mol. Microbiol. 18, 661-670, 1995

A;Title: Expression of two csg operons is required for production of fibronectin- and CA; Reference number: 870788; MUID:96414468; PMID:8817489

A;Reference number: 870788; MUID:96414468; PMID:8817489

A;Reference number: S70783; MUID:96414468; PMID:8817489

A;Residues: 1-151 cHAM>
A;Residues: 1-151 cHAM>
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A;Residues: 1-151 cHAM>
A;Residues: 1-151 cHAM>
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                    major curlin chain precursor [imported] - Salmonella enterica subsp. enterica serovar Typin (Species: Salmonella enterica subsp. enterica serovar Typin A;Note: this species has also been called Salmonella typhin (Species) as also been called Salmonella typhin (Species) as also been called Salmonella typhin (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as a foreign (Species) as 
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A,Residues: 1-151 <BLAT>
A,Residues: 1-151 <BLAT>
A,Residues: 1-151 <BLAT>
A,Cross-references: GB:AB000205; GB:U00096; NID:G1787265; PIDN:AAC74126.1; PID:G1787279; A;Experimental source: strain K-12, substrain MG1655
R;Olsen, A; Arnqvist, A; Hammar, M.; Sukupolvi, S.; Normark, S.
Mol. Microbiol. 7, 523-536, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKLLKVAAFFAAIVVSGSALAGVVPQWGGGGNFNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 683; DB 2;
Pred. No. 1.4e-51;
1; Mismatches 14
            NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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Best Local Similarity 90.1%;
Matches 136; Conservative
                 121
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A,Accession: $42135

A,Molecule type: DNA

A,Rolecule type: DNA

A,Rolecule 1164-1174.1179-1198,1233-1252,1285-1293,1297-1309,1316-1326,1331-1341,1343-

A,Cross-references: EMBL:L03710

R,Martindale: D.W.; Taylor, F.M.

R,Martindale: D.W.; Taylor, F.M.

A,Title: Multiple introns in a conjugation-specific gene from Tetrahymena thermophila.

A,Reference humber: S03650; MUID:88189811; PMID:335771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A/Genetic code: SGC5
A/Genetic code: SGC5
A/Introns: 85/3; 136/1; 157/3; 201/2; 290/2; 327/3; 499/1; 573/2; 607/3; 708/3; 777/3;
C/Keywords: zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       onia protein - Tetrahymena thermophila
C;Species: Tetrahymena thermophila
C;Species: Tetrahymena thermophila
C;Species: Tetrahymena thermophila
C;Species: Tetrahymena thermophila
C;Species: Tetrahymena thermophila
C;Date: 1997
C;Accession: S42136; S42135; S03550
R;Taylor, F.M.; Martindale, D.W.
submitted to the EMBL Data Library, October 1992
A;Reference funmber: S42136
A;Accession: S42136
A;Accession: S42136
A;Molecule type: DNA
A;Residues: 1-1748 -TAY
A;Cross-references: EMBL:L03710; NID:g161751; PID:g161752
A;Cross-references: EMBL:L03710; NID:g161751; PID:g161752
A;Cross-references: EMBL:L03710; NID:g161751; PID:g161752
A;Tetraylor, F.M.; Martindale, D.W.
Nucleic Acids Res. 21, 4610-4614, 1993
A;Title: Retroviral-type zinc fingers and glycine-rich repeats in a protein encoded ba;Reference number: S42135; MUID:94051569; PMID:8233798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 DQLVTRVVTHEMAHAFRNNATIDQWNAKONSDITVGQYGGNNAALVNQTASDSSVMVRQVG 141
                                                                                                                                                                                                                                                 66 SETTITOSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAK---NSDITVGQYGGNN 122
                                                                                                                                                                                                                                                                                          150 GLTLTTQGSHAAG------IVAQSVGGGGTGGTASSYSAGIGFTASVAVGCTGGNG 800
                                                                                                                                   65
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                                                                                                                                                                                  AIATAGAGAVGILAÓSIGGGGGN---GGNATGGDAGFGSFGJGGGGGGGGGGYANTANVGFK
                                                                                                                                11 AIVVSGSALAGVVPQ--WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR---K
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40;
                                                                           22;
                  Length 2174;
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                                                                              Indels
                                                                              61;
                  13.8%; Score 107; DB 2; 26.2%; Pred. No. 0.62; ive 21; Mismatches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession:;803650
A;Molecule type: DNA
A;Residues: 236-250,'I',252-255,'N',257-773 <MAR>
A;Cross-references: EMBL:X06462
C;Genetics:
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Filt64-1450/Region: zinc finger CCHC motif
Filt78-1464/Region: zinc finger CCHC motif
Filt78-1514/Region: zinc finger CCHC motif
Filt78-1568/Region: zinc finger CCHC motif
Filt78-1568/Region: zinc finger CCHC motif
Filt602-1615/Region: zinc finger CCHC motif
Filt602-1615/Region: zinc finger CCHC motif
Filt602-1615/Region: zinc finger CCHC motif
Filt602-1615/Region: zinc finger CCHC motif
Filt602-1615/Region: zinc finger CCHC motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                    821
                                                                                                                                                                                                                                                                                                                                                                                                                    801 GAGGEVSVSLTDSAIRTGOGG
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                                                                                    Conservative
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                                                                                    37;
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Best Local S:
Matches 36
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                         Query Match
Best Local S:
Matches 37
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S42136
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                                                                                                                                                                                                                                                             hypothetical protein csgA [imported] - Escherichia coli (strain O157:H7, substrain EDL93 hypothetical protein csgA [imported] - Escherichia coli (5.5peciese Escherichia coli (5.5peciese Escherichia coli (5.5peciese) and the coli (5.4cession: H8565 | Herberon H8565 | Herberon H8565 | Harkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001 | A;Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7. A;Acference number: A85480; MUID:21074935; PMID:11206551 | A;Acterus: preliminary A;Aclerus: preliminary A;Aclerus: preliminary A;Aclerus: preliminary A;Aclerus (Fig. 10.7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-152 <STO>
A;Coss.references: GB.AE005174; NID:g12514574; PIDN:AAG55788.1; GSPDB:GN00145; UWGP:Z16
A;Experimental source: strain O157:H7; substrain EDL933
C;Genetics:
A;Gene: csgA
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Local Similarity 62.9%; Score 487.5; DB 2;
Local Similarity 66.4%; Pred. No. 7.6e-35;
les 101; Conservative 16; Mismatches 34;
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                                                                                              GNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                GGNGAAVDOTASNSTVNVTQVGFGNNATAHQY
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Qy 11 AIVVSGSALAGVVPQWGGGGNHN-GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETT 69	Db 294 AVPTPGNGNVGIGNGGNGNFGGGNTGNANIGLGNVGDG 331	OY 1TOSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGOYGGNNAALVNOT 129	130 ASDSSVMVRQVGFGNNATAN 149	:           Db   370 SGSGNIGFCNSGTGN 384	סו ביווסממ	ae. PL021 19   PL021	N.Alternate names: promastigote surface proteinase; surface endopeptidase glycoprotein C. Species: Leishanain major major (C. Date: 16.Sep. 1992 #semionne revision 16.Sep. 1992 #semionne		0. AAP. Ned		A,Cross-references: GB:Y00647, NID:99554, PIDN:CAA68673.1, PID:99555 A,Note: this is a revision to the sequence from reference A27598	יים דים הים בים מים בים מים בים מים בים מים בים מים בים מים בים מים בים מים בים מים בים מים בים מים מים בים מי מים בים מים מים מים מים מים מים מים מים מים מ	A Arcefording Country of the major surface antiger of A. Arcefording and A. Arcefording a	A;Accession: A,7.738 A;Status: significant sequence differences A;Molecule type: DNA	R; Bouvier, J.; Bordier, C.; Vogel, H.; Reichelt, R.; Etges, R. Mol. Biochem. Parasitol. 37, 235-246, 1989	A; Title: Characterization of the promastigote surface protease of Leishmania as A; Reference number: A60648; NUID:90114330; PMID:2608099	A; Molecule type: protein A; Molecule type: protein A; Residues: 101, 'E', 103-118, 'SV', 121-123 <bou></bou>	A; Experimental source: strain LEM513 R; Schlagenhauf, E.; Etges, R.; Metcalf, P.	A;Contents: annotation; X-ray crystallography, 1.86 angstroms, residues 100-407,412-49 A;Note: strain LRC-Li19 C:Complex: homedimer	C; Function: A; Description: catalyzes the hydrolysis of peptide bonds between two hydrophobi	A;Note: the activated form can activate the proenzyme form , \$ C;Superfamily: leishmanolysin	Holroyd, S. C;Keywords: blocked carboxyl end; cell adhesion; glycoprotein; homodimer; hydrolase; F:1-39/Domain: signal sequence #status predicted <sig></sig>	F:40-100/DOMAIN: activation peptide #status predicted <atp> F:101-577/Product: leishmanolysin #status experimental <mat> F:518-602/Domain: carboxyl-terminal propeptide #status predicted <ctp></ctp></mat></atp>	E E E	F;125-142,191-230;344-386,393-455,406-425,415-489,466-510,515-565,535-558/Disul F;264,568,334/Binding site: 2.n.c, catalytic (His) (active) #status experimental F;264,700:00 2:00 01:00 0	F:285/ACLIVE SIGE: CLU #SEGRUS PICALCEG F:300,407/Binding site: Carbohydrate (Asn) (covalent) #status experimental F:57//Modified site: GPI-anchor drahamine amidated carbovyl end (in mature	THE CHANGE THE PARTY OF THE PAR	th 602;
Oy 142 FGNNATAN 149	: :   : 1723 WGSNNQAS 17	RESULT 8	JC6040 Finbrin protein agfB precursor - Salmonella enteritidis	c;species: Salmonalia enteritidis C;Date: 31-Dace:1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999 C;Accession: JC6040	R;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W. J. Bacteriol. 178, 662-667, 1996	A; Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fimbri A; Reference number: JC6039; MUID:96146512; PMID:8550497	A;Accession: JC6040 A;Molecule type: DNA A;Residues: 1-151 <ccl></ccl>	A;Cross-references: GB:U43280; NID:g1184712; PIDN:AAC43598.1; PID:g1184713 A;Experimental source: strain 276755-3b C.Generics:	A Gene: agfB () Function:	*/prescription: minor component of thin aggregative inmortae A;Note: fimbriae bind to fibronectin, plasminogen, tissue plasminogen activator C;Keywords: fimbria	F;1-21/Domain: signal sequence #status predicted <sig> F;22-151/Product: fimbrin protein agfB #status predicted <mat></mat></sig>	Query Match 12.2%; Score 94.5; DB 2; Length 151; Best Local Similarity 26.9%; Pred. No. 0.34;	; Conservative 1	10 AAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETT 6	S8 ARVRQEGSKLLSVISQEGGNNRAKVDQAGNYNFAYIEQTGNAN	OY 70 ITOSOYGNGADYDQLVTRVYTHEMAHAFRNNATIDQWNAKNSDITVGGYGGNNAALVNQT 129 DD 104 ISOSAYGNSA	ASDSSWWWQ 139	Db 141 QSHWAIRVIQ 150	RESOLI 9 FOOSES probable PPE protein - Mycobacterium tuberculosis (strain H37RV)	<pre>C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 15-Sep-2003</pre>	Ď.,		Addition of Salares, R., Sulston, J.E., Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete		A, October 1971 Increase del Sequence not snown; translation not snown A, Molecule type: DNA A. Molecule type: DNA A. Molecule type: DNA A. Molecule S. 1-645 < COL>	;	(.c.p.np+1,0x.	C.Genetics: A.Gene: PPE Onerw Match 12 1%. Some 64. DB 2. Tondth 646.

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Escherichia coli (strain O157:H7, subs C;Species: Escherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bscherichia coli (5.5pecies: Bsch
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A;Experimental source: strain K-12, substrain MG1655
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() Species: Mycobacterium tuberculosis

() Species: Mycobacterium tuberculosis

() Accession: B70663

R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A, Muthors Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A, Aluthors Complexing the biology of Mycobacterium tuberculosis from the complete genome A, Reference number: A70500; MUID: 98295987; PMID: 9634230
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A;Cross-references: GB:Z83860; GB:AL123456; NID:G3261681; PIDN:CAB06165.1; PID:e290763; A;Experimental source: strain H37Rv C;Genetics: A;Genetics: A;Gene: PPE
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                 YDQLVTRVVTHEMAHALGFSGPFFEDARIVANVPNVRGKNFDVPVINSSTAVAKAREQYG 313
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A,Status: preliminary; nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                       F3F19.21 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
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Best Local Similarity
Matches 36; Conserv
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Cutinn minor chain precursor, CsgA homolog [imported] - Escherichia coli (strain O157:H7 C.Species: Escherichia coli (Species: Escherichia coli (Species: Escherichia coli (Species: Escherichia coli (Species: Escherichia coli (Species: Escherichia coli (Species: Escherichia coli (Species: Escherichia coli (Species: Escherichia coli (Species: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Especies: Esp
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A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: C90806
A;Accession: C90806
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-151 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34842.1; PID:913360879; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics: A;Gene: ECS1419
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11.5%; Score 89.5; DB 2; Length 151;
Best Local Similarity 28.1%; Pred. No. 0.92;
Matches 32; Conservative 15; Mismatches 62; Indels
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CORA MEDSA P33_WYCPE ACMA_LACLA Y442_WYCTU YFCU_ECOLI YFCU_ECOLI P35_MYCAUCR P	ALIGNMENTS	SGA_SALTY  SGA_SALTY  SGA_SALTY  C CSGA_SALTY  C D CACCI-1996 (Rel. 34, Created)  O 1-OCT-1996 (Rel. 34, Last sequence update)  T O1-OCT-1996 (Rel. 34, Last sequence update)  T O1-OCT-1996 (Rel. 34, Last sequence update)  E Major curtin subunit precursor (Fimbrin SEF17).  C CGA OR AGRA OR STMILL4 OR STY1181 OR T1776.  S Salmonella typhimurium, S Salmonella typhimurium, S Salmonella typhimurium, S Salmonella typhimurium, S Salmonella typhimurium, S Salmonella typhimurium, S Salmonella typhimurium, S SALOHONELE RNOM NA.  C Enterobacteriaceae; Salmonella.  NOEL TaxID=602, 601, 592;  (1) P SEQUENCE RNOM NA.  SPECIES=S typhimurium; STRAIN=SR-11; MEDILINE=98117058; PubMed=9457880; A Romling U. Bian Z., Hammar M. Sierralta W.D., Normark S.; CURII fibers are highly conserved between Salmonella typhimurium.  E Scherichia coli with respect to operon structure and requiation.  I J. Bacteriol. 180:722-731(1998).  C SPECIES=S typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720; X MEDILINE=21534948; PubMed=11677609; X MEDILINE=21534948; PubMed=11677609; X MACLElland M., Sanderson K.E., Spieth J., Cirewal N., Milvaney E. SPECIES=S typhimurium S. Soctt R., Holmes A., Grewal N., Milvaney E. Courtney L., Porwollik S., Ali J., Dante M., Carewal N., Malvaney E. Ryan E.; Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; I LT2."; I LT2."; I LT2."; I Nature 413:852-856(2001).	18; 167768; 168. Thomson N.R., P. Bentley S.D., Holden M.T. S.K., Chillingworth T., Co S.R., Dowd L., White N., ye A., Hien T.T., White N., Simmonds M., Skelton J., 5f a multiple drug resists 3.",  / ATCC 700931; 5644504; btt G. III, Mayhew G.F., I Schwartz D.C., Blattner I
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch.)
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SPECIES=S.enteritidis; STRAIN=27655-38;
MEDLINE=91310586; PubMed=1677357;
Collinson S.K., Emcedy L., Mueller K.-M., Trust T.J., Kay W.W.;
Collinson and characterization of thin, aggregative fimbriae from "Purification and characterization of thin, aggregative fimbriae from "Salmonella enteritidis.";
J. Bacteriol. 173:4773-4781(1991).
-! FUNCTION: CURLIN IS THE STRUCTURE SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSERBLE PREFERENTALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
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Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W.W.;
"Salmonella enteritidis agfBAC operon encoding thin, aggregative
                                                                                                                                                                                                                                                                                                 SPECIES-S.enteritidis; STRAIN=27655-3B; BEDLIKE=94013373; PubMed=8104955., Doran J.L. Collinson S.K., Burian J., Sarlos G., Todd E.C.D., Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., Kay W.W.; "DNA-based diagnostic tests for Salmonalla species targeting agfa, the structural gene for thin, aggregative fimbriae."; J. Clin. Microbiol. 31:2263-2273(1993).
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StyGene; SG10608; csgA.
Fimbria; Signal; Complete proteome.
                                              Bacteriol. 185:2330-2337(2003).
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  RRETHER RREAL BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BRANCH BR
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BECCETIOI. 173:4773-4781(1991).
FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURPACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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MEDLINE-91310586; PubMed=1677357;
Collinson S.K., Emody L., Trust T.J., Kay W.W.;
"Purification and characterization of thin, aggregative fimbriae from Salmonella enteritidis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-KI2 / W3110;
MEDLINE=93211294; PubMed=8459772;
Olsen A., Arnqvist A.;
"The RpoS sigma factor relieves H-NS-mediated transcriptional
renression of csga, the subunit gene of fibronectin-binding curli in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=K12;
MEDILINE=9061202; PubMed=8905322;
MEDILINE=90661202; PubMed=8905322;
Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Iskemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Moril H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.,
A. Taskb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12.7-28.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97426617; PubMed=9278503; Battner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                     Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
VCBI_TaxID=562;
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                                                               01-DEC-1992 (Rel. 24, Created)
01-007-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Major curlin subunit precursor.
151 AA
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STANDARD;
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STRAIN=K12 / MC4100;
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STRAIN=K12 / MG1655;
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STRAIN=K12 / W3110;
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Mau B., Shao Y.;
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ECOLI
CSGA_EC
P28307,
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SEQUENCE FROM N.A.
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                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Burpaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MDDLINE-2118556; PubMed-11318-125;
Unlich G.A., Keen U.E., Elder R.O.;
"Mutations in the csgD promoter associated with variations in curli
expression in certain strains of Escherichia coli 0157:H7.";
Appl. Environ. Microbiol. 67:2367-2370(2001).
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SEQUENCE FROM N.A.

MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 1 Last annotation update)
Major curlin subunit precursor.
SCAA OR 21676 OR ECS1420.
ESCHARICHIA COli 10157.H7.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
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7 7 A -> E (IN REF. 1).

151 AA; 15049 MW; C003470D208D395F CRC64;
-!- SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.7%; Score 509; DB 1; 68.2%; Pred. No. 8.7e-37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152
                                                                                                                                                                                                                                                                      EMBL; D90742; BAA3...
EMBL; D90742; BAA3...
PIR; S70788; S70788.
ECGGene; EG11489; CSGA.
Finbria; Signal; Complete proteome.
7 A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A -> E A
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EMBL; X90754; CAA62282.1; -.
EMBL; AE000205; AAC74126.1; -.
EMBL; D90741; BAA35832.1; -.
EMBL; D90742; BAA35840.1; -.
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                                                                                                            QSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYG
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MEDLINE=8817058; PubMed=9457880;
Romling.U., Blan Z., Hammar M., Sierralta W.D., Normark S.;
"Curli fibers are highly conserved between Salmonella typhimurium and
Escherichia coli with respect to operon structure and regulation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
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01-027-1996 (Rel. 34, Last sequence update)
01-027-1996 (Rel. 34, Last sequence update)
Minor cúrlin subunit precursor (Fimbrin SEF17 minor subunit)
CSGB OR AGRE OR STM1143.
Salmonella typhimurium, and
Salmoneila enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EE2D2D94DDE91243 CRC64;
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EMBL, AE005315; AAG55788.1; -.
EMBL, AP005254; BAB34443.1; -.
EMBL, AP005554; BAB34443.1; -.
EMBL, AP00606; D90806.
PIR, D90806; D90806.
FIR, H85665, H85665.
FIRMATA, Signal; Complete proteome.
FIGNAL
21 152 MAJOR CURLIN SUBUNIT.
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[3]
SEQUENCE FROM N.A.
STRAIN-O157:H7 / RIMD 0509952;
MEDLINE-21156231; PubMed=11259796;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 AA; 15099 MW;
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Matches 101; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----AIIQKGSGNKANIT--QYGTQKTAVVVQK 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 AAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETT 69
                                                                                                                                                                                                                                                                                                                                                                                                                     finbriae.";
J. Bacteriol. 178:662-667(1996).
-(- FUNDTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI. CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 ARVRQEGSKLLSVISQ--EGGNNRAKVDQAGNYNFAYİEQTGNAN------DAS
                                                    SEQUENCE FROM N.A.
SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latraille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96146512; PubMed=8550497;
Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W.W.;
"Salmonella enteritidis agfBAC operon encoding thin, aggregative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GP63_LBIMA

GP63_LBIMA

C P08148, P15906;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Leishmanolysin precursor (EC 3.4.24.36) (Cell surface protease)

DE (Major surface glycoprotein) (GP63 protein) (Promastigate surface DE endopeptidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37;
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MINOR CURLIN SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Mismatches
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SPECIES=S.enteritidis; STRAIN=27655-3B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; JC6040; JC6040.
StyGene; SG10609; csgB.
Fimbria; Signal; Complete proceome
SIGNAL
J. Bacteriol. 180:722-731(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AJ002301; CAA05316.1; --
EMBL, AE008749; AAL20073.1; --
EMBL; U43280; AAC43598.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 26.9<sup>3</sup>
Matches 35, Conservative
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141 QSHMAIRVTQ 150
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Structure 6:1035-1046(1998).

C. -!- FUNCTION: Has an integral role during the infection of macrophages in the mammallan host.

C. -!- CATALYTIC ACTIVITY: Preference for hydrophobic residues at Pl and Pl' and basic residues at P2 and P3'. A model nonapeptide is cleaved at -Ala-Tyr-1-Leu-Lys-Lys.

C. -!- CATALYTIC ACTIVITY: Preference for hydrophobic residues at P1 and P3'. A model nonapeptide is cleaved at -Ala-Tyr-1-Leu-Lys-Lys.

C. -!- CATALYTIC ACTIVITY: Preference for hydrophobic residues at P1 and P3'. A model nonapeptide is cleaved at -Ala-Tyr-1-Leu-Lys-Lys.

C. -!- CATALYTIC ACTIVITY: A mached to the membrane by a GPT-anchor.

C. -!- PTM: THE PHOSPHATIDYILANSITOL MOIETY OF THE GPI-ANCHOR CONTAINS A FULLY SATURATED UNBRANCHED 2-0-ACYL CHAINS (C12:0, MIXTURE OF FULLY SATURATED UNBRANCHED 2-O-ACYL CHAINS (C12:0, C14:0, C16:0, AND C18:0).
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InterPro; IPRO06025; Pepti M_Zn_BS.
InterPro; IPRO06025; Peptidase_M8.
InterPro; IPRO01577; Peptidase_M8: 1.
PRINYS; PRO07482; LSHMANOLYSIN.
PRINYS; PRO07482; LSHMANOLYSIN.
PROSITE; PSO0142; ZINC PROTEASE; 1.
Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc;
Zymogen; Signal; Cell adhesion; GHI-anchor; 3D-structure; Lipoprotein.
SIGNAL 1 39 POTENTIAL.
SIGNAL 40 100 ACTIVATION PEPTIDE.
CHAIN 101 577 LEISHMANOLYSIN.
nnonde 578 602 REMOVED IN MATURE FORM.
                  Leishmania major.
Eukaryota, Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95406217; PubMed=7675788; Schlagenhauf B., Etges R., Metcalf P.; diffraction studies of "Crystallization and preliminary X-ray diffraction studies of leishmanolysin, the major surface metalloproteinase from Leishmania
                                                                                                                                                                                                                                                                                                                                                                                                    당
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (1.86 ANGSTROMS).
MEDLINE=98416698, PubMed=9739094;
Schlagenhauf E., Etges R., Metcalf P.;
"The crystal structure of the Leishmania major surface proteinase
                                                                                                                                         Button L.L., McMaster W.R.;
"Molecular cloning of the major surface antigen of leishmania.";
J. Exp. Med. 167:724-729(1988).
                                                                                                                                                                                                                                                                                                                                                                                                       membrane anchor
                                                                                                                                                                                                                                                                                                                                     MEDLINE=91009116; PubMed=2145267; Schneider P., Ferguson M.A.J., McConville M.J., Mehlert A., Homans S.W., Bordier C.; "Structure of the glycosyl-phosphatidylinositol membrane and the Leishmania major promastigote surface procease."; J. Biol. Chem. 265:16955-16964(1990).
                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 101-123.
MEDLINE=88154764; PubMed=3346625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
                                                                                                                                                                                                                                                    Button L.L., McMaster W.R.;
J. Exp. Med. 171:589-589(1990)
[3]
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REVISIONS.
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                                                                                                                                                                                                                                                                                                                                                                                                                   ---GONG
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MEDLINE=9641466; WC4100,
MEDLINE=9641466; WC4100,
MEDLINE=9641466; WC4100,
MEDLINE=5641466; WC4100,
MEDLINE=5650 of two csg operons is required for production of fibronectin- and congo red-binding curli polymers in Bscherichia coli Kr.12.";
Mol. Microbiol. 18:661-670(1995).
                                                                                                                                                                                                                                                                                                                                                               Gaps
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STRAIN=KIZ / MGJ655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gragor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., "The complete genome sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                               21;
                                                                                                                                                                                                                                                                                                                                                                                81 YDQLVTRVVTHEMAHAF------RNNATIDQWNAKNSDITV-----
                                                                                                                                                                                                                                                                                                                                       11.8%; Score 91.5; DB 1; Length 602; 41.7%; Pred. No. 1.6; ive 2; Mismatches 12; Indels 2
                                                                                                                                                                                                                                                                                                                    63953 MW; 982EF3245D87C43E CRC64;
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Best Local Similarity
Matches 25; Conserva
   SEQUENCE
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N-LINKED (GLCNAC. . .) (POTENTIAL)
GPI-anchor amidated asparagine.
                      (CATALYTIC).
 (CATALYTIC)
  ZINC
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Science 277:1453-1474(1997)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arnquist A., Olsen A., Normark S.;
"Sigma S-dependent growth-phase induction of the csgBA promoter in
Escherichia coli can be achieved in vivo by sigma 70 in the absence
of the nucleoid-associated protein H-NS.";
Mol. Microbiol. 13:1021-1032(1994).
-! FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE
COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH
TEMPERATURES BELOW 37 DEGREES CELGIUS. CURLI CAN BIND TO
FIBRONECTIN. THE MINOR SUBJNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=0157:H7 / RIMD 0509952;
MEDLINB=21156231; PubMed=11258796;
MEDLINB=21156231; PubMed=11258796;
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.,
"Complete genome sequence of enterchemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                       STRAIN=K12;
MEDLINE=97061202; PubMed=8905232;
MEDLINE=97061202; PubMed=8905232;
Ikemoro K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Ikemoro K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Morri H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
Yano M., Horiuchi T.;
MA Sequence of the Escherichia coli K-12 genome
Corresponding to the 12-28.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of enterchaemorrhagic Escherichia coli O157:H7."; Nature 409:529-533(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=0157:H7 / BDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MINOR CURLIN SUBUNIT.
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EMBL, POO741, BAA35831.1, --
EMBL, AE005315, AAG55787.1, --
EMBL, AP002554, BAB34842.1, --
PIR, C90806, C90806, PIR, G85665, PIR, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S70787, S7078
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Fimbria; Signal; Complete
SIGNAL 1 21
CHAIN 22 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-21 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0157:H7 and genomic comp
DNA Res. 8:11-22(2001).
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                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 AHAFRNNATIDQWNAKNSDITVGQYG-----GNNAALV-----NQTASDSSVMVRQVGFG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 GGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADYDQLVTRVVTHEM 93
                                                                                                         97
                                                                                                                                            76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              933 GSTSTAGPDSSL-IAGYGSTQTA------GYNSILTAGYGS------
                                                                                                                                          21 AAGYDLANSEYNF----AVNELSKSSFNQAALIGQAGTNNSAQLROGGSKLLAVVAQEGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-90092494; PubMed=2599095;
Abe K., Watabe S., Emori Y., Watanabe M., Arai S.;
Implication active gene of Erwinia ananas. Sequence similarity
to those of Pseudomonas species and regions required for ice
                                                                                                         38 SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAF
                                                                        Gaps
                                                                                                                                                                                                         151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- FUNCTION: Ice mucleation proteins enable bacteria to nucleate crystallization in supercooled water.
-:- SUBCELLULAR LOCATION: Outer membrane (By similarity).
-:- DOMAIN: CONTAINS MANY IMPERPEZT REPEATS OF THE CONSENSUS OCTAPEPTIDE A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
-:- SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae; Pantoea.
                                                                                                                                                                                   98 RNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                          5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.5%; Score 89.5; DB 1; Length 1322; 26.8%; Pred. No. 5.9;
                                     Length 151;
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                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 1281 OCTAPEPTIDE PERIODICITY.
1322 AA, 131094 MW, 89BOEEE24AA837039 CRC64;
151 AA; 15882 MW; B18D266B964014B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26;
                                                                      62;
                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                    01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                   11.5%; Score 89.5; DE 28.1%; Pred. No. 0.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18; Mismatches
                                                                          15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIK; DOUGLY, INNA.
INCEPPRO) INNA.
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INCEPPRO) INCEPPRO) INCEPPRO) INCEPPRO) INCEPPRO) INCEPPRO) INCEPPRO) INCEPPRO) INCEPPRO) INCEPPRO) INCEPPRO) INCEPPRO) INCEPPRO) INCEPPRO) INCEPPRO) INCEPPRO) INCEPPRO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Pantoea ananas (Erwinia uredovora)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleation activity.";
FEBS Lett. 258:297-300(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X17316; CAA35194.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                             ce nucleation protein inaA.
                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=553;
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Best Local Simi
Matches 34;
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                                                                                                                                                                                                                                                                                                                   ICEA PANAN
P20469;
   SEQUENCE
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NCBI_TaxID=553;
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ID ICEN PANAN
AC Q47879;
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                                                                                                                                                                                                          SEQUENCE
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60 Q-----SDARKSETTITQSGYG----NGAD-----YDQLVTRVVTHEMAHAFRNNAT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VYGSTLITGADQSRLVAGYGSTETAGDHSDLIAGYGSTGTAGSDSSI-LAGYGSTQTAAGR 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STLTAGYGSTQTAQEGSRLISGYGSTATSGSDSAVISGYGSTQTAGSESSLTAGYGSTQT 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 IDQWNAKNSDITVGQYG-----GNNAALV-----NQTASDSSVMVRQVGFGNNATANQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   324 A----RKGSDITAG-YGSTGTAGSDSALIAGYGSTQTAGSESSLT--AGYGSTQTARK 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 VSGSALAG-----VVPQWGG---GGNHN-----GGGNSSGPDSTLSIXQYGSANAALAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                        Xanthomonas campestris pv. translucens.";
Mol. Gen. Genet. 223:163-166(1990).

-! FUNCTION: Ice mucleation proteins enable bacteria to nucleate crystallization in supercooled water.

-! SUBCELULIAR LOCATION: Outer membrane (By similarity).

-! DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE PERIODICITY IS SUGGESTED IN WHICH THE ICH WINCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.

-! MISCELLANDOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICH WINCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.

-! SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                    Xanthomonas campestris (pv. translucens).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1567;
                                                                                                                                                                                                                                                                                                                                                Zhao J., Orser C.S.; "Conserved repetition in the ice_nucleation gene inaX from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR000258; Ice_nucleatn.
Pfam; PF00818; Ice_nucleation; 81.
PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE NUCLEATION; 57.
Ice nucleation; Repeat; Outer membrane.
SEQUENCE 1567 AA; 152548 MW; C8B451D959ECAD63 CRC64;
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                                                                                                                                                                 (Rel. 16, Created)
(Rel. 16, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                    STRAIN=X56S;
MEDLINE=91080859; PubMed=2259339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X52970; CAA37140.1; -. HSSP; P06620; 11NA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47; Conservative
                                                                                                                                        STANDARD;
                                                                                                                                                                                                           Ice nucleation protein.
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1014 SSQTARE 1020
                                        144 NNATANO 150
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Best Local Similarity
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01-NOV-1990
16-OCT-2001
                                                                                                                                     ICEN XANCT P18127;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 ALQSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----TOTGMKGSDLTAG- 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                       161 IATYGSTLSGTHQSQLIAGYGSTETAGDSSTLIAGYGSTGTAGSDSTL-VAGYGSTQTA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 IVVSGSALAGVVPQW--GGGGNHNGGGNSS------GPDSTLSIYQYGSANAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                             MEDLINE=94264407; PubMed=7764866;
Michigami Y., Watabe S., Abe K., Obata H., Arai S.;
"Cloning and sequencing of an ice nucleation active gene of Erwinia
                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 1034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 YG-----GNNAALV-----NQTASDSSVMVRQVGFGNNATANQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 YGSTGTAGDDSSLIAGYGSTQTAGEDSSLT--AGYGSTQTAQK 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OCTAPEPTIDE PERIODICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41;
1034 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.3%; Score 87.5; DE 25.2%; Pred. No. 6.6; ive 18; Mismatches
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                                                                       update)
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PIR; JC2143; JC2143.
HSSP; P06620; INA.
InterPro; IPR000258; Ice_nucleatn.
Pfam; PF00818; Ice nucleation; 51.
PRINTS; PR00327; ICENUCLEATION
PROSTIE; PS00347; ICE NUCLEATION; 34.
Ice nucleation; Repeat; Outer membrane.
DOMAIN 162 993 OCTAPEPTIDE
                                  01.NOV-1997 (Rel. 35, Created)
01.NOV-1997 (Rel. 35, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219 -----GEESSQMAGYGS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                         (Erwinia uredovora)
                                                                                                                       Ice nucleation protein inaU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1034 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                FROM N.A.
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ID ICEN ERWHE
AC P16239;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 ALQSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 IVVSGSALAGVVPQW--GGGGNHNGGGNSS------GPDSTLSIYQYGSANAAL 57
                                                                                                                                                                                                                  -!- FUNCTION: Ice nucleation proteins enable bacteria to nucleate crystallization in supercooled water.
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- DOMAIN: CONTAINS 126 INPRERFECT REPEATS OF A CONSENSUS OCTAPEPTIDE A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE PRENDUCITY IS SUPERIMPOSED.
-!- MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                   Warren G.J., Corotto L.V.; "The consensus sequence of ice nucleation proteins from Erwinia "The consensus sequence of ice nucleation proteins syringae."; dene 85:239-242(1989).
                                                                                                                                                                                                                                                                                                                          SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 1217 OCTAPEPTIDE PERIODICITY.
1258 AA; 125084 MW; 590E8A130077FBD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----GNNAALV-----NQTASDSSVMVRQVGFGNNATANQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 YGSTGTAGDDSSLIAGYGSTQTAGEDSSLT--AGYGSTQTAQK 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Minor curlin subunit precursor.
CSGB OR STY1180 OR T1777.
             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.3%; Score 87.5; DE
25.2%; Pred. No. 8.2;
tive 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 -----GEESSQMAĠŸĠS-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000258; Ice_nucleatn.
Pfam; PF00818; Ice_nucleation; 65.
PRINTS; PR00327; ICENUCLEATN.
PROSITE; P800314; ICE NUCLEATION; 45.
Ice_nucleation; Repeat; Outer membrane.
                                                                                                                                           STRAIN=M1;
MEDLINE=90152370; PubMed=2515997;
  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M26382; AAA24823.1; -.
                                                                                          Enterobacteriaceae; Pantoea.
NCBI_TaxID=549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                       Ice nucleation protein.
 (Rel. 14, C
(Rel. 14, I
(Rel. 40, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J20188.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                SEQUENCE FROM N.A.
                                                                 Erwinia herbicola.
 01-APR-1990 (
01-APR-1990 (
16-OCT-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8Z7M3;
28-FEB-2003
28-FEB-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 YG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41;
                                                                                                                                                                                                                                                                                                                                         family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SALTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
CSGB_SALTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSGB
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  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Ty2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol. 185:2330-2337 (2003).
-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 AAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETT
                                                                                                                                                                                                               Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G. Sebaihia M., Backer S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davis R.M., Dowd L., White N., Farrar J., Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Interford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Simmonds M., Skelton J., Stevens K., Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.2%; Score 86.5; DB 1; Length 151; 26.2%; Pred. No. 0.89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
MINOR CURLIN SUBUNIT.
; 161C54326E573495 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
GP63 LEIDO
ID GP63 LEIDO STANDARD; PRT; 590 AA.
AC P23223;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17; Mismatches
                                                                                                                                                                                                     MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fimbria; Signal; Complete proteome
                                   Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AL627269; CAD08267.1; -. EMBL; AE016840; AAO69400.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16254 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURLIN MONOMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 AA;
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Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                  SEQUENCE FROM N.A.
                                                                  NCBI_TaxID=601;
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7
                                                                                                                                                                                    Webb J.R., Button L.L., McMaster R.W.,
Webb J.R., Button L.L., McMaster R.W.,
"Heterogeneity of the genes encoding the major surface glycoprotein
of Leishmania donovani.",
Mol. Biochem. Parasitol. 48:173-184(1991).
-!- FUNCTION: Has an integral role during the infection of macrophages
in the mammalian host.
-!- CATALYIC ACTIVITY: Preference for hydrophobic residues at Pl and
Pl' and basic residues at P2 and P3'. A model nonapeptide is
cleaved at -Ala-Tyr-|-Leu-Lys-Lys-.
-!- COFACTOR: Binds I zinc ion per subunit (By similarity).
-!- SUBCELDULAR LOCATION: Attached to the membrane by a GPI-anchor.
-!- SIMILARITY: Belongs to peptidase family M8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEISHWANGLYSIN.
REMOUTED IN MATURE FORM (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
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                                                                     Leishmania donovani.
Eukaryota, Buglenozoa, Kinetoplastida, Trypanosomatidae, Leishmania.
VSB_TaxID=5661;
10.-OCT-2003 (Rel. 42, Last annotation update)
Leibmanolysin precursor (EC 3.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface endopeptidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR001577; Peptidase_M8.
Pfam; PF01457; Peptidase_M8: 1.
PRINTS; PR001782; ISHMANOLYSIN.
HYdrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc; Zymogen; Signal; Cell adhesion; Gl-anchor; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 86; DB 1; Length 590;
Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OFB315D299659F58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTIVATION PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity
                                                                                                                                                         STRAIN=LV9;
MEDLINE=92107220; PubMed=1762629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        590 AA; 62950 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M60048; AAA29244.1; -- HSSP; P08148; 1LML.
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48.8%;
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Best Local Similarity
Matches 21; Conserv
                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; M08.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METAL
ACT_SITE
METAL
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DISULFID
DISULFID
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PROPEP
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YDQLVTRVVTHEMAHA-----FRNNATIDQ-WNAKNSDITV 115 241 YDQLVTRVVTHEMAHALGFSVVFFRDARILESISNVRHKDFDV 283

81

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SEQUENCE FROM N.A.

STRAIN-AMYC/BZ/62/37379,

MEDLINE-93149206; PubMed-8426614;

Medina-Acosta B. T. Karess R. B., Russell D.G.;

Medina-Acosta B. T. Karess R. B., Russell D.G.;

Medina-Acosta B. B., Raress R. B., Russell D.G.;

Medina-Acosta B. B., Raress R. B., Russell D.G.;

Medina-Acosta B. B., Raress R. B., Russell D.G.;

Medina-Acosta B. R. B., Raress R. B., Rosell D.G.;

Medina-Acosta B. R. B., Raress R. B., Rosell D.G.;

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Eukaryota: Euglenozoa, Kinetoplastida, Trypanosomatidae, Leishmania.
                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin C1 precursor (EC 3.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amastigote forms. SIMILARITY: Belongs to peptidase family M8.
   STANDARD;
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GP63 LEIME
P43150;
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93 MAHA 96
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P15320;
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 SOTTERESTATIONS
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"Three distinct RNAs for the surface protease gp63 are differentially expressed during development of Leishannia donovani chagasi

"Three distinct RNAs for the surface protease gp63 are differentially promastigotes to an infectious form.",

"Deal Chem. 267-1888-1895(1992)."

"FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.

"C-I- CATALYTIC ACTIVITY: Preference for hydrophobic residues at Pl and Pl' and basic residues at P2 and P3'. A model nonapeptide is cleaved at Ala-Tyr-|-Leu-Lys-Lys-.

"C-I- COPACTOR: Binds 1 zinc ion per subunit (By similarity).

"SUNCELLULAR LOCATION: Actached to the membrane by a GPI-anchor.

"STMILARITY: Belongs to peptidase family M8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                        YDQLVTRVVTHEMAHAFRNNAT------IDQWNAKNSDITV-------GQYG 119
                                                                                                                                              256 YDQLVTRVVTHEMAHAVGFSGTFFGAVGIVQEVPHLRRKDFNVSVITSSTVVAKAREQYG 315
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=44271;
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=90205976; PubMed=2320059;
Miller R.A., Reed S.G., Parsons M.;
Leishmania gp63 molecule implicated in cellular adhesion lacks an
Arg-Gly-Asp sequence."
Mol. Biochem. Parasitol. 39:267-274(1990).
                                                                                                                                                                                                                                                                                   01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 33.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
(GLCNAC. .) (POTENTIAL). (GLCNAC. .) (POTENTIAL). (GLCNAC. .) (POTENTIAL). (GLCNAC. .) (POTENTIAL).
                                                                                                21;
                                                                      Score 84.5; DB 1; Length 646;
Pred. No. 6.9;
7; Mismatches 12; Indels 21
                                         LINKED (GLCNAC. . .) (PO
FE448DDC78C10B0A CRC64;
                                                                                                                                                                                                                                                              599 AA
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MEDLINE=92112918; PubMed=1370484;
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InterPro; IPR001577; Peptidase_M8.
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Best Local Similarity 36.5'
Matches 23, Conservative
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466
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646 AA;
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                                                                                                                                                                          120 GNN 122
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MEROPS; M08.001;
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                        CARBOHYD
CARBOHYD
SEQUENCE
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               CARBOHYD
   CARBOHYD
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GP63_LEICH
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                                                                                                                                                                                                                                                                                                                                                  ACTIONALM PEPTIDE.
LEISHMANOLYSIN.
REMOVED IN MATURE FORM (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
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Poole K., Schiebel E., Braun V.;
"Molecular characterization of the hemolysin determinant of Serratia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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J. Bacteriol. 170:3177-3188(1988).
-!- FUNCTION: Bacterial hemolysins are exotoxins that attack blood
-e!- FUNCTION: Bacterial hemolysins are exotoxins that attack blood
cell membranes and cause cell rupture by mechanisms not clearly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE BRYTHROCYTE MEMBRANE. SHLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Serratia.
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Pfam; PF01457; Peptidase M8; 1.
PRINTS, PR00742; LSHMANDISIN.
Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Zinc; Zymogen; Signal; Cell adhesion; GBI-anchor; Lipoprotein.
SIGNAL
PROPEP 40 97 ACTIVATIAN DEFENSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.8%; Score 84; DB 1; Length 599; 37.5%; Pred. No. 7;
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-!- SUBCELLULAR LOCATION: Outer membrane.
-!- SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 7;
5; Mismatches
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Best Local Similarity
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EMBL; M22618; AA56182.

InterPro; IPR008638; Haemagg_act.
Pfam; PF05860; Haemagg_act.
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SEQUENCE 1608 AA; 165078 MW; D669B476FE7DAD51 CRC64;
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Search completed: August 2, 2004, 14:49:32 Job time : 5.3 secs

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61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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MEDLINE=98053981; PubVed=9293832;
Sukupolvi S.S., Lorentz R.G., Gordon J.I., Bian Z., Pfeifer J.D.,
Normark S.J., Rhen M.;
Normark S.J., Rhen M.;
Expression of thin, aggregative fimbriae promotes interaction of
Salmonella typhimurium SR-11 with mouse small intestinal epithelial
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
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88.7%; Pred. No. 1.1e-47;
ive 2; Mismatches 15; Indels
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Infect. Immun. 65:5320-5325 (1997).
EMBL; AJ000514; CAA04151.1; -.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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QSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYG 119
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                                       61 SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG
1 MKLLKVAAFAAIVVSGSALAGVVPQW--GGNHHGGGSNYGPDSSLSIYQYGSNNSANALQ
                                                                          59 SDARKSDVTITOHGRGNGAVVGOGADDSTISLKOTGFONSATIDOWNAKNADISVTOFGG
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STRAIL=O6:II / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
MEDLINE=22388234; PubMed=12471157;
MWEICH R.A. B. Buthan V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhaw G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mayhaw G.F., T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coll.";
Proc. Natl. Acad. Scil. U.S.A. 99:17020-17024(2002).
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Enterobacter.
                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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NCBI_TaxID=217992;
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nes 101; Conservative
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SEQUENCE 152 AA
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Zogal X., Bokranz W., Nimtz M., Romling U.;
Zogal X., Bokranz W., Nimtz M., Romling U.;
Zogal X., Bokranz W., Nimtz M., Romling U.;
Zogal X., Bokranz W., Nimtz M., Romling U.;
Zogal X., Bokranz W., Nimtz M., Production of Cellulose and Curil Finbriae by Members of the Family
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 72:4151-4158(2003).
EMBL, AJ515701; CD566751; --
SEQUENCE 149 AA, 15260 MW; 946DD52017F648FD CRC64;
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"Production of Cellulose and Curli Fimbriae by Members of the Family
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 72:4151-4188(2003).
EMBL. AJ515700; CAD56672.1; -.
SEQUENCE 150 AA; 15016 MW; 1D7141B8D6973DC6 CRC64;
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Enterobacteriaceae, Citrobacter.
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Bacteria; Broteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
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76.8%; Pred. No. 6.5e-39;
ive 10; Mismatches 24
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Matches 116; Conservative
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"Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract."; Infect. Immun. 72:4151-4158 (2003). EMBL, AJS15702; CADS66781: -.
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Enterobacteriaceae, Salmonella.
NCBI_TaxID=592;
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Enterobacteriaceae, Escherichia.
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Cox J.M., Eglezos S., Woolcock J.B.;
virulence of Salmonella enteritidis in chickens correlates with colony morphology and expression of SEF17 fimbriae.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U53207; AAA98671.1;
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                                                                   53.1%; Score 411.5; DB 2; Length 150; 57.6%; Pred. No. 3.1e-26; ive 25; Mismatches 38; Indels 1
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Pred. No. 4.7e-17;
1; Mismatches 15; Indels
                                               15112 MW; 5D8BB2D872DF15F3 CRC64;
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78.9%;
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01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
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                                           MEDLINE=99314153; PubMed=10386375; La Ragione R.W., Collighan R.J., Woodward M.J.; La Ragione R.W., Collighan R.J., Woodward M.J.; Is a Secondated with "Non-curliation of Escherichia coli 078:K80 isolates associated with IS1 inserti on in csgB and reduced persistence in poultry infection."; FEMS Microbiol. Lett. 175:247-253(1999).
EMBI, AJ131756; CAB45380.1; -- 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSNNATTLQFGATNTA-----TTLQTGSLLTV--NTAVTGQGGTTATASNTALT-GQVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 LKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
DNA Res: 9:189-197(2002).
EMBL; APO05954; BAC50564.1; -.
Complete proteome.
SEQUENCE 130 AA; 12699 MW; ACFB2D66A48D260F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22484998, PubMed=12597275,
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Kasamoto S., Watenabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada Tabata S.,
                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bradyrhizobiaces, Bradyrhizobium.
                                                                                                                                                                                                                                                              2; Length 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                29 AA; 2789 MW; E290DFC07ABBB243 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; DB 16; 1
0.085;
ches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
                                                                                                                                                                                                                                                            Score 122; DB 2;
Pred. No. 0.0021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNNAALVNOTASDSSVMVRQVGFGNNATANQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |:|::|: | ::| | :| | :| | CSNSSLIGQIGANNTAGVGQLGILNGSTILQ 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.5%; Score 112; DB 26.5%; Pred. No. 0.08 ive 28; Mismatches
                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                      1 MKLLKVAAFAAIVVSGSALAGVVPQWGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
SEQUENCE FROM N.A.
TRANSPOSON=Insertion sequence IS1;
                                                                                                                                                                                                                                                              15.7%;
89.7%;
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24,
24,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bradyrhizobium japonicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40; Conservative
                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
Bll5299,protein.
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Gaps

27;

26

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:: | | : : | | : | | : | | 3.486 KSYQYQARTGDITYSGSGISALSDVDLLAKQGKVDIVA----GNDTSSR-HEDHSDRTIG 2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2430 SGSHFSTAGPSWGDLGRNVGGGPNSSG----VGLAPYGSAHSADNAAGNSSRQNASVVIG 2485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 SGRDNLIDLVQQGTANQGIVFQSGSDNS-AYVTQAGNDN----ISLVTQIGT----- 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Taspin A., Scott J., Bearan M., Brinkac L., Daugherty S., Bacy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mellblyum T.V., Smith H.O., Vutter B.C., Nealson R.H., Fraser C.M., "Genome sequence of the dissimilatory metal ion-reducing bacterium Shewarella oneidensis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 LALQSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 SGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Alteromonadaceae; Shewanella.
NCBI_TaxID=70863;
                                                                                                                                                                                                                                                                                                                                                           DB 16; Length 3552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.2%; Score 110; DB 16; Length 13
28.3%; Pred. No. 0.13;
ive 19; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                          3552 AA; 352934 MW; C5432AABE2CCF59C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 SGSALAGVVPQWGGGGNHNGGG-NSSGPDSTLSIYQYGSANAA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 AA; 14811 MW; 41EC1CFA76957920 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Minor curlin subunit CsgB, putative.
                                                                                                                                                                                                                                                                                                                                                                                                              52;
  Nature 415:49/->uccorrections

EMBL, ALG46079, CAD1769111, -.
GO; GO:0046821; C:extrachromesomal DNA; IEA.
GO; GO:0004519; F:endonuclease activity; IEA.
GO; GO:003676; F:nucleic acid binding; IEA.
InterPro; IPR008619; Fil haemagg.
InterPro; IPR008638; Haemagg_act.
The Pro; IPR008638; Haemagg_act.
The Pro; IPR008638; Haemagg_act.
                                                                                                                                                                                                                                                                                                                                                     14.4%; Score 111.5; D
29.3%; Pred. No. 5.3;
tive 20; Mismatches
                                                                                                                                                                                                   pfam; PF05594; Fil_haemagg; 70.
Pfam; PF05860; Haemagg_act; 1.
PROSITE; PS01070; NUCLEASE NON_SPEC; 1.
Plasmid; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nat. Biotechnol. 20:1118-1123(2002).
EMBL; AE015532; AAN53942.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2541 DLGGNGYSGTVGVRSASSTL 2560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=MR-1;
MEDLINE=22297686; PubMed=12368813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 QYGGNNAALVNQTASDSSVM 136
                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 29.3
(es 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 28.3 les 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shewanella oneidensis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome
SEQUENCE 139 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S00866;
                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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OSEIH3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 LALQSDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                            Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Bilault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Roher C.A.;

"Genome sequence of the plant pathogen Ralstonia solanacearum.", Nature 415:497-502 (2002).
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MEDLINE-ZAMINOO;
MEDLINE-ZAMINOO;
MEDLINE-ZAMINOO;
MEDLINE-ZAMINOO;
MEDLINE-ZAMINOO, Artiguard F., Gouzy J., Mangenot S.,
Arlat M., Billault A., Brottier P., Camis J.C., Cattolico L.,
Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
Weissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 3501;
                                                                      Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGSALAGVVPQWGGGGNHNGGG-NSSGPDSTLSIYQYGSANAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.4%; Score 111.5; DB 16; Length 29.3%; Pred. No. 5.2; rindels ive 20; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3501 AA; 348421 MW; 290B41C99018A107 CRC64;
01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Probable hemagglutinin-related protein. RSC0887 OR RSO6116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probable hemagglutinin-related protein.
SRSD540 OR RS06117.
Ralstonia solanacearum (Pseudomonas solanacearum).
Plasmid megaplasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMEL, AL646061, CADI4589.1, -.
GO; GO:0004519; F:endonuclease activity; IEA.
GO; GO:0003676; F:nuclea caid binding; IEA.
InterPro; IPR00169; F:nuclease.
InterPro; IPR008619; Fill haemagg.
InterPro; IPR008619; Fill haemagg.
Fam; PF05594; Fill haemagg. act.
Pfam; PF05594; Fill haemagg. act.
Pfam; PF05860; Haemagg act.
Pfam; PF05860; Haemagg act.
PROSITE; PS01070; NUCLEASE_NON_SPEC; 1.
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                                                                                                                                                                                                                                                      MEDLINE=21681879; PubMed=11823852;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 QYGGNNAALVNQTASDSSVM 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome
SEQUENCE 3501 A
                                                                                                                                                       NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=305
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12

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Matches

QBXSD6;

RESULT 10

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Gaps

RESULT 12 **OBEFU3** 

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502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 AA--LVNQTASDSSVMVRQVG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        801 GAGGEVSVSLTDSAIRTGQGG 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conserved hypothetical protein. S00865.
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24.2%;
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EMBL; AE015532; AAN53941.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 26.2 Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shewanella oneidensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical
SEQUENCE 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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QBEIH4
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MEDLINE-22297686, PubMed=12368813;
MEDLINE-22297686, PubMed=1.T., Nelson K.E., Gaidos E.J., Nelson W.C.
Read T.D., Elsen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
Wadupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
Wamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,
Meller J. V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.;
"Genome sequence of the dissimilatory metal ion-reducing bacterium
Shewanella oneidensis.";
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Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
NCBI_TaxID=382;
1422 AA; 148253 MW; 840DB6300C993DE8 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical glycine-rich protein SMb21548.
Rhizobium meliloti (Sinorhizobium meliloti)
Plasmid pSymB (megaplasmid 2).
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Last annotation update)
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EMBL, AE015630, AAN54924.1; -.
TIGR; SO1872; -.
                                                                                                                                                                                                                                               Created)
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STRAIN=1021;
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66 SETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAK---NSDITVGQYGGNN 122
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MEDLINE=21396508; PubMed=11481431;
Pinan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
A Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
Golding B., Puehler A.,
The complete sequence of the 1,683-kb psym8 megaplasmid from the Nz-
frixing endosymbiont Sinorhizobium mellloti.";
Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894 (2001).

BRI, MS5965; E95965.
BS965; E95965.
BOS GO:004681; C:extrachromosomal DNA, IEA.

GO; GO:006491; F:peroxidase activity; IEA.

GO; GO:006991; P:peroxidase activity: IEA.

GO; GO:006991; P:peroxidase.

InterPro; IPR005546; Autotransporter.

InterPro; IPR005013; PfkB.

RPOSTIE: PS00445; PEROXIDASE 1; 1.

PROSTIE: PS00445; PEROXIDASE 1; 1.

PROSTIE: PS00683; PFKB KINASE_1; 1.

PROSTIE: PS00683; PFKB KINASE_1; 2.

PROSTIE: PS006845; PEROXIDASE 1; 1.

PROSTIE: PS006845; PEROXIDASE 1; 1.

PROSTIE: PS006845; PEROXIDASE 1; 1.

PROSTIE: PS006845; PEROXIDASE 1; 1.

PROSTIE: PS006845; PEROXIDASE 1; 1.

PROSTIE: PS006845; PEROXIDASE 1; 1.

PROSTIE: PS006845; PEROXIDASE 1; 1.
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MEDIJIRE=2229686, PubMed=12368813;
MEDIJIRE=2229686, PubMed=12368813;
MEDIJIRE=2229686, PubMed=12368813;
Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Britkac L., Daugherty S., DeBoy R.T., Dodson R.J., Umayam L.A., White O., Wolf A.M., Wadthou R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Wamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Musler H., Gill J., Utterback T.R., McDonald L.A., Gelblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; Medenome sequence of the dissimilatory metal ion-reducing bacterium Shemanella oneidensis.";
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502 AA; 52441 MW; D08CA23D6C46B62D CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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79 ADYD-----QLVTRVVTHEMAHAFRNNATIDQW------NAKNSDIT 114
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                                                                         29 GGNHNGGGNSSGPDSTLSIYQYGSANAA-----LALQSDARKSETTITQSGYGNG 78
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    Gaps
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MEDLINE=22484998; PubMed=12597275;
Raneko T., Nakamura Y., Saro S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
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ENBL, AP005954; BAC50565.1; -.
Complete proteome.
SEQUENCE 171 AA; 17448 MW; 995DB08C01498381 CRC64;
    35;
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12.8%; Score 99.5; DB 16; Length 171;
Best Local Similarity 24.7%; Pred. No. 1.2;
Matches 39; Conservative 26; Mismatches 56; Indels 37,
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Bracteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Bradyrhizobiaceae, Bradyrhizobium.
NCBI_TaxID=375,
    59; Indels
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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25; Mismatches
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38; Conservative
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Search completed: August 2, 2004, 14:54:42 Job time : 30.7 secs

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2, 2004, 14:35:42; Search time 44.9 Seconds (without alignments) 950.215 Million cell updates/sec
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768
1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Agfa::P	6352	4625 Agf	Aab36341 Salmonell	Aaw23570 Salmonell	Aab36347 AgfA::PT3	Aab36351 AgfA::PT3	Aab36354 AgfA::PT3	Aab36346 AgfA::PT3	Aab36353 AgfA::PT3	Aab36349 AgfA::PT3	Aab36350 AgfA::PT3	Aab36348 AgfA::PT3	Aab36343 Escherich	Abr82651 E. coli C	Aar62761 AgfA segu	Aaw23569 Salmonell	O.	ıΩ	5316	8 Sa	36325 Sal	6339 Salmon	0 Salmon	Abr82644 E. coli c
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The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use, of thin aggregative fimbriae (SE17/TAF) nucleation depended assembly system of strains of Salmonella. Bscherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA. CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene back into the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromosome of the chromo

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## ALIGNMENTS

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal. Salmoneila; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen. AgfA::PI3#10 amino acid sequence SEQ ID NO:30. Kay WW; Disclosure, Page 139, 139pp, English. Collison SK, AAB36355 standard; protein; 151 AA. 05-APR-2000; 2000WO-CA000356. 99US-0127888P (first entry) Salmonella enteritidis. Escherichia coli. (UYVI-) UNIV VICTORIA Doran JL, WPI; 2000-672631/65. N-PSDB; AAC64631. WO200060102-A2 05-APR-1999; 26-FEB-2001 12-OCT-2000. White AP, Synthetic. AAB36355; RESULT 1 

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AAR74625;
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compy of that gene, and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foregan amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong communogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and the presentive to purify in large amount. The present sequence is given in
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                                                                                                                                                                                                                                                                                                                                                                     61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
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                                                                                                                                                                                                                                                100.0%; Score 768; DB 3; Length 151; 100.0%; Pred. No. 1.7e-66; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                    inexpensive to purify in large amount. The puthe exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AgfA::PT3#7 amino acid sequence SEQ ID NO:24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella; agfA; chromosomal gene ravaccine; immune response; immunogen.
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Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella enteritidis
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N-PSDB; AAC64628.
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                                                                                                                                                                                                                           Sequence 151 AA;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative finbriae (SEB17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and and Enterobacteriaceae for the production of fimbriae comprising recombinant of Enterobacteriaceae for the production of fimbriae comprising recombinant of AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) directing recombinant gene into the chromosome of the homologus species, replacing the native comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino protein containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino protein containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful consequencity and adhesion properties relevant for an efficient live vaccine, the carrier finbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response in an animal immune response in an animal important for an efficient live vaccine, the carrier finbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response in any properties relevant for an efficient live vaccine, the carrier finbrial subunit. The present sequence is given in the exemplification of the present invention
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Pred. No. 6.8e-60;
0; Mismatches 0
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89.9%;
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Best Local Similarity
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26-JUN-1995
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assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and Enterpolateriaceae for the production of fimbriae comprising recombinant of gracting recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, copy of that gene; and (4) eliciting an immune response in an animal, protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant ApfA protein which is useful for useful for the expension of recombinant ApfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogens, which may be important for directing an immune response immunogens, which may be important for directing an immune response in an immune response in an expensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enteropathogenic bacteria, enterobacteria, S.enteritidis, antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 681; DB 3;
Pred. No. 4.7e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 4.7e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NNAALVNOTASDSSVMVROVGFGNNATANOY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VICTORIA INNOVATION &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW23570 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94US-00233788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 90.7
es 137; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kay ww,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 151 AA;
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Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collinson SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-APR-1994;
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29-SEP-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW23570;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDARKSETTIITQSGYGNGADVGQGADNSTIELTQNGFRNNAIYDQLVTRVVTHEMAHAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are.
                                                                                                               Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
                                                                                                                                                                                                                                            immunization compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                      Salmonella AgfA protein and DNA are used in vaccine and genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             la, agfA; chromosomal gene replacement; fimbrin; epitope; immune response; immunogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella enteritidis AgfA amino acid sequence SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                   Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                   Score 681; DB 2; I
Pred. No. 4.7e-58;
2; Mismatches 12;
           Doran JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kay WW;
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        Clouthier SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 135; 139pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB36341 standard; protein; 151 AA
                                                                                                                                                                              7B; 95pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
        Collinson SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella enteritidis.
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                                                 WPI; 1994-358275/44.
N-PSDB; AAQ87467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-672631/65.
                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                              Disclosure; Fig
                                                                                                                                                                                                                                                                                                                             Sequence 151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                             137;
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                                                                                                                                                                                                                                                                                                                                                                                            Local
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Gaps

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protein useful for eliciting immune response in animal
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ilarity 81.9%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                            Sequence 151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB36351;
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Matches
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                                                                                                   The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 27655-3b. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                 61 SDARKSETTITIQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
                                                                                                                                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGFDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                           1 MKLLKVAAFPAIVVSGSALAGVVPQWGGGGNHNGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                Gaps
                                               Isolated Salmonella gene agfA - used for diagnosis of Salmonella or enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
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                                                                                                                                                                                                                                                           Length 151;
                                                                                                                                                                                                                                                                               13; Indels
                                                                                                                                                                                                                                                        Score 676; DB 2;
Pred. No. 1.4e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AgfA::PT3#2 amino acid sequence SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                              151
                                                                                                                                                                                                                                                                                                                                                                                                                    121 NNPALVNOTASDSSVMVRQVGFGNNATANOY 151
                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              NNAALVNOTASDSSVMVRQVGFGNNATANQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine; immune response; immunogen.
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                                                                                  7; 85pp; English
                                                                                                                                                                                                                                                         88.0%;
90.1%;
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                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella enteritidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-672631/65.
               WPI; 1997-309886/28
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 136; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
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                          N-PSDB; AAT74142
                                                                                                                                                                                                                                   Sequence 151 AA;
                                                                                 2; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200060102-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB36347;
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                                                                                  Example
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEPI)/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and aggregative fimbriah subunits, respectively; (2) assembly system of strains of Salmonella, Escherichia coli and containing the combination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene comprising species; (3) directing recombination of a recombinant gene comprising separating an aminologous species, replacing the native comprising separating an amino acid polymer comprising a replacement segment or segments of foreign animo containing a replacement segment or segments of foreign amino protein containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments or diluent. (T) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the hererologous antigens are presented in high numbers (up to system the hererologous antigens are presented in high numbers (up to system the hererologous antigens are presented in high numbers (up to vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention researched in given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNAT-------YDQ 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SDARKSETTITOSGYGNGADVGQGADNSTIELTONGFRNNATIDOWNAKNSDITVGQYDQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKLLKVAAFPAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 LVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----SVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 659; DB 3;
Pred. No. 6.4e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AgfA::PT3#6 amino acid sequence SEQ ID NO:22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
Disclosure; Page 136; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ą
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epicope or antigen. Also described are: (I) use of thin aggregative fimbriae (SET1/TAR) nucleation depended assembly system of strains of Salmonella Escherichia coli and AffA-homologue finbrin subunits, respectively; (2) alrecting recombination of a recombinant gene into the chromosome of the homologues species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, copy of that gene; and (4) eliciting an immune response in an animal, copy of that gene; and (4) eliciting an immune a replacement segment or segments of foreign amino acid polymer comprising separating an amino acid polymer comprising separating an animal and a salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a salmonella, E. coli or acid sequence or sequences grown on a salmonella, E. coli or acid sequence or sequences grown on a salmonella, E. coli or acid in minume response in an animal. In a finbrial presentation copyetem the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial presented in a minumal response in an animal protein are usually strong immunogens, which may be important for directing an immune response in an appearant secures as and secured sequence or experience or experience or experience or experience or experience or experience or experience or experience or experience or experience or experience or experience or experience or experience or experience or experience or experience or experience or expe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                         Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 137; 139pp; English.
                                                                                                                                                                                                                                                         Collison SK,
99US-012788BP
                                                                                                                         (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                         Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                   WPI: 2000-672631/65,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAC64627.
05-APR-1999;
                                                                                                                                                                                                                                                                White AP,
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SDARKSETTITQSGYGNGADVGQGADNSTIBLTQNGFRNNATYDQLVTRVVTHEMAHA-- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SDARKSETTITQSGYGNGADVGQGADN------YDQLVTRVVTHEMAHADQ 105
                                                                                                                                                                                                                                                                                                                                                                                             1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGCNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                             1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                              30;
                                                                                                                                                                                                                                                                                                                                                            85.5%; Score 657; DB 3; Length 151;
81.9%; Pred. No. 1e-55;
ive 0; Mismatches 0; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------GGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 WNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                              Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                              Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                              119
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                                                                                                                                                                               Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen.
                                                                                                                                    AgfA::PT3#9 amino acid sequence SEQ ID NO:28,
AAB36354 standard; protein; 151 AA
                                                                                         (first entry)
                                                                                           26-FEB-2001
                                             AAB36354;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbrise (SERI)/TAF) nucleation depended assembly system of strains of salmonella, Escherichia coli and assembly system of strains of salmonella, Escherichia coli and assembly system of strains of salmonella, Escherichia coli and assembly system of strains of salmonella, Escherichia coli and assembly system of strains of a recombination of a recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal. Comprising a recombinant AgfA comprising separating an aminon acid polymer comprising a replacement sequence of sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences in an animal. In a fimbrial presentation cystem the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response in manner easy and immune to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHA-- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------YDQLVTRVVTHEMAHAFR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MKLLKVAAFAAIVVSGSALAGVVPQWGGGCNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --GGNNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 613; DB 3; Length 151;
Pred. No. 1.9e-51;
0; Mismatches 0; Indels 4
                                                                                                                                                                                                                                                                                                                                        Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 SDARKSETTITQSGYGNGAD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 138; 139pp; English.
                                                                                                                                                                                                                                                                                                                                        Collison SK,
                                                                                                                                                                                                      05-APR-2000; 2000WO-CA000356.
                                                                                                                                                                                                                                                 99US-0127888P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 129; Conservative
                     Salmonella enteritidis.
                                                                                                                                                                                                                                                                                            (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                                                                                        Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-672631/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                         Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAC64630,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 151 AA;
                                                                                                            WO200060102-A2.
                                                                                                                                                                                                                                                 05-APR-1999;
                                                                                                                                                        12-OCT-2000
                                                                                                                                                                                                                                                                                                                                          White AP,
                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119
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RESULT

99 NNATIDQMNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEPI7/TAP) mucleation depended assembly system of strains of Salmonella. Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant CC directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an ending a replacement segment or segments of foreign amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Encertaceae host cell. from the host cell and introducing the polymer into the animal in conjunction with a carrier or dilutent. (I) is useful for the expression of recombinant AgfA protein which is useful for useful for the expression of recombinant AgfA protein which is useful conjuncient, the carrier fimbrial submit proteins are usually strong immunogens, which may be important for directing an immune response conjunction, and hybrid fimbriae are easy and intexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                          Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 151;
                                                                                                                                   AgfA::PT3#1 amino acid sequence SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 135; 139pp; English.
                                                                                                                                                                                                 vaccine; immune response; immunogen.
              AAB36346 standard; protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                           05-APR-2000; 2000WO-CA000356.
                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0127888P.
                                                                                           (first entry)
                                                                                                                                                                                                                                  Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000-672631/65.
                                                                                                                                                                                                                                                       Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAC64622.
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                                                                                                                                                                                                                                                                                                                WO200060102-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-1999;
                                                                                           26-FEB-2001
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                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               White AP,
                                                        AAB36346;
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AAB36346
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGCNSSGPDSTLSIYQYGSANAALALQ 23; Indels 78.5%; Score 603; DB 3; 80.8%; Pred. No. 1.7e-50; iive 6; Mismatches 23; Conservative Local Similarity les 122; Conserv Matches

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA cequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEPI)/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coll and AgfA-homologue fimbria of fimbriae comprising recombinant of a recombination of a recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the homologous species; (3) directing recombinant of a recombinant gene copy of that gene, and (4) eliciting an immume response in an animal, comprising separating an amino all additional and interoducing a recombinant AgfA protein containing a replacement segment or segments of foreign amino comprising separating an amino and salmonella, E. Coll or.

Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein mounders (up to coll of the expression of recombinant protein prosent of a suschil for caliciting an immume response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to coll occ an immume response in an animal. In a fimbrial presentation immune response in an animal are usually strong immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong capainst the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
                                  61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella, agfA, chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                        AgfA::PT3#8 amino acid sequence SEQ ID NO:26.
                                                                                      151
                                                                                                                             121 NNAALVNYDQLVTRVVTHEMAHANNAFANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kay WW;
                                                                                      121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 138; 139pp; English
                                                                                                                                                                                                                                          AAB36353 standard; protein; 151 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-APR-2000; 2000WO-CA000356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0127888P
                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-672631/65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200060102-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         )5-APR-1999;
                                                                                                                                                                                                                                                                                                                                 26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               White AP,
                                                                                                                                                                                                                                                                                    AAB36353;
                                                                                                                               g
                                                                                                                                                                                                                                                                                       Db
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                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                         61 LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                   Length 151;
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                                                                                                   24;
                                                                  Score 600; DB 3;
Pred. No. 3.4e-50;
4; Mismatches 24
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 of the present invention
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                                                                  Match 78.1%;
Local Similarity 81.5%;
es 123; Conservative
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the exemplification
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N-PSDB; AAC64625.
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Escherichia coli.
                                  Sequence 151 AA;
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Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a finbrial presentation system the heterologous antigens are presented in high numbers (up to $500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDYDQLVTRVVTHEMAHALQ
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Pred. No. 4.2e-50;
5; Mismatches 23;
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ilarity 81.5%;
Conservative
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N-PSDB; AAC64624.

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assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant of Enterobacteriaceae for the production of fimbriae comprising recombinant of directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence in mimule nesponse in an aminal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the carrier fimbrial submit proteins are usually strong immunogens, which may be important for directing an immune response immunogens, which may be important for directing an immune response immunogens the exemplification of the present invention
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Pred. No. 6.6e-50;
5; Mismatches 23;
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Matches 123; Conservative
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA segment with the encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative fimbries (BER17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and affA. CsgA and AgfA. homologue fimbrin subunits, respectively. (2) directing recombination of fimbries comprising recombinant of homologous species; (3) directing recombination of a recombinant of the chromosome of the homologous species; (3) directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising speraring an amino acid polywer comprising a replacement segment comprising a recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to sout mannogenicity and adhesion properties relevant for a efficient live in mannogenicity and adhesion properties relevant for a mefficient live in mannogenicity and adhesion properties relevant for an efficient live
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKLLKVAARAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine, the carrier finbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                   Recombinant agfA gene having a segment replaced by a foreign DNA segwhich encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli CsgA amino acid sequence SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 566; DB 3;
Pred. No. 6.7e-47;
5; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                            Disclosure, Page 136; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine; immune response; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB36343 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.7%;
80.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 80.8
Matches 122, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200060102-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB36343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB36343
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The invention relates to an isolated peptide capable of binding a mammalian plasma protein or of generating an immune response in a mammal selected from sequences shown in ABR82642, ABR82648-49. The peptide or antibody is useful for treating a bacterial infection in a human or animal or in the manufacture of a medicament for the prophylactic treatment of a bacterial infection, such as Escherichia coli, Salmonella or Shigella infection. The peptide that is immobilized on a solid support is also useful as a reagent for determining the ability of a plasma protein to bind to bacteria. The present sequence represents an E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDARKSETTITOSGYGNGADVGOGADNSTIELTONGFRNNATYDOLVTRVVTHEMAHAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated peptide capable of binding a mammalian plasma protein, useful in the manufacture of a medicament for the prevention and/or treatment of a bacterial infection, such as Escherichia coli, Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MKLLKVAAFAAI VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSI YQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MKLLKVEAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ
Plasma protein; immune response; antibacterial; vaccine; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 512; DB 7;
; Pred. No. 1.2e-41;
17; Mismatches 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                               Herwald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2, 2004, 14:48:29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 41-42; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  Wikstroem M,
                                                                                                                                                                                                                             30-JAN-2003; 2003WO-EP000943
                                                                                                                                                                                                                                                                                   31-JAN-2002; 2002GB-00002275
                                                                                                                                                                                                                                                                                                                                         (HANS-) HANSA MEDICAL RES AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shigella infections.
                                                                                                                                                                                                                                                                                                                                                                                               Olsen A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                completed: August
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-646136/61.
N-PSDB; ACF36153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                     Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 151 AA;
                                                                                                              WO2003064446-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Job time : 44.9 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 kDa protein
                                                                                                                                                                    07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                  Bjoerck:L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA comparison encoded a foreign epicope or antigen. Also described are: (1) use of thin aggregative finbriae (SFBI)/TAP) mucleation depended assembly system of strains of Salmonella, Escherichia coli and contained strains of Salmonella, Escherichia coli and contained and AgfA-homologue fimbriae (SFBI)/TAP) mucleation depended assembly system of strains of a recombination of inprising recombinant containing recombination of a recombination of a recombination of a recombinant gene into the chromosome of the homologue species, replacing the native comprising separating an amino acid polymer comprising a recombinant gene comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a namino acid polymer comprising recombinant AgfA protein containing a namino acid polymer of acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriacee host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful containing an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein sare usually strong immunogens, which may be important for directing an immune response contains and properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong against the inserted epitope, and hybrid fimbriae are usually strong immunogens, which may be important for directing an immune response in example in a properties are usually sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                           Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.3%; Score 517; DB 3;
69.5%; Pred. No. 3.8e-42;
iive 17; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNAALVNOTASDSSVMVRQVGFGNNATANQY, 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GNGAAVDOTASNSSVNVTQVGFGNNATAHQY 151
                                                                                                                                                                       Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E. coli CsgA subunit 15 kDa protein.
                                                                                                                                                                       Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABR82651 standard; protein; 151 AA.
  05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Page 135; 139pp;
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                                                                                                              (UYVI-) UNIV VICTORIA
                                                                                                                                                                       White AP, Doran JL,
                                                                                                                                                                                                                                2000-672631/65.
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                                                                                                                                                                                                                                                        N-PSDB; AAC64619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABR82651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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Gaps ; 0

Length 151; 30; Indels

(0108N) YUDI8 860d SIUJ

5434, Ap 7, Appli 9, Appli 9, Appli 8, Appli 6, Appli 2, Appli

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Sequence 2, Appli
Sequence 10, Appl
Sequence 3827, Appl
Sequence 42, Appl
Sequence 10, Appl
Sequence 22, Appl
Sequence 28148, A
Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                             Sequence 54
Sequence 7,
Sequence 9,
Sequence 9,
Sequence 8,
                              Sequence 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-233-788A-59

Sequence 59, Application US/08233788A

Patent No.; 5635617

GENERAL INFORMATION

APPLICANT: Doran, James L.

APPLICANT: Kay, William W.

APPLICANT: Collinson, Karen S.

APPLICANT: Clouther, Sharen C.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION

TITLE OF INVENTION: OF SALMONELLA

NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry

STREET: 6300 Columbia Center, 701 Fifth Anners

CITY: Seattle
                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: FIDOPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT: APPLICATION DATA:
APPLICATION NUMBER: US/08/23,788A
FILING DATE: 26-APR-1994
FILING DATE: 26-APR-1994
FILING DATE: 26-APR-1994
TLING DATE: APPLICATION:
NAME: King, JOSHUR: 35,570
REFERENCE/DOCKET NUMBER: 35,570
REFINENCE/DOCKET NUMBER: 35,570
TELEFRATION NUMBER: 35,570
TELEFRATION INFORMATION:
TELEFRAX: (206) 622-4900
TELEFRAX: (206) 622-4900
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TELEFRAX: (206) 622-631
US-09-252-991A-26658

US-09-595-664B-39

US-08-604-267C-3

US-09-543-61A-5434

US-09-336-447A-9

US-08-336-447A-9

US-08-336-447A-9

US-08-94-818B-8

US-08-9445-472-6

US-08-9445-472-6

US-08-9445-472-6

US-08-95A-10

US-09-540-685A-10

US-09-540-685A-10

US-09-540-685A-10

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amino acid
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Best Local Similarity 90.1
Matches 136; Conservative
     , MOLECULE TYPE: protein US-08-233-788A-59
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ZIP: 98104-7092
     RESULT 1
US-08-233-788A-59
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Sequence 8, Appli
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Sequence 8, Appli
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11518, A
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Sequence 4764, Ap
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1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-841-835-10

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                                                                       SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                         SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV 60
1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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APPLICANT: Kay, William W.
APPLICANT: Collinson, Karen C.
APPLICANT: Collinson, Karen C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TITLE OF INVENTION: OF SALMONELLA
NUMBER OF SEQUENCES:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 496; DB 1; Length 120;
Pred. No. 4e-43;
2; Mismatches 12; Indels
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CITY: Seattle
STATE: Washington
COUWTRY: U.S.A.
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,788A
FILING DATE: 26-415
                                                                                                                                                       121 NNPALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                              121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 920043.403C2
TELEPHONE: (206) 622-4900
TELEFRAX: (206) 682-6031
TELEFRAX: (206) 682-6031
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TELEFRAX: 0208) 622-6031
SEQUENTION FOR SEQ ID NO: 57: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                            Sequence 57, Application US/08233788A Patent No. 5635617
GENERAL INFORMATION:
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US-08-864-038A-3
; Sequence 3, Application US/08864038A
; Patent No. 6001592
; GENERAL INFORMATION:
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87.5%;
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Best Local Similarity
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TITLE OF INVENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
TITLE OF INVENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
TITLE OF INVENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
TITLE OF INVENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
TITLE OF INVENTION: TO SAID POLYPEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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Patent No. 6277613

GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
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IBM Compatible
SYSTEM: Microsoft Windows 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
12.0%; Score 92.5; DB 3;
Best Local Similarity 27.7%; Pred. No. 0.46;
Matches 43; Conservative 12; Mismatches 61;
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                                                                                                                                                                                                                                                                                                                                                                                MEDLUM
COMPUTE: IBM Comparize Compoures Computer: IBM Comparize OPERATING SYSTEM: Microsoft Windows SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/864,038A
FILING DATE: May 28, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 8-184459
FILING DATE: 15-July-1996
ATTORNEY/AGENT INFORMATION:
NAME: C. BRUCE Hamburg
REGISTRATION NUMBER: 22,389
REFERRENCE/DOCKET NUMBER: F-5610
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: From 1 to 738 IDENTIFICATION METHOD: E
                                                                                                                                                                                                812-5 Hirano
                                                                                                                                                                                                                                                                 STATE: Mie-prefecture
COUNTRY: JAPAN
ZIP: 514-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 AALVNQTASDSS-
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                       STREET: Isshind
CITY: Tsu-city
STATE: Mie-pred
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us-09-543-407-30.rai

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99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPGSSLAESPEAA 157
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US-09-196-387-10

Sequence 10. Application US/09196387

Patent NO. 6277613

PAPPLICANT: de Lange, Titia

APPLICANT: Smith, Susan

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue, 4th Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 673;
        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
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APPLICATION NUMBER: US/09/196,387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 29.4%; Pred. No. 0.51;
Matches 42; Conservative 17; Mismatches 65;
                                                                                                                                                                                                                                                        NAME: Jackson Egg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPRONE: 201-487-580
TELEPRONE: 201-343-1684
TELERA: 133521
INFORMATION FOR EGG ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
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                                                                                                  FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 09/196,387
FILING DATE:
ATTORREY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 07601
COMPUTER READABLE FORM:
NEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION UNMER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY AGENT INFORMATION:
NAME: Jackson Esq., David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jackson Esq., David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-09-841-835-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
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Patent No. 6506587
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
11.9%; Score 91.5; DB 3; Length 673;
Best Local Similarity 29.4%; Pred. No. 0.51;
Matches 42; Conservative 17; Mismatches 65; Indels 12
                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSBE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Klauber & Jackson
411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           600-1-230 CIP1
                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
ATORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-23
TELEPHONE: 201-487-5800
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ. ID NO: 8:
SEQUENCE CHARATERISTICS:
LENGTH: 673 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDTUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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STREET: 411 Hacke
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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: USA
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11.9%; Score 91.5; DE
29.4%; Pred. No. 0.8;
tive 17; Mismatches
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APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
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INFORMATION FOR SEQ ID NO: 2:
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, MOLECULE TYPE: protein US-09-841-835-10
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STRANDEDNESS: sin
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                                                                                                                         Best Local Similarity
Matches 42; Conserv
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New COUNTRY: US ZIP: 07601
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                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGD------VSRV--KRLVDAAN 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 VAAFAAI-VVSGSALAGVVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR
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| Sequence 10. Application US/09841835
| Sequence 10. Application US/09841835
| PAPLICANT: GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GEORGE 10. GE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 11.9%; Score 91.5; DB 3; Length 949; 1 Similarity 29.4%; Pred. No. 0.8; 42; Conservative 17; Mismatches 65; Indels 15
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APPLICATION NUMBER: US/09/841,835 FILING DATE:
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIPI
TELECOMOUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 949 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         600-1-230 CIP1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 VNAK--DMAGRKSSPLHFAAGFG 227
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REFERENCE/DOCKET NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
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SEQUENCE CHARACTERISTICS:
LENGTH: 949 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: linear
                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-196-387-10
                                                                                                                                                                                                                                                                                                       amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 42; Conserv
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                                                                                                                                                                                                                                                                                                  158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGD------VSRV--KRLVDAAN 206
                                                                                                                                                              99 VAAADVVPAVGISSAAGVAPNPAGSGSNNSPSSSSSPISS-SSSSPSSPGSSLAESPEAA 157
                                                                                                                   6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 VAAFAAI-VVVSGSALAGVVPQWGGGGNHNGGGNSSGFDSTLSIYQYGSANAALALQSDAR
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11.9%; Score 91.5; DB 3; Length 1327;
Best Local Similarity 29.4%; Pred. No. 1.3;
Matches 42; Conservative 17; Mismatches 65; Indels 19; Gaps
                                                        Gaps
                                                        19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09196387

Patent No. 6277613

GENERAL INFORMATION:

APPLICANT: de Lange, Titia

APPLICANT: Smith, Susan

TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS

TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS

TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS

TITLE OF INVENTION: A DRUGGES 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue, 4th Floor
Length 949;
                                                        65; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
DB 4;
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us-09-543-407-30.rai

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 KSETTIT----QSGYGNGADVGQGADNSTIELIQNGFRNNATYDQLVTRVVTHEMAHAGG 120
99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
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US-09-841-835-2
US-09-841-835-2
Sequence 2, Application US/09841835
patent No. 6506897
GENERAL INFORMATION:
APPLICANT: Ge Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Alauber & Jackson
STREET: Hackensack
STREET: Hackensack
STATE: New Jersey
COUNTRY: LOSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65;
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11.9%; Score 91.5; DE
Best Local Similarity 29.4%; Pred. No. 1.3;
Matches 42; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   600-1-230 CIP1
                                                                                                       121 NNAALVNQTASDSSVMVRQVGFG 143
                                                                                                                                          207 VNAK--DMAGRKSSPLHFAAGFG 227
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APPLICATION NUMBER: US/09/841,835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REPERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 133521
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1327 amino acids
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99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSPSSPGSSLAESPEAA 157
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TITLE OF INVENTION: LT and CT in Parenteral Immunization
TITLE OF INVENTION: Methods Against Helicobacter Infection
FILE REFERENCE: 06132/055002
CURRENT APPLICATION NUMBER: US/09/336,115C
CURRENT FILING DATE: 1999-06-19
PRIOR FILING DATE: 1998-06-19
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                     APPLICANT Greeg, Morin B.
APPLICANT Walter, Funk D.
APPLICANT Walter, Funk D.
APPLICANT Walter, Funk D.
TITLE OF INVENTION: A Second Mammalian Telomerase FILE REFERENCE: 080/003C
CURRENT APPLICATION VMBER: US/09/972,115A
CURRENT FILING DATE: 2001-10-05
PRIOR PILING DATE: 2000-04-10
PRIOR PILING DATE: 1999-04-13
PRIOR PILING DATE: 1999-04-13
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COTHER INFORMATION: Xaa = Any Amino Acid
US-09-336-115C-6
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                       Sequence 8; Application US/09972115A Patent No. 6599728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6 Application US/09336115C
Patent No. 6576244
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 29.4%;
Matches 42; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Weltzin, Richard A. APPLICANT: Guy, Bruno
                                                                          GENERAL INFORMATION:
APPLICANT: Geron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1327
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: SIGNAL
LOCATION: (1)...(20)
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US-09-972-115A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS-09-972-115A-8
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RESULT 15
US-09-540-236-2676
US-09-540-236-2676
US-09-540-236-2676
Sequence 2677, Application US/09540236
Sequence 2677, Application US/09540236
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAF
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RELATING TO KLEBSIELLA
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                                                                                                                                                                                                                          181 VTGNTSLVVNDSGGRIASI---YGGGYGTNATNTANVTGNVSTKVAITNAATGFQLSTYY
                                                                                                                                                                                                                                                                                                                  238 GGVQYGNIG------GKVTNDISGYGRWYTAGORFIGGSSRGDIGTNRATDGITT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 GGLDRNGANANGQTDTFGIYAFDTLTLTERIEINGGLRLDNYHTKYDSATACGGSGRGAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 -- DVGQ--GADNSTIELTQNG----FRNNATYDQLVTRVVTHEMAHAGGN---NAALVNQ
                                                                                                                                                                                                                                                                        --GADNSTIELTQ
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                                                                                                                                     78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATI
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATI
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENY APPLICATION NUMBER: US/09/489,039A
CURRENY FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 589;
                                                                                     Query Match 10.8%; Score 83; DB 4; Length 1216; Best Local Similarity 24.4%; Pred. No. 8.2; Matches 49; Conservative 19; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                  ----GFRNNATYDQLVTRVVTHEMAHAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                      49 ---QYGSANAALALQSDARKSETTITQSGYGNGADVGQ-----
                                                                                                                                                                                 6 VAAFAAIVV -- SGSALAGVV PQWGG -- GGNHNGGGNSSGPDST -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56;
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llarity 24.5%; Pred. No. 4.5;
Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7849, Application US/09489039A Patent No. 6610836 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 TASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           368 PPGGSSFALAASGSGNSANRTDF 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 SDSSVMVRQVGFGNNATANQY 151
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|-----QIGASNEALYDAY
TYPE: PRT
ORGANISM: Enterococcus faecalis
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Matches 35; Conserv
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US-09-489-039A-7849
                                                US-09-134-000C-5130
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US-00-252-91A-30227
iSequence 30227, Application US/0925291A
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sequence 30227, Application US/09252991A
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; Sequence 5130, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
APPLICANT: LYNN DOUGETCE-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUMBER: US/09/134,000C
; TITLE REPERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US 60/055,778
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR PILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SEQ ID NOS: 6812
; SEQ ID NO 5130
; LENGTH: 1216
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                                                                                                                                          102 ÁYQÁVFLAINÁAVGL---WNTIGYAVMCGNĠNGTESGÞGSVIFNDQÞGQDSTQITCNRFE 158
                                                                                                                                                                                                                                    159 STGPGKSMSIDEFKKLNEAYQIIQQALKNQSGFPELG-GNGTKV---SVNYNYECRQTAD 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 GQA------EAGASVGIDTNGDGKPDLTVIADANGNFTAPLNPPLTNGGTVTV 252
                                                                                                                                                                                      SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 VAAFAAIVVSGSAL-AGVV--PQWGGGGNHNGGGNSSGPDST-----LSIYQYGSANA 55
                                                   Gaps
                                                                                                                                                                                                                                                                             98 RNNATYDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVGFGNNAT 147
                                                                                                                                                                                                                                                                                                               INGGVYQPCKAKNGSSSSSNGGNGSSTQTTATTTQDGVTITTTYNNKAT 264
                                                37;
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    DB 4; Length 745;
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10.9%; Score 84; DB 4; Length 2736;
Best Local Similarity 29.7%; Pred. No. 19;
Matches 43; Conservative 17; Mismatches 49; Indels
                                                   Indels
    11.3%; Score 86.5; DB 4; I 20.0%; Pred. No. 1.9; ive 27; Mismatches 72;
                                                                                                 AFAAIVVSGSALAGVVPQW-------GGGGNHNGGGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 VVTHEMAHAGGNNAALVNQTASDSS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                34; Conservative
       Query Match
Best Local Similarity
Matches 34; Conserv
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Query Match
Best Local Similarity 26.8%; Pred. No. 11;
Matches 49; Conservative 23; Mismatches 65; Indels 46; Gaps 10;
                                                                                                                                                                                                                                                                                        93 TIA----GGRN------NQATKENSTVGGGKFNQAKGRNSTVAGGYNNEATGIDSTIAGG 142
                                                                                                                                                                                                                                                                                                                                       98 R-NNATYDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVMV-----RQVGFGNNAT 147
                                                                                                                                                                                                                                                                                                                                                             4 LKVAAFAAIVVSGSALAG--VVPQWGG-----GGNHN------GGG---NSSGPDS 43
                                                                                                                                                                                                                    44 TLSIYQYGSANAALALQSDARKSETTITQSGY----GNGADVGQGADNST--IELTQNGF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: August 2, 2004, 14:58:37 Job time: 13 secs
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2676
; LENGTH: 867
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2676
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August 2, 2004, 14:54:48; Search time 36.8 Seconds (without alignments) 1287.123 Million cell updates/sec
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768
1 MKLLKVAAFAAIVVSGSALA.......DSSVMVRQVGFGNNATANQY 151
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1291235 segs, 313682936 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                              Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 20638, Sequence 21, Appl Sequence 21, Appl Sequence 64364, A Sequence 64364, A Sequence 64364, A Sequence 6264, A Sequence 6264, A Sequence 6264, A Sequence 6264, A Sequence 6264, A Sequence 10, Appli Sequence 10, Appli Sequence 2, Appli Description 2 US-09-741-873B-4 2 US-09-741-873B-4 2 US-09-741-873B-2 2 US-09-741-873B-2 3 US-10-369-493-20638 6 US-10-369-493-141342 6 US-09-833-141342 1 US-09-833-141342 2 US-10-282-122A-64364 2 US-10-282-122A-64364 2 US-10-282-122A-64364 2 US-10-282-122A-64364 2 US-10-282-122A-64364 2 US-10-282-122A-652848 US-09-841-835-10 US-09-841-835-10 US-09-841-835-2 0 US-09-972-115A-8 SUMMARIES Query Match Length DB Result No.

Sequence 4, Appli	Sequence 53269, A	eguer	Sequence 108981,	Sequence 48048, A	Sequence 147748,	Sequence 2, Appli	Sequence 49757, A	Sequence 105413,	Sequence 56041, A	Sequence 275468,	Sequence 57763, A	Sequence 146, App	Sequence 67750, A	Seguence 6, Appli	Sequence 58683, A	Sequence 68152, A	Sequence 122263,	Sequence 47486, A	Sequence 1074, Ap	Sequence 590, App	Seguence 172276,	Sequence 26, Appl	Sequence 26, Appl	Sequence 749, App	Sequence 24, Appl	Sequence 64573, A	Sequence 16, Appl	Sequence 33, Appl	Sequence 115033,
-10-199-9	-282-1	-424-	-437-9	-282-	-437-	-311-4	-282-	-437-	-425-	-424-	US-10-425-114-57763	793-30	-425-	834-66	-282-122A	-425-	1-437-963-	-282-122A	-412-699B	0-374-780A	1-437-963-	-628-659-0	-021-811-	1-238-075-	905-176-2	0-282-	9-996-194-16	10-164-	10-437-963-1
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## ALIGNMENTS

US-01-11-8/30-4

Sequence A Application US/09741873B

Publication No. US2020081722A1

GENERAL INFORMATION:
APPLICANT: Normark, Staffan
APPLICANT: Normark, Staffan
APPLICANT: Normark, Staffan
APPLICANT: Normark, Staffan
APPLICANT: Normark, Staffan
APPLICANT: Normark, Staffan
APPLICANT: Normark, Staffan
APPLICANT: Normark, Staffan
APPLICANT: Normark, Staffan
CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR PLING DATE: 1999-11-26
PRIOR PLING DATE: 1991-11-06
PRIOR PLING DATE: 1991-11-03
PRIOR PLING DATE: 1994-01-28
PRIOR PLING DATE: 1994-01-28
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-01-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE PLEATION NUMBER: US 08/187,865
PRIOR FILING DATE: 1994-01-06
NUMBER OF SEQ ID NOS: 10
SOFTWARE PLEATION NUMBER: US 08/318,519
PRIOR FILING DATE: 1994-01-06
SOFTWARE PLEATION NUMBER: US 08/318,519
PRIOR FILING DATE: 1994-01-06
SOFTWARE PLEATION NUMBER: US 08/318,519
PRIOR FILING DATE: 1994-01-06
SOFTWARE PLEATION NUMBER: US 08/318,519
PRIOR FILING DATE: 1994-01-06
SOFTWARE PARE PARENTH VERSION 3.0 ö Gaps ; 0 Length 151; Indels Query Match 66.9%; Score 514; DB 12; Best Local Similarity 68.9%; Pred. No. 1.4e-43; Matches 104; Conservative 18; Mismatches 29; ORGANISM: Escherichia coli RESULT 1 US-09-741-873B-4 SEQ ID NO 4

1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ

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US-09-741-873B-2
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US-US-141-873B-4

PUBLICATION OF US20040096965A9

GENERAL INFORMATION:
APPLICANT: Normark, Staffan

APPLICANT: Normark, Staffan

TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation

TITLE OF INVENTION: Pibronectin Binding Protein As Well As Its Preparation

TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation

TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation

TITLE OF INVENTION: Pibronectin Binding Protein As Well As Its Preparation

TITLE OF INVENTION: WOMBER: US 09/741,873B

CURRENT FILING DATE: 1998-05-06

PRIOR FILING DATE: 1999-11-26

PRIOR PRILING DATE: 1991-11-06

PRIOR FILING DATE: 1991-11-03

PRIOR FILING DATE: 1994-01-28

PRIOR FILING DATE: 1994-01-05

PRIOR FILING DATE: 1994-10-05

NUMBER OF SEQ ID NOS: 10

SOUTHARE: PATENTIN VERSION 3.0
                                                                                          61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
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Publication No. US20020081722A1
GENERAL INFORMATION:
APPLICANT: Obsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 01289-084
CURRENT APPLICANTON UNMER: US/09/741,873B
CURRENT FILING DATE: 2003-04-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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66.9%; Score 514; DB 12; Length 15

Best Local Similarity 68.9%; Pred. No. 1.4e-43;

Matches 104; Conservative 18; Mismatches 29; Indels
                                                                                                                                                      121 NNAALVNOTASDSSVMVRQVGFGNNATANOY 151
                                                                                                                                                                                    121 GNGAAVDQTASNSSVNVTQVGFGNNATAHQY 151
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Sequence 2, Application US/09741873B

Dublication No. US20040096965A9

Fublication No. US20040096965A9

GENERAL INFORMATION:

APPLICANT: Normark, Staffan

APPLICANT: Olsen, Arne

TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation

FILE REPERENCE: 01289-084

CURRENT APPLICATION NUMBER: US/09/741,873B

CURRENT FILING DATE: 1998-05-06

PRIOR FILING DATE: 1998-05-06

PRIOR FILING DATE: 1998-05-04

PRIOR FILING DATE: 1991-11-06

PRIOR FILING DATE: 1991-11-06

PRIOR FILING DATE: 1991-11-06

PRIOR PLING DATE: 1994-01-28

PRIOR PLING DATE: 1994-01-28

PRIOR PLING DATE: 1994-01-05

PRIOR FILING DATE: 1994-01-05

PRIOR FILING DATE: 1994-01-06

PRIOR FILING DATE: 1994-01-06

PRIOR FILING DATE: 1994-01-06

PRIOR FILING DATE: 1994-01-06

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PRIOR FILING DATE: 1994-01-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VGQGSDDSSIDLIQRGFGNSATLDQWNGKNSEMTVKQPGGGNGAAVDQTASNSSVNVTQV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GVVPQYGGGGNHGGGGNNSGPNSELNTYQYGGGNSALALQTDARNSDLTITQHGGGNGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.8%; Score 436; DB 12; 65.6%; Pred. No. 7.7e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17; Mismatches
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1989-05-04
PRIOR FILING DATE: 1989-10-07/89,437
PRIOR PILING DATE: 1991-11-06
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR PILING DATE: 1991-11-03
PRIOR FILING DATE: 1994-11-03
PRIOR FILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PALENTIN VERSION 3.0
SEQ ID NO 2
LENGTH: 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Escherichia coli
US-09-741-873B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 GFGNNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 86; Conserv
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DB 12; Length 131;

56.8%; Score 436;

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RESULT 7

1 Sequence 21, Application US/09820843A

2 Sequence 21, Application US/09820843A

3 Fublication No. US20030039963A1

3 GENERAL INFORMATION:

4 APPLICANT COUNCIL OF Scientific and Industrial Research

5 TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTE

7 TITLE OF INVENTION: USFUL AS ANTI-INFECTIVES

7 TITLE OF INVENTION: USFUL AS ANTI-INFECTIVES

7 CURRENT APPLICATION NUMBER: US/09/820,843A

7 CURRENT FILING DATE: 2001-03-30

7 NUMBER OF SEQ ID NOS: 118

7 SOFTWARE: Patentin version 3.0

7 SOFTWARE: Patentin version 3.0
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 141342
LENGTH: 537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               400 EPAGTLP-----QMSATALLQXAAQMGATTSSYNAGGAGGASSLLRGASSHGISVGEGPA 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 WNGGSTNTGLANAGAGNTGFFDAGNYNFGSLNAGNINSFGNSGDGNSGFLNAGDVNSGV 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                Length 537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            455 NERSSYQNL----IMGSMA-SGGGGGGGFAGSFSGAS-----GFG 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 RNNATYDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVGFG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 WGGGGNHNGGGNSSGPDS---TLSIYQYGSANAALALQSDARKSETTI-
                                                                                                                                                                                                                                                                                                     ; CTHER INFORMATION: Clone ID: PAT_MRT4530_42455C.1.pep
US-10-437-963-141342
                                                                                                                                                                                                                                                                                                                                                                                  12.3%; Score 94.5; DB 16; 27.1%; Pred. No. 0.71;
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Pred. No. 0.47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Mismatches
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CTHER INFORMATION: PPE
NAME/KEY: misc_feature
CTHER INFORMATION: gi|1781260
US-09-820-843A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 12.2%;
1 Similarity 25.0%;
35; Conservative 16
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Best Local|Similarity 27.1%
Matches 45; Conservative
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                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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Publication No. US20030233675A1
GENERAL INFORMATION
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: BARRY S.
TITLE REFERENCE: 38-10(52052) B
CURRENT APPLICATION UNBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
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                                                                                                                                                                                                                         19 AAFAADSNIVVINQIGUDQQANIIQSGUGNSVGAFNGNSGFLQENGILSGA-NLLIVKQS 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 AAFAA-----IVVSGSALAGVVPQWGGGG-----NHNGG-----GNSSGPDSTLSIYQY 50
                                                                                                                                      1 GVVPQYGGGGNHGGGGGNNSGPNSELNTYQYGGGNSALALQTDARNSDLTITQHGGGNGAD 60
                                                                                               21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 DOLVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVGFGNNATANQ 150
                       Best Local Similarity 65.6%; Pred. No. 7.7e-36;
Matches 86; Conservative 17; Mismatches 28;
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DCATION: (1)..(445)

CORTION: (1)...(445)

COTHER INFORMATION: unsure at all Xaa locations

US-10-369-493-20638
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; Publication No. US20040123343A1
; GENERAL INFORMATION:
APPLICANT: LA ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-1
NUMBER OF SEQ ID NOS: 47374
LENGTH: 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Rhodopseudomonas palustris
                                                                                                                                                                                                                                                                                                  GFGNNATANOY 151
                                                                                                                                                                                                                                                                                                                                              121 GFGNNATAHÓY 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 44; Conserv
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Squence 49960, Application US/10425114

Sublication No. US2004034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: Screen, Seven E

APPLICANT: Screen, Seven E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 49960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  895 SGFLNVVAGASGI-----SGYLNVGALGSGVTNVGHTVSGFYNASALDLVTPAFASGLM 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 NAALALQSDARKSETTITQSGYGNGADVGQGADN-----STIELTQNGFRNNAT 102
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PRIOR APPLICATION NUMBER: 60/255,025

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-25

PRIOR FILING DATE: 2000-12-25

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-04

SOFTWARE: Patentin version 3.1

SEQ ID NO 64364

LENGTH: 2204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 YDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVM----VRQVGFGN 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: Clone ID: 700071884_FLI.pep
US-10-425-114-49960
                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Mycobacterium tuberculosis US-10-282-122A-64364
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 12.2%
Best Local Similarity 26.1%
Matches 43; Conservative
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ORGANISM: Zea mays
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US-10-425-114-49960
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Best Local S
Matches 33
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                                                Sequence 196554, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: About Withan
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICANTON PUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 196154
LENGTH: 498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Xu, H. WINTERTON: Identification of Essential Genes in Microorganisms FILE OF INVENTION: Identification of Essential Genes in Microorganisms FILE OF INVENTION: Identification of Essential Genes in Microorganisms CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT APPLICATION NUMBER: 00/191,078 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21 PRIOR PILING DATE: 2000-05-23 PRIOR PAPLICATION NUMBER: 60/207,727 PRIOR PAPLICATION NUMBER: 60/207,727 PRIOR PILING DATE: 2000-05-06 PRIOR PILING DATE: 2000-09-06 PRIOR APPLICATION NUMBER: 60/230,335 PRIOR PILING DATE: 2000-09-09 PRIOR APPLICATION NUMBER: 60/230,347 PRIOR APPLICATION NUMBER: 60/230,347 PRIOR APPLICATION NUMBER: 60/230,247 PRIOR APPLICATION NUMBER: 60/230,247 PRIOR PILING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DVGQGADNSTIEL----TQNGFRNNATYDQLVTRVVTHEMAHAGG-NNAALVNQTASDSS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             355 GSSNSDNNASQSDTSSEQNNKEGSSNSDNS--NDANQNGSNSNENANDNGNASHEAQNNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.2%; Score 94; DB 12; Length 498; 28.1%; Pred. No. 0.72; ive 24; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Clone ID: PAT_MRT3847_19152C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 64364, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Wall, Judith
APPLICANT: Trawick, John
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Yamamoto, Robert
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Best Local Similarity 28.1%
Matches 34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Glycine max
                                US-10-424-599-196154
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US-10-282-122A-64364
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APPLICANT:
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: 05/10/282,122A
CURRENT FILING DATE: 2003-02-20
REICR APPLICATION NUMBER: 60/291,078
PRIOR FILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PELICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
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29.5%; Pred. No. 4.8
                                                                                                                                                                              Sequence 62548, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 29.5
Matches 39; Conservative
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188 SGA 190
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RESULT 12 US-09-841-835-8 ; Sequence 8, Application US/09841835

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99 VAAADVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSPSSPGSSLABSPEAA 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGD-----VSRV--KRLVDAAN 206
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Patent No. US20020076795A1
GENERAL INFORMATTON:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THAT BINDS TO TRF1 AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9;
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Sequence 10, Application US/09841835
Sequence 10, Application US/09841835
Setent No. US2002006795A1
GENERAL INFORMATION:
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO T
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSES: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
                                                                                                                                                                                  ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17; Mismatches
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RR: 600-1-230 CIP1
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Pred. No. 1.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 VNAK - - DMAGRKSSPLHFAAGFG 227
                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFRENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 29.4%;
                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-841-835-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC OPERATING SYSTEM:
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US-09-841-835-10
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99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGD------VSRV--KRLVDAAN 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9; Length 1327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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PUBLICATION NO. US2003003769A1

GENERAL INFORMATION:
APPLICANT: Gerea Corporation
APPLICANT: Gregg, Morin B.
APPLICANT: Maler, Funk D.
ITILE OF INVENTION: A Second Mammalian Telomerase
FILE REFERENCE: 080/003C
CURRENT APPLICATION NUMBER: US/09/972,115A
CURRENT APPLICATION NUMBER: US 60/128,577
FRIOR APPLICATION NUMBER: US 60/129,123
FRIOR APPLICATION NUMBER: US 60/129,123
FRIOR APPLICATION NUMBER: US 60/129,123
FRIOR PILING DATE: 2000-04-10
FRIOR FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 64
SOFTWARE PATENTING VERSION 3.1
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65;
          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIPI
TELEPHONE: 201-487-5800
TELEPHONE: 201-437-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 133521 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.9%; Score 91.5; DB
29.4%; Pred. No. 4.3;
Live 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 NNAALVNQTASDSSVMVRQVGFG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207 VNAK--DMAGRKSSPLHFAAGFG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 29.4
Matches 42; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CRGANISM: Homo sapiens
US-09-972-115A-8
                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                        linear
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Best Local Similarity
Matches 42; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGD------VSRV--KRLVDAAN 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
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APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 29.4%; Pred. No. 2.9; Length 949;
Matches 42; Conservative 17; Mismatches 65; Indels 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/841,835 FILING DATE:
                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: JACKSON ESQ., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIPI
TELECOMMUNICATION INFORMATION:
TELECPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 NNAALVNQTASDSSVMVRQVGFG 143
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                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 2, Application US/09841835; Patent No. US20020076795A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 949 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                    COMPUTER READABLE FORM:
New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Hacke
STATE: New
COUNTRY: US
                                     07601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-841-835-10
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US-09-841-835-2
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Gaps

Db 158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGD------VSRV--KRLVDAAN 206
Qy 121 NNAALVNQTASDSSVMVRQVGFG 143
Db 207 VNAK--DMAGRKSSPLHFAAGFG 227

Search completed: August 2, 2004, 15:36:14 Job time : 37.8 secs

(Oldsu) Anold 9604 2141

GenCore version Copyright (c) 1993 - 2004

protein search, using sw model August 2, 2004, 14:48:33

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Run on:

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Sequence 7, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 55, Appli
Sequence 5834, Ap
Sequence 5834, Ap
Sequence 34, Appli
Sequence 34, Appli
Sequence 37, Appli
Sequence 37, Appli
Sequence 37, Appli
Sequence 39, Appli
Sequence 383, Ap
Sequence 5833, Ap
Sequence 5833, Ap
Sequence 5833, Ap
Sequence 20638, A
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Sequence 20638, A
Sequence 20638, A
Sequence 20638, A
Sequence 20638, A
                 Sequence 5, Ap
Sequence 57, App
Sequence 14, A
Sequence 22, A
Sequence 28, A
                                                          Sequence 1
Sequence 2
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Sequence 2
Sequence 3
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                                                                                                                                                                                                                                                                                                                                                      Sequence
  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEP'
FILE SPERENCE: 920043466
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 151
19 US-09-543-407-30
US-09-543-407-24
US-09-543-407-24
US-09-543-407-24
US-09-543-407-14
US-08-233-4407-12
US-09-543-407-12
US-09-543-407-12
US-09-543-407-12
US-09-543-407-12
US-09-543-407-12
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US-09-543-407-13
US-09-543-407-13
US-08-23-643-62
US-08-23-643-62
US-08-23-643-63
US-08-23-691-5834
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US-08-23-691-5834
US-08-23-691-5833
US-08-243-407-35
US-09-543-407-35
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US-09-543-407-35
US-09-543-407-35
US-09-543-407-35
US-09-733-089-23325
US-09-733-089-23323
US-09-733-089-23333
US-09-719-358
                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1
US-09-543-40,-30
Sequence 30, Application US/09543407
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                            237
217:5
1114.5
114:5
114:5
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101:5
99.5
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                                                                           / Search time 167.9 Seconds
(without alignments)
877.809 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                             1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                               6019581
             5.1.6
Compugen Ltd.
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hits satisfying chosen parameters: 6019581 segs, 976053577 residues

Total number of

Searched:

Gapop 10.0 , Gapext 0.5

BLOSUM62

Scoring table:

US-09-543-407-30 768

Perfect score:

Title:

Sequence:

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database

seq length: 0 seq length: 200000000

Minimum DB Maximum DB

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Query Match Length DB Score Result Š.

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CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-233-642A-57; Sequence 57; Application US/08233642A; GENERAL INFORMATION:
                                                                                                                                    ; TYPE: PRT
; ORGANISM: Salmonella enteritidis
US-09-543-407-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPACNE: (206) 622-4900
TELERAX: (206) 682-6031
TELEX: 3723836 SEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 amino acids
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Best Local Similarity 90.1
Matches 136, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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                                                                                                                                                                                                                                                                                                                    61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNAT------YDQLVTRVVT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNYDQLVTRVVT 120
                                                                                                                                                                 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALO 60
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                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Moran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.466
CURRENT FILING DATE: 2000-04-05
CURRENT FILING DATE: 2000-04-05
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO S. 59
SOFTWARE: FASLSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09543407

Sequence 5, Application US/09543407

GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: AAPLICANT: AAPLICANT: AS WIlliam W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGGUS PEPTIDE SEQUENCES
FILE REFREENCE: 920043.406

CURRENT APPLICATION NUMBER: US/09/543,407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                   Score 768; DB 19; Length 151;
Pred. No. 7e-73;
                                                                                                          Indels
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                                              100.0%; Score 768; DI
100.0%; Pred. No. 7e-
tive 0; Mismatches
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US-09-543-407-24
; Sequence 24, Application US/09543407
; GENERAL INFORMATION:
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                                                 Query Match
Best Local Similarity 100.
Matches 151; Conservative
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Best Local Similarity
  US-09-543-407-30
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                                                                                                                                          Gaps
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APPLICANT: Kay, william W.
APPLICANT: Collinson, S. Karen
APPLICANT: Clouthier, Sharon C.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: BASED VACCINES
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
Query Match

88.7%; Score 681; DB 19; Length 151;
Best Local Similarity 90.7%; Pred. No. 1.2e-63;
Matches 137; Conservative 2; Mismatches 12; Indels
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ZIPTE: Washington
COUNTRY: U.S.A.
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentle Forms:
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STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
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us-09-543-407-30.rapm

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61 ŞDARKSETŢŢŢĢSGYĞNGADVĞQĞADNŞŢĪELTQNĞFRNNATYBQLVTRVVTHEMAHAĞĞ 120
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Doran, James L.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

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APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: SOO043,406

CURRENT APPLICATION WUMBER: US/09/543,407

CURRENT APPLICATION WUMBER: US/09/543,407

CURRENT APPLICATION WUMBER: US/09/543,407

SOOTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 22

LENGTH: 151
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US-09-543-407-14

SQUENCE 14, Application US/09543407

SQUENCE 14, Application US/09543407

SQUENCE 14, Application US/09543407

APPLICANT: White, Aaron P.

APPLICANT: White, Aaron P.

APPLICANT: Kay, William W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

FILE REFERENCE: 920043.406

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT PILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FASLSEQ for Windows Version 4.0
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85.8%; Score 659; DB 19; Length 151;
Best Local Similarity 81.9%; Pred. No. 2.7e-61;
Matches 136; Conservative 0; Mismatches 0; Indels 30
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US-09-543-407-22
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LENGTH: 151
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61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHA-- 118
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                                                                                                                                                                                                                                                               0; Indels 30; Gaps
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APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMERIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
                                                    OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA porter information: sequence containing the replacement fragment orther information: encoding PT3 from GP63 of Leishmania major. US-09-543-407-22
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81.9%; Pred. No. 4.3e-61;
tive 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FRSESEQ for Windows Version 4.0
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ORGANISM: Artificial Sequence
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Best Local;Similarity 81.94
Matches 136; Conservative
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Best Local Similarity
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LENGTH: 151
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US-09-543-407-12; Sequence 12, Application US/09543407; GENERAL INFORMATION:

, APPLICANT: White, Aaron P.

151

121 NNAALVNQTASDSSVMVRQVGFGNNATANQY

3 10:54:46 2004

Tue Aug

DB 19; Length 151;

77.7%; Score 597;

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APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMERIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTERQ for Windows Version 4.0
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
FILE REPERENCE: 920043.406
CURRENT FILING DATON NUMBER: US/05/543,407
CURRENT FILING DATON NUMBER: US/05/543,407
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASLSEQ for Windows Version 4.0
LENGTH: 151
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78.1%; Score 600; DB 19;
Best Local Similarity 81.5%; Pred. No. 4.9e-55;
Matches 123; Conservative 4; Mismatches 24;
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|21 NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
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Best Local Similarity 80.8
Matches 122; Conservative
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US-09-543-407-26
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LENGTH: 151
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61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGGUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 151
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APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 92004-406
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA, OTHER INFORMATION: sequence containing the replacement fragment, OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-18
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121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                      ; Sequence 18, Application US/09543407; GENERAL INFORMATION:
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GENERAL INFORMATION:
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                                                                                            RESULT 10
US-09-543-407-18
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61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: NORMARK.
TITLE OF INVENTION FIRENDECTIN BINDING PROTEIN AS WELL AS ITS PREPARATION
FILE REPERENCE: 012889-081
CURRENT APPLICATION NUMBER: US/08/978,878
CURRENT PILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: SE 8801723-1
EARLIER PILING DATE: 1988-05-06
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GENERAL INFORMATION:
APPLICANT White, Aaron P.
APPLICANT Doran, James N.
APPLICANT Collinson, S. Karen
APPLICANT Collinson, S. Karen
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                                OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                     Length 151;
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                                                                                                                                                                                              Query Match 73.7%; Score 566; DB 19; Length 1: Best Local Similarity 80.8%; Pred. No. 2e-51; Matches 122; Conservative 5; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM; Escherichia coli
US-09-543-407-7
                                                                                                                                    US-09-543-407-16
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US-08-978-878-4
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                                                                                                                                                                                                                                                                                 61 VGQGADNSTIELTQNGFRNNATIDQWNAKONSDITVGQYGGNNAALVNQTASDSSVMVRQV 120
                                                                                                                                                                                                                                     SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQV 140
                                                                                                    1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                 1 MKLLKVAAFAAIVVSGSALAGVVPOWGGGGNHNGGGNSSGPDSTLSIYOYGSANAALALO 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 31, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
TITLE OF INVENTION: BRCTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT PILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFFWARE: FastSEQ for Windows Version 4.0
                                Gaps
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 151
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Pred. No. 1e-54;
5; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 594; DB 19;
Pred. No. 1.8e-54;
2; Mismatches 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       121 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
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US-09-543-407-16
Sequence 16, Application US/09543407
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Salmonella enteritidis US-09-543-407-31
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Best Local Similarity 89.3%;
Matches 117; Conservative
81.5%;
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ORGANISM: Artificial Sequence
Best Local Similarity 81.53
Matches 123; Conservative
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US-09-543-407-31
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Sequence 21, Appli
Sequence 301344,
Sequence 30134,
Sequence 312468,
Sequence 34512,
Sequence 35751, Appl
Sequence 49, Appl
Sequence 49, Appl
Sequence 7907, Appl
Sequence 7907, Appl
Sequence 7907, Appl
Sequence 11109, Appl
Sequence 11109, Appl
Sequence 1109, Appl
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9194, Ap
                                                                      August 2, 2004, 14:49:38; Search time 17.8 Seconds (without alignments) 888.146 Million cell updates/sec
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                                                                                                                      US-09-543-407-30
768
1 MKLLKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151
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Sequence
Sequence
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1: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/USO3_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO3_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO3_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/USO3_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USO3_NEW_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-741-873C-2
US-10-425-115-301334
US-10-425-115-301334
US-10-425-115-301334
US-10-425-115-301334
US-10-425-115-301334
US-10-425-115-301334
US-10-425-115-301334
US-10-425-115-301391
US-10-10-205E-741
US-10-425-115-304391
US-0-56-632-7907
US-0-56-632-7907
US-0-56-632-7906
US-0-579-062-7906
US-0-579-062-7906
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Maximum Match 100%
Listing first 45 summaries
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Match 1
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No.
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APPLICANT Normark, Staffan
APPLICANT Olsen, Arne
TITLE OF INVENTAURON: Fibronectin Binding Protein As Well As Its Preparation
TITLE OF INVENTAURON: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084
CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT APPLICATION NUMBER: US 8801723-1
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-04
PRIOR FILING DATE: 1998-11-26
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1991-11-06
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR APPLICATION NUMBER: US 07/789,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR PRIUNG DATE: 1994-10-28
PRIOR PILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PARCETIN VARIABE: PARCETIN NUMBER: US 08/318,519
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 11
Sequence 9194, Ap Sequence 17.5 Appli Sequence 17.5 Appli Sequence 9810, Ap Sequence 343835, Sequence 11, Appl Sequence 285214, Sequence 385214, Sequence 34256, Sequence 511, Ap Sequence 511, Ap Sequence 1872, Ap Sequence 1872, Ap Sequence 190187, Sequence 1872, Ap Sequence 1872, Ap Sequence 1872, Ap Sequence 1872, Ap Sequence 1872, Ap Sequence 1872, Ap Sequence 1872, Ap Sequence 180187, Ap Sequence 180187, Ap Sequence 180187, Ap Sequence 180187, App Sequence 180187, Ap Sequence 180187, Ap Sequence 180187, Ap Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, App Sequence 180187, Ap
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9807, Ap
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                                                                                                                                                                                                                                                                                                                                                     Sequence 3
Sequence 2
Sequence 3
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; Pred. No. 3.7e-37;
18; Mismatches 29; Indels
US-60-579-062-9194
US-10-491-73-2
US-09-248-7954-175-9
US-60-581-351-9810
US-10-10-68-7968
US-10-10-68-7968
US-10-778-804-11
US-10-178-804-11
US-10-425-115-285216
US-10-425-115-285216
US-10-425-115-342526
US-10-425-115-342526
US-10-425-115-342526
US-10-6854-439-511
US-10-854-439-511
US-10-854-135-190187
US-60-581-35-190187
US-60-581-35-190187
US-10-864-138-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 4; Application US/09741873C; GENERAL INFORMATION:
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Best Local Similarity 68.99
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT;
; ORGANISM: Escherichia coli
US-09-741-873C-4
    758
376
630
630
1358
201
201
1127
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631
132
1132
1132
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    US-09-741-873C-4
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34; Conservative
Best Local Similarity
Matches 34; Conserv
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US-10-425-115-300390
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                                                                                                                 APPLICANT: Olsen, Arme
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 01289-084
CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT APPLICATION NUMBER: US 8801723-1
PRIOR APPLICATION NUMBER: US 8801723-1
PRIOR FILING DATE: 1999-10-26
PRIOR FILING DATE: 1999-11-26
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR FILING DATE: 1999-11-06
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR FILING DATE: 1999-11-06
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1991-11-06
PRIOR PELING DATE: 1994-10-05
PRIOR APPLICATION NUMBER: US 08/318,519
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PREDITTION NUMBER: US 08/318,519
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 11

LENGTH: 131

LENGTH: 131

LENGTH: 131
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; Sequence 21, Application US/10479638
; GENERAL INPORMATION:
; APPLICANT: Don A. Roth
; APPLICANT: The University of Wyoming
; TILE OF INVENTION: Expression of Spider Silk Proteins in Higher Plants
; TILE OF INVENTION: Expression of Spider Silk Proteins in Higher Plants
; TILE OF INVENTION: Expression of Spider Silk Proteins in Higher Plants
; CURRENT APPLICATION NUMBER: US/10/479,638
; CURRENT APPLICATION NUMBER: DCT/US02/18256
; PRIOR FILING DATE: 2002-66-06
; PRIOR FILING DATE: 2002-66-06
; PRIOR FILING DATE: 2001-66-06
; PRIOR FILING DATE: 2001-66-06
; RIOR FILING DATE: 2001-66-06
; SEQ ID NOS: 54
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
LENGTH: 520
; TYPE: PRT
; ORGANISM: Argiope trifasciata
US-10-479-638-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 VGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 VGQGSDDSSIDLTQRGFGNSATLDQWNGKNSEMTVKQFGGGNGAAVDQTASNSSVNVTQV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GVVPQYGGGGNHGGGGNNSGPNSELNTYQYGGGNSALALQTDARNSDLTITQHGGGNGAD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 GVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 520;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.8%; Score 436; DB 5; Length 13
65.6%; Pred. No. 1.7e-30;
tive 17; Mismatches 28; Indels
                                              Sequence 2, Application US/09741873C GENERAL INFORMATION:
APPLICANT: Normark, Staffan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 65.67
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 GFGNNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-741-873C-2
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Sequence 300390, Application US/10425115

Sequence 300390, Application US/10425115

Sequence 300390, Application US/10425115

APPLICANT: La Rosa, Thomas J.

APPLICANT: Exvalic, David K.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21 (53222) B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 300390

LENGTH: 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: La Rovalicu:
APPLICANT: La Rovalic. David K.
APPLICANT: Sovalic. David K.
APPLICANT: Thou, Yihua
APPLICANT: Caou, Yorkua
APPLICANT: Cao, Yorguan
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (5322) B
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 301334
LENGTH: 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---ATGGG 182
                                                                                                                                                                        74 GYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGNNAALVNQTASDS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 SALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDA----RKSETTITQ 72
                                                                     15 SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSET-TITQS
                                                                                                        347 AGAGAAAASAGAGAGAGGYGGGYGVAGGSS----ISYGATSSSATSSSTASSSRSGIVTSG
                                                                                                                                                                                                        13;
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Best Local Similarity 25.2%; Pred. No. 1.5;
Matches 38; Conservative 15; Mismatches 51; Indels 4
                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 GGMGGGADGAYGSGAGGGVGKGQGESGVALAPSSDGYYNGGAAD----
                     99
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US-10-425-115-301334
24.6%; Pred. No. 0.68;
tive 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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Sequence 301334, Application US/10425115
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                             157 --VISNIFSGVSSSAGSY 472
                                                                                                                                                                                                                                                                             134 SVMVRQVGFGNNATANQY 151
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ORGANISM: Zea mays
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APPLICANT ADAMS, Mark
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE REFERENCE: CLOOD381
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: Patentin version 3.2
SEQ ID NO 35751
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ADAMS, Mark
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT APPLICATION NUMBER: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                             64 IDGILGSLGGGGGGGLTGGGGGNKENAQADSGNAQEGSGNA----QEDSGNAQ--- 116
                                                                                                                                                                                                                                                                                                                                                                                          TQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGNNAALVN-QT 129
                                                                                                                                                                                                                                                                                                                                                                                                                       65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGD------VSRV--KRLVDAAN 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
                                                                                                                                                                                                                                                                                                19 LAGVVPQWGGGG------NHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTI
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                                                                                                                                                                                                        Length 179;
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                                                                                                                                                                                                        9
                                                                                                                                   OTHER INFORMATION: Clone ID: MRT4577_78839C.1.pep
                                                                                                                                                                                                     11.9%; Score 91.5; DB 27.7%; Pred. No. 1.5; iive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 35751, Application US/10170205E GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 VNAK--DMAGRKSSPLHFAAGFG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 ASDSSVMVRQVGFGNNATANQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 QIEGEDEQAQGNAGNENAAEE 176
NUMBER OF SEQ ID, NOS: 369326
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Best Local Similarity 29.4%
The A2; Conservative
                                                                                                                                                                                                                           Best Local Similarity 27.73
Matches 39, Conservative
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US-10-170-205E-35751
                                                             TYPE: PRT
ORGANISM: Zea mays
FEATURE:
                                                                                                                                                         US-10-425-115-346132
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US-10-170-205E-35751
                 SEQ ID NO 346132
LENGTH: 179
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US-10-170-205E-741
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 312468
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Lou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPRENCE: 38-21(53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
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                                                                                                                                                                                                                                                                                                                                                                                            133 GGMGGGANGAYGSGAGGGVGKGEGVSGVALAPSSNGYYNGGAAD-----ATGGG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 YGGGYSSGGGYSSG-GYAANGYGVGSGSGNYSNASGGGYSGS----DGYGNGAASGGYA 192
                                                                                                                                                                                                                                                                                                  17 SALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGNN-----AALVNQTASDSS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                          12.1%; Score 93; DB 6; Length 258; 26.8%; Pred. No. 1.7; tive 16; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: MRT4577_37025C.1.pep
US-10-425-115-300390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: MRT4577_48027C.1.pep
US-10-425-115-312468
                   LOCATION: (1)..(258)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-425-115-312468
; Sequence 312468, Application US/10425115
; GENERAL INFORMATION:
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; Sequence 346132, Application US/10425115
; GENERAL INFORMATION:
                                                                                                                                                                      Query Match
Best Local Similarity 26.84
Matches 33, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 30.28
Matches 35; Conservative
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 NNA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGA 184
              NAME/KEY: unsure
LOCATION: (1)..(:
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Sequence 17306, Application US/09248796A
Sequence 17306, Application US/09248796A
GENERAL INPORMATION:
TILLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TILLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
TILLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
TILLE REPERIOR: 10196-132
CURRENT PAPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 17306
LENGTH: 388
                                              TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With FILLE OF INVENTION: Plants FILE REFERENCE: 38-21(5322)B CURRENT APPLICATION NUMBER: US/10/425,115 ... CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 369326 SEQ ID NO 304391 LENGTH: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G--QGADNSTIELTQNGFRNNATYDQL-VTRVVTHEMAHAGGNNAALVNQTASDSSVMVR 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 QSGYGNGADVGQ--GADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGNNAALVN-Q 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 -GGTGGGGAGGAMNSNAQGSGSGTGSGSSYANRYWYGSNEAGASANGNGGGTGNSQ 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 SGSALAGVVPQWGGGGNHNGGGNSSGPDSTLS---IYQYGSANAALALQSDARKSETTIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.5%; Score 88.5; DB 6; Length 197; 27.3%; Pred. No. 3;
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27.1%; Pred. No. 6.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Clone ID: MRT4577_40676C.1.pep
                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/FEXY: unsure
1)..(197)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 NGGGGGGGGAGSGYGNAXTPSFY 196
Kovalic, David K.
Zhou, Yihua
Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 QVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 27.3
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
US-09-248-796A-17306
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                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches
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Sequence 49 Application PC/TUS0402338

SEQUENCE ALL INFORMATION:
TITLE OF INVENTION: MAPCAXS AS MODIFIERS OF THE APC AND AXIN PATHWAYS AND METHODS OF TITLE OF INVENTION: USE
FILE REFERENCE: EXA-0030-CPC
CURRENT APPLICATION NUMBER: US60/443,484
PRIOR APPLICATION NUMBER: US60/447,358
PRIOR APPLICATION NUMBER: US60/447,358
PRIOR FILING DATE: 2003-02-10
PRIOR FILING DATE: 2003-02-11
PRIOR FILING DATE: 2003-04-10
PRIOR FILING DATE: 2003-04-10
PRIOR FILING DATE: 2003-04-10
PRIOR FILING DATE: 2003-05-14
PRIOR PILING DATE: 2003-05-14
PRIOR FILING DATE: 2003-05-14
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                                                                                                                                                                                                                                                                                             99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPESSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                                                                                                                                                                                                                                                                                                                 65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
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                                                                                                                                                                                                                                                                                                                                                                                                                  -----VSRV--KRLVDAAN 206
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                                                                                                                                                                                                                                                               6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
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11.9%; Score 91.5; DB 1; Length 1327;
Best Local Similarity 29.4%; Pred. No. 15;
Matches 42; Conservative 17; Mismatches 65; Indels 19,
                                                                                                                                                        Length 1203;
                                                                                                                                                        11.9%; Score 91.5; DB 6; Length 1 larity 29.4%; Pred. No. 13; Conservative 17; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGD--
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GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
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     ; SEQ ID NO 741
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-205E-741
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Best Local Similarity
Matches 42; Conserv
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US-10-425-115-304391
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PCT-US04-02338-49
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MS-10-425-115-254240
Sequence 254240, Application US/10425115
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                                                                                                                                                                        81 VGQGADN-STIELTQN------GFRNNATYDQLVTRVVTHEMAHAGGNNA 123
                                                                                                                                                                                                                 300 AAQGTDNGAAABINTGNADPAQGNDNGAAABNSGNENGTAABNNANADVQNDAAQVNDNGA 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 --GADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGNNAALVNQT-----ASDSS 134
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                                                             30 GNHNGGG--NSSGPDSTLSIYQYGSANAALA-----LQSDARKSETTITQSGYGNGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 GGGGNHNGG---GNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQ
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           54; Indels
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11.3%; Score 86.5; DB 6;
Best Local Similarity 26.9%; Pred. No. 4.3;
Matches 35; Conservative 15; Mismatches 53;
           16; Mismatches
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Job time : 18.8 secs
           34; Conservative
                                                                                                                                                                                                                                                                                 124 ALVNOTASDSS 134
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ORGANISM: Zea mays
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                                                                                                                                                                           APPLICANT: Monsanto Technology, LLC
APPLICANT: Baum, James A
APPLICANT: Baum, James A
APPLICANT: Evovalic, David K.
APPLICANT: Larcas, Thomas J.
APPLICANT: Larcas, Thomas J.
APPLICANT: Larcas, Thomas J.
APPLICANT: Munyikwa, Tichifa R. I.
APPLICANT: Roberts, James K.
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Wo, Wei
APPLICANT: Wo, Wei
APPLICANT: Shang, Bei
TITLE OF INVENTION: Mchods for Genetic Control of Insect Infestations in Plants and
TITLE OF INVENTION: Compositions Thereof
CURRENT APPLICATION NUMBER: US/60/565,632
CURRENT APPLICATION NUMBER: 2004-04-27
NUMBER OF SEQ ID NOS: 15449
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Baum, James A
APPLICANT: Baum, James A
APPLICANT: Baum, James A
APPLICANT: Baum, James J
APPLICANT: Lu, Maolong
APPLICANT: Lu, Maolong
APPLICANT: Munyikwa, Tichifa R. I.
APPLICANT: Moberts, James K
APPLICANT: APPLICANT: Wa, Wei
APPLICANT: Ziang, Bei
TITLE OF INVENTION: Compositions thereof
FILE REPERENCE: 38-21 (53403) C
CURRENT APPLICATION NUMBER: US/60/579,062
CURRENT APPLICATION NUMBER: US/60/579,062
CURRENT APPLICATION NUMBER: US/60/579,062
CURRENT PILING BATE: 2004-06-11
NUMBER OF SEQ ID NOS: 414445
SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 GNHNGGG--NSSGPDSTLSIYQYGSANAALA-----LQSDARKSETTITQSGYGNGAD 80
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Pred. No. 12;
16; Mismatches
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Pred. No. 12;
                                                                                                                               Sequence 7907, Application US/60565632 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7907, Application US/60579062
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Diabrotica virgifera
US-60-565-632-7907
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US-60-579-062-7907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 26.0%;
Matches 34; Conservative 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.4%;
26.0%;
240 GAGFGDNSNTSSY 252
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Best Local Similarity
                                                                              RESULT 13
US-60-565-632-7907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
US-60-579-062-7907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 7907
LENGTH: 573
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 2, 2004, 14:39:53 ; Search time 9.4 Seconds (without alignments) 1545.204 Million cell updates/sec

US-09-543-407-30 768 1 MKLIKVAAFAAIVVSGSALA......DSSVMVRQVGFGNNATANQY 151 Title: Perfect score: Sequence:

Scoring table:

283366 seqs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	in prote	$\Xi$	curlin protein cag	curlin major subun	hypothetical prote	curlin nucleator p		curlin minor chain	cnjB protein - Tet	fimbrin protein ad	nucleation compone	hypothetical qlyci	d hyp	hypothetical prote	probable PPE prote	prot	PE prot	prot	prot	probable PPE prote	DNA-binding protei	ovo protein - frui	protein kinase sgg		21 protein	probable adhesin h	urface anti	le disease	e PPE prot
SUMMARIES	ID	~	~	~	0	10	S70787	C30806										B70663									F03	9785	468	7052
	DB	0	~1	N	7	N	~	N	(1	~	C)	(1)	~	N	Ŋ	C)	N	N	N	~1	C)	7	7	(7)	N	~	~	7	7	7
	Length	15	15	15	15	15	15	7	15	174	15	15	217	14	14	64	31	32	65	25	220	102	121	57	40	57	191	65	44	96
æ	Query	88.7	œ	7	S	IJ	3	m	3	3	3	m	3	2	7	3	N	a	$^{\circ}$	$^{\circ}$	$^{\circ}$	N	N	2	н	ч	н.	М	н	-
	Score	681	681	Ŋ	02	02	9	104.5	9	Н	σ	99.5	σ	9 8		97.5	9	94		93.5	m	N	CA.		н	91.5	Н	16	90.5	σı
	Result No.	•	7	m	4	Ŋ	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	23 09	70

	probable exported	hypothetical prote	nuclear pore compl	hypothetical prote	sericinlB - silkwo	hypothetical prote	hypothetical prote	probable nucleopor	probable PPE prote	probable PPE prote	large repetitive p	tail fiber protein	leishmanolysin (EC	outer membrane pro	probable PPE prote	leishmanolysin (EC
	AH0038	T05221	B44402	S66852	S52714	T21956	T26667	T50074	B70987	E70946	AD0835	800275	A45621	E64559	F70675	C42049
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	1238	343	959	296	1217	407	586	1778	1053	590	3624	262	590	745	582	639
	11.7	11.6	11.6	11.5	11.5	11.5	11.5	11.5	11.4	11.3	11.3	11.3	11.3	11.3	11.2	11.2
-7:	89:5	89	68	88.5	88.5	88	88	88	87:5	87	87	86:5	86:5	86:5	98	9 .
	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

	RESULT 1	
	fimbrin pr	
	C.Species:	Cibbocies: Salmonella enfertidis Cibate: 31-Dec.1996 #semience revision 31-Dec.1996 #text channe 08-Oct-1999
	C, Accessio	,
	R;Collinso	nn,:S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.
	A,Title: S	A)Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fimbriae. A:Reference mimber: IC6019: MITD:06146512: DMTD:8560497
	A; Accession: JC6039	n: (UC6039
	A;Molecule A;Residues	A;Molecule type: DNA A;Residues: 1-151 <col/>
	A; Cross-re	A, Cross-references: GB: U43280; NID: g1184712; PIDN: AAC43599.1; PID: g1184714
	A; Accessio A; Molecule	n: PC6015 : type: protein
	A; Residues	A; Residues: 21-52 < CO2>
	A; Experime	ntal source: strain 27655-3b a anthors translated the order ACC for residue 44 an Tlo
	R, Collinso	hydria manning the mody L.; Muller, K.H.; Trust, T.J.; Kay, W.W.
	J. Bacteri	
	A;Titie: F	WINITICATION AND CNATACTERIZATION OF THIN, AGGREGATIVE IIMDRIAE IFOM SAIMONEII — himber: 144888: MITH:0111686: DMTD:147327
	A; Contents	: 27655
	A; Accession: A44898	n: A44898
	A; Status:	A;Status: preliminary
	A;Molecule A:Residues	A!Molecule type: protein A:Regidnes: 21-33 <7073
	A; Note: se	A;Note: sequence extracted from NCBI backbone (NCBIP:45936)
	C, Genetics:	u
	C:Function:	EA.
	A, Descript	on: major component of thin aggregative
	A;Note: Ilmorlae Dil	2
	F;1-20/Dom	Civernos : Institute aguence #status predicted <sig> Fig.1-20/Domain: signal sequence #status predicted <sig> Fig.1-15/(Prodint: fimbin protein anti-theratus experiments) which</sig></sig>
	3/TCT_T7/3	#פרשרתפ פאהפדדוופוורשד
	Query Ma Best Loca Matches	Query Match Best Local.Similarity 90.7%; Pred. No. 3.3e-49; Matches 137; Conservative 2; Mismatches 12; Indels 0; Gaps 0;
	67	Ì MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
	Db	1 MKLEKVAAFAAIVVSGSALAGVVPQWGGGONHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
	δý	61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
	ΩÞ	61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQMNAKNSDITVGQYGG 120
	ð	121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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csg

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Curin major subunit CsgA [imported] - Escherichia coli (strain O157:H7, substrain RIMD C.Species: Escherichia coli C.Species: Escherichia coli C.Species: Bs.Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C.Accession: D90806 C.Accession: D90806 C.Accession: D90806 C.Accession: D90806 C.Accession: D90806 C.Accession: D.Y. Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Yokoyama, K.; Han, C.G. DNA Res: 8, 11-22, 2001 A.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DA, Alitle: Complete genome sequence of enterchemorrhagic Escherichia coli O157:H7 and gency A, Reference number: A99629; MUD:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Description: major component of wild-type curli, interaction between CsgA and CsgB tri
A,Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli that
and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-151/Product: curlin #status experimental <MAT>
A,Title: The RpoS sigma factor relieves H-NS-mediated transcriptional repression of A,Reference number: S31202; MUID:93211294; PNID:8459772
A,Rocession: S31202
A,Molecule type: DNA
A,Rocesicule type: DNA
A,Cossicules: 1-6, 'V', 8-15 < OLS1>
A,Cossicules: EMBL:L04979
A,Rocession: S34560
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A;Cross-references: GB:BA000007; PIDN:BAB34843.1; PID:g13360880; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKLIKVAAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSELNIYQYGGGNSALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKLLKVAAFAAIVVSGSALAGVVPQW-GGGGNHNGGGNSSGPDSTLSIYQYGSANAALAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: DNA
A,Residues: 1-13, RQRDSGWLW' <0LS3>
A;Cross-references: EMBL:L04979; NID:9230424; PIDN:AAA23616.1; PID:9230425
A;Experimental source: strain K-12, substrain W3110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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ilarity 68.4%; Pred. No. 1.6e-34;
Conservative 18; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 517; DB 2;
Pred. No. 1e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 GNGAAVDOTASNSSVNVTOVGFGNNATAHÓY 151
                                                                                                                                                                                                                                                                           A, Molecule type: protein
A, Residues: 21-42;44-50 <01.52>
R;Olsen, A.N.; Armqvist, A.M.
submitted to the EMBL Data Library, October 1992
A, Reference number: S34559
A, Accession: S34559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 67.3°
Best Local Similarity 69.5°
Matches 105; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C,Genetics:
A,Gene: csgA
A,Map position: 23.15
C,Function:
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Simi
Matches 104;
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A,Gene: ECs1420
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NyAlternate names: csgA protein; major curlin protein

C,Species: Escherichia coli

C,Species: Escherichia coli

C,Species: 12-Peb-1998 #text_change 01-Mar-2002

C,Accession: 570788, G4846; S31302; S34569; S34559

R;Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S.

Mol. Mcrobiol. 18, G41840; J995

R;Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S.

Mylitle: Expression of two csg operons is required for production of fibronectin- and CA

A;Reference number: 570783; MUID:96414468; PMID:8817489

A;Reference number: 570783; MUID:96414468; PMID:8817489

A;Retern mucleid acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Resperimental source: strain K12, substrain W3110

A;Rose, D.J; Mau, B.; Shao, Y.

Sience 277, 1453-1464 sequence was submitted to the EMBL Data Library, August 1995

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Reference number: A64720; MUID:97426617; PMID:9278503

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A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                    Cydes: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
Cydcession: Al635
Kyarkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Mature 413, 848-852, 2001
Mature 413, 848-852, 2001
Myature 413, 848-852, 2001
Myature 513, 848-852, 2001
Myature 513, 848-852, 2001
Myature 513, 848-852, 2001
Myature 513, 848-852, 2001
Myature 513, 848-852, 2001
Myature 513, 848-852, MulD:21534947; PMID:11677608
Myaccession: Al0652
Myaccession: Al0652
Myaccidue: 1512 cpan
Myaccidues: 1-151 cpan
Myaccidues: 1-151 cpan
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R;Olsen, A.; Arnqvist, A.; Hammar, M.; Sukupolvi, S.; Normark, S. Mormolvi, J. 523-536, 1993
                                                                                                                                                                                                               - Salmonella enterica subsp. enterica serovar Ty
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                      major curlin chain precursor [imported] - Salmonella enterica subsp. enteric
C;Species: Salmonella enterica subsp. enterica servora Typhi
A;Note: this species has also been called Salmonella typhi
A;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
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Pred. No. 3.3e-49;
2; Mismatches 12,
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                                             NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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Best Local Similarity 90.7%;
Matches 137; Conservative
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A,Description: minor component of wild-type curli, interaction between CsgA and CsgB tr A,Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli that and H-kinindgen; in the absence of CsgA, CsgB can self-assemble into polymers
F;1-21/Domain: signal sequence #status predicted <SIG>F;22-151/Product: minor curlin chain #status predicted <MAT>
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Date: 10-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
R;Perna, NT:; Plunkett III, G;; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca
Nature 409, 529-533, 2001
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A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: G85665

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-151 <STO>

A;Cross-references: GB:AE005174; NID:g12514573; PIDN:AAG55787.1; GSPDB:GN00145; UWGP:Z1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               minor curlin subunit precursor CsgB [imported] - Escherichia coli (strain O157:H7, si CiSpecies: Escherichia coli CiSpecies: Escherichia coli CiSpecies: Escherichia coli CiSpecies: 18-Jui-2001 #sequence_revision 18-Jui-2001 #text_change 18-Jui-2001 GiAccession: C90806

R;Hayashi, T;, Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, Sasawara, N.; Yashi, K.; Yokoyama, K.; Han, M.; Hayashi, T;, Makino, K.; Ohnishi, M.; Shiba, T.; Hattori, M.; Shinagawa, H.
A;Hille: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and A;Accession: C90806
A;Status: préliminary
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A;Crossreferences: GB:BA000007; PIDN:BAB34842.1, PID:g13360879; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 AAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAĞTNNSAQLRQĞGSKLLAVVAQEĞS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 RNNATYDQLVTRVVTHEMAH----AGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNNATYDQLVTRVVTHEMAH - - - AGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNRAKIDQ----TGDYNLAYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQY
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13.6%; Score 104.5; DB 2;
Best Local Similarity 29.1%; Pred. No. 0.087;
Matches 34; Conservative 15; Mismatches 57;
                  source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                               ; Score 104.5; DB
; Pred. No. 0.087;
15; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                               13.6%;
29.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                    23.15
       A;Experimental sc
C;Genetics:
A;Gene: csg8;
A;Map position: 2
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NyAlternate names: csgB protein; curlin nucleation component; minor curlin protein
C;Species: Escherichia coli
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 01-Mar-2002
C;Accesion: $707897, F64846

R;Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S.
Mol. Microbiol. 18, 661-670, 1995

A;Title: Expression of two csg operons is required for production of fibronectin- and Cc
A;Reference number: $70783; MUD:96414468; PMID:8817489

A;Reference number: $70783; MUD:96414468; PMID:8817489

A;Ression: $70787

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                                                                                                                                                                                                                                                                                                                                       Apportherical protein csgA [imported] - Escherichia coli (strain O157:H7, substrain EDL93 C, Species: Escherichia coli (Species: Escherichia coli (Species: Escherichia coli (Species: Escherichia coli (Species: Escherichia coli (Species: Escherichia coli (Species: Escherichia coli (Species: Escherichia coli (Species: Escherichia (Species: N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew Inler: A.; Grotheck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, N.Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A, Reference number: A85480; MUID:21074935; PMID:11206551
A, Accession: H8565
A, Status: preliminary
A, Residues: DNA
A, Residues: DNA
A, Residues: 1-152 < STO>
A, Cross-references: GB:ABC05174; NID:g12514574; PIDN:AAG55788.1; GSPDB:GN00145; UMGP:216
C, Genetics:
A, Gene: csgA
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A,Residues: 1-151 <BLAT>
A,Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74125.1; PID:g1787278;
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Gaps
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68.4%; Pred. No. 1.6e-34;
live 18; Mismatches 29;
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Best Local Similarity 68.4%
Matches 104; Conservative
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Salmonella enterica sero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aggregative fimbriae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C,Function:
A,Description: minor component of thin aggregative fimbriae
A,Note: fimbriae bind to fibronectin, plasminogen, tissue plasminogen activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4,
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                                                                                                                                                                                                                                                                     fimbrin protein agfB precursor - Salmonella enteritidis
C,Species: Salmonella enteritidis
C,Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999
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R/Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.
J. Bacteriol. 178, 662-667, 1996
A, Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fila, Reference number: JC6039, MUID:96146512; PMID:8550497
A,Accession: JC6040
A,Rolecule type: DNA
A,Residues: 1-151 < COD.
A,Residues: 1-151 < COD.
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R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, J. S.; Moule, S.; O'Gare, P.
Nature 413, 848-852, 2001
A, Authors: Parry, C.; Quall, M.; Rutherford, K.; Simmonds, M.; Skein, A; Title: Complete genome sequence of a multiple drug resistant Sala, A; Reference number: AB0502; MUID:21534947; PMID:11677608
A; Accession: AH6635
A; Statuts: preliminary
A; Molecule type: DNA
A; Residues; 1-151 cPAR>
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1723 WGSNNQAS 1730
142 FGNNATAN 149
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Best Local Similarity
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Best Local Similarity
Matches 33; Conserv
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                                                                                                                                                                                                                                                                                                                      38 SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGF 97
                                                                                                                                                                                                                                                                                                                                                                       21 AAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNRAKIDQ----TGDYNLAYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNNATYDOLVTRVVTHEMAH----AGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                   Length 151;
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                                                                                                                                                                                                                                        Indels
        strain O157:H7, substrain EDL933
                                                                                                                                                           13.6%; Score 104.5; DB 2; 29.1%; Pred. No. 0.087; ive 15; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 13.2%; Score 101; DB 2; Best Local Similarity 29.7%; Pred. No. 2.6; Matches 38; Conservative 18; Mismatches 32;
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                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                   Query Match
Best Local Similarity
Matches 34; Conserva
            A,Experimental source:
C,Genetics:
A,Gene: csgB
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hypothetical protein AGR L_228 [imported] - Agrobacterium tumefaciens (strain C58, Ceres Species: Agrobacterium tumefaciens agrobacterium tumefaciens (5) Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens 20-0ct-2001 #sequence_revision 22-0ct-2001 #text_change 18-Nov-2002 C; Accession: H98144

R;Goodner, B; Hinkle, G; Gattung, S; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman A; Iiu, F; Wollam, C; Allinger, M.; Doughty, D; Scott, C; Lappas, C; Markelz, B. Airitle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu A; Reference number: A97359; MUID:2160851; PMID:11743194
A;Reference number: A97359; MUID:2160851; PMID:11743194
A;Residues: I-145 <KUR>
A;Residues: 1-145 <KUR>
A;Residues: CB:AE007870; PIDN:AAK88682.1; PID:g15158413; GSFDB:GN00170
C;Genetics: A;Gene: AGR L_228
A;Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ajaccession: F70825
Ajataus: preliminary; nucleic acid sequence not shown; translation not shown
Ajataus: preliminary; nucleic acid sequence not shown; translation not shown
Ajataus: 1-645 cou.>
Ajataus: 1-645 cou.>
Ajataus: references: GB:AL021958; GB:AL123456; NID:g3261536; PIDN:CAA17522.1; PID:e12532:
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.; Hamlin, N.; Holroyd,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Uul-1998 #sequence_revision 17-Jul-1998 #text_change 15-Sep-2003
C;Accession: F70825
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gor, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holrc Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Natures: 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Reference number: A10805
A;Accession: F10825
A;Accession: F10825
                                                                                                                                                                                                                                                                                                                                                                                                                             45 LSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYD 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45 LSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYD 104
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                                                            Length 145;
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                                                                                                                                       Indels
                                                                                                                                       57;
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12.8%; Score 98; DB 2;
Best Local Similarity 27.1%; Pred. No. 0.29;
Matches 38; Conservative 25; Mismatches 57
                                               12.8%; Score 98; DB 2;
27.1%; Pred. No. 0.29;
:ive 25; Mismatches
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                                           Query Match
Best Local;Similarity 27.1
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105
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                                                                                                                                                                                                                     Pypothetical glycine-rich protein [imported] - Sinorhizobium meliloti (strain 1021) maga CjBecies: Sinorhizobium meliloti
CjBecies: Sinorhizobium meliloti
CjBecies: Sinorhizobium meliloti
CjBecies: Sinorhizobium meliloti
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CjBecies: Sinorhizobium meliloti
CjBecies: Sinorhizobium meliloti
CjBecies: Sinorhizobium meliloti
CjBecies: Sinorhizobium meliloti
CjBecies: Sinorhizobium meliloti
CjBecies: Na. 1969 1989, 2001
AjTille: The Complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endc
AjReference number: Aj8842; MUID:21396508; PMID:11481431
AjReference number: Aj8842; MUID:21396508; PMID:11481431
AjReference number: Aj8842; MUID:21396508; PMID:11481431
AjReference number: Aj8842; MUID:21396508; PMID:11481431
AjReference number: Aj8842; MUID:21396508; PMID:11481431
AjReference number: Aj8842; MUID:21396508; PMID:11481431
AjReference number: Aj8842; MUID:21366234; PMID:11474104
AjReference number: Aj8842; MUID:21366234; PMID:11474104
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C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AD3143
R;Mood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell i, Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Ster, E.W.
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A;Reference number: AB2577; MUID:21608550; PMID:11743193
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A;Experimental source: strain C58 (Dupont)
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 AIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTI 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     933 ADIGVSVGGSGSAGGNGGAVTAALKDSASVTTADDYANAIVVQSIGGGGGNGGV-----
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27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
13.0%; Score 99.5; DE
Best Local Similarity 23.0%; Pred. No. 4.3;
Matches 32; Conservative 14; Mismatches
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A,Map position: linear chromosome
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A; Residues: 1-145 < KUR>
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C, Genetics:
A, Gene: SMb21548
A, Genome: plasmid
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Query Match
Best Local Similarity 25.9%; Pred. No. 1.6;
Matches 43; Conservative 15; Mismatches 59; Indels 49; Gaps
A,Experimental source: strain H37Rv C,Genetics:
A,Gene: PPE
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Total number of hits satisfying chosen parameters:

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SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;

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J. Bacteriol. 173:4773-4781(1991).
-!- FUNCTION: CURLIN 18 THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
"Comparative genomics of Salmonella enterica serovar Typhi strains {\rm Ty2} and CT18.";
                                                                                                                                                                                                                                                                                  SEQUENCE OF 21-33.
SPECIES=S.enteritidis; STRAIN=27655-3B;
MEDLINE=91310586; PubMed=1677357;
MEDLINE=91310586; Emoedy L., Mueller K.-M., Trust T.J., Kay W.W.;
"Purification and characterization of thin, aggregative fimbriae from
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SPECIES-S. enteritidis; STRAIN-27655-3B;
MEDLINE=96146512; PubMed=8550497;
Collinson S.K., Clouther S.C., Doran J.L., Banser P.A., Kay W.W.;
"Salmonella enteritidis agfBAC operon encoding thin, aggregative
                                                                                                                                                                          SPECIESS. enteritidis; STRAIN=27655-3B; MEDLINE=94013373; PubMed=8104955, Doran J.L., Collinson S.K., Burian J., Sarlos G., Todd B.C.D., Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., Kay W.W.; "DNA-based diagnostic tests for Salmonella species targeting agfA, the structural gene for thin, aggregative fimbriae."; J. Clin. Morobiol. 31:2263-2273(1993)
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151 AA; 15305 MW; B7DACOD16B621359 CRC64;
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PIR; UC6039; UC6039.
StyGene; SG10608; CsgA.
Fimbria; Signal; Complete proteome.
SIGNAL
                                 Bacteriol. 185:2330-2337(2003).
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[6]
SEQUENCE OF 21-151 FROM N.A.
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Bacteriol. 173:4773-4781(1991).
FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN.
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MEDLINE-91310586; PubMed=1677357;
Collinson S.K., Emocedy L., Trust T.J., Kay W.W.;
"Purification and characterization of thin, aggregative fimbriae from Salmonella enteritidis.";
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Grejor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.,
                                                                                                                                                                                                                                                                                      Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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SEQUENCE FROM N.A.
STRAIN=KI2 / W3110;
STRAINE=93211294; PubMed=8459772;
MEDLINE=93211294; PubMed=R459772;
Olsen A., Arnqvist A.;
The RpoS sigma fact. relieves H-NS-mediated transcriptional
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"The complete genome sequence of Escherichia coli K-12.";
Science 27:1453-1474(1997).
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01-07-1996 (Rel. 34, Last sequence update)
8-FBE-2003 (Rel. 41, Last annotation update)
Major curlin subunit precursor.
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MEDLINE=93023873; PubMed=1357528;
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Mol. Microbiol. 7:523-536(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKLLKVAAIAAIVFSGSALAGVVPQYGGGGHGGGGGHNSGPNSELNIYQYGGGNSALALO 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=21218556; Pubmed=11319125;

Which G.A., Keen J.E., Elder R.O.;

Whatelons in the csgD promoter associated with variations in certain strains of Escherichia coli 0157:H7.";

Appl. Bnviron. Microbiol. 67:2367-2370(2001).

MEDLINE=21074935; Pubmed=11205551;

SEQUENCE FROM N.A.

STRAIN-0157:H7 / EDL933 / ATCC 700927;

SEQUENCE FROM N.A.

STRAIN-21074935; Pubmed=11205551;

ROSE D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Dutin A., Shao Y., Miller L.,

Rose D.J., Mayhew G.F., Link S., Boutin A., Shao Y., Miller L.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Apodaca Sequence of enterchaemorrhagic Escherichia coli 0157:H7.";

Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGFDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAJOR CURLIN SUBUNIT.
A -> E (IN REF. 1).
C003470D208D395F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.3%; Score 517; DB 1; L/69.5%; Pred. No. 9.7e-37; ive 17; Mismatches 29;
  -!- SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Major curlin subunit precursor.
CSGA OR Z1676 OR ECS1420.
Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 NNAALVNOTASDSSVMVROVGFGNNATANOY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, L04979; AAA23616.1; -.
EMBL; X90754; CAA62282.1; -.
EMBL, AE000205; AAA74126.1; -.
EMBL; D90741; BAA35842.1; -.
EMBL; S70788; S70788.
E.CGGene; EG11489; csgA.
Finbria; Signal; Complete proteome.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 AA; 15049 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI TaxID=83334;
[1]
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ID CSGA_E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 OSDARKSETTITOSGYGNGADVGOGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAG 119
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                                                                     MKLLKVAAFAAIVVSGSALAGVVPQW-GGGGNHNGGGNSSGPDSTLSIYQYGSANAALAL
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STRAIN=K12 / MC4100;
MEDLINE=96414468; PubMed=8817489;
MEDLINE=96414468; PubMed=817489;
MEDRINE=MATAYSE A., Bian Z., Olsen A., Normark S.;
"Expression of two csg operons is required for production of fibronectin- and congo red-binding curli polymers in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minor curlin subunit precursor.

CSGB OR B1041 OR Z1675 OR ECS1419.

Escherichia coli, and

Escherichia coli 0157:H7.

Escherichia coli 0157:H7.

Enterobacteriacebacteria; Gammaproteobacteria; Enterobacteriales;

Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.4%; Score 502.5; DB 1; Length 152; 68.4%; Pred. No. 1.6e-35; ive 18; Mismatches 29; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
MAJOR CURLIN SUBUNIT.
FE2D2D94DDE91243 CRC64;
                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fimbria; Signal; Complete proteome
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=0157:H7 / RIMD 0509952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15099 MM;
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Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                       FIBRONECTIN.
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'Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."; SEQUENCE FROM N.A.
STRAIN=0157:H7 / EDD1933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck B.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.; 

Hayashi T., Makino K., Ohtsuboh M., Kurokawa K., Ishii K., Yokoyama K., Han C.G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H., Complete genome sequence of enterchemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12."; SEQUENCE FROM N.A. STRAIN=0157:H7 / RIMD 0509952; MEDLINE=21156231; PubMed=11258796;

STEAIN=K12; MEDLINE=95157246; PubMed=7854117; SEQUENCE OF 1-21 FROM N.A.

Arnquist A., Olsen A., Normark S.,

"Sigma S-dependent growth-phase induction of the csgBA promoter in

"Sigma S-dependent growth-phase induction of the csgBA promoter in

Escherichia coni can be achieved in vivo by sigma 70 in the absence

of the nucleoid-associated protein H-NS.";

Mol. Microbiol. 13:1021-1032(1994).

-! FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE

COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERRITALLY AT GROWTH

TEMPERATURES BELOW 37 DEGREES CELGIUS. CURLI CAN BIND TO

FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF

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CURLIN MONOMERS

EMBL; X90754; CAA62281.1; -.

76 Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., Simmonds M., Skelton J., Stevens K., Complete genome sequence of a multiple drug resistant Salmonella enterica servovar Typhi CT18.", STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett II, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.,
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 98 RNNATYDQLVTRVVTHEMAH---AGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151 38 SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGF 21 AAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS ". Bacteriol. 185:2330-2337(2003).
-!- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI AR COLLED SURPACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF Gaps Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; DB 1; Length 151; B18D266B964014B8 CRC64; POTENTIAL. MINOR CURLIN SUBUNIT. 57; SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY. 13.6%; Score 104.5; DB 29.1%; Pred. No. 0.033; 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-007-2003 (Rel. 42, Last annotation update)
Minor curlin subunit precursor.
CSGB OR STY1180 OR T1777. 151 AA 15; Mismatches EMBL; AE000205; AAC74125.1; -... EMBL; D807411, BAA3831.1; -... EMBL; AE005315; AAG55787.1; -... EMBL; AP002554; BAB34842.1; -... EMBL; C90806; C90806. PTR; G98665; G85665. PTR; G85665; G85665; Finbria; S10787; S10787. MEDLINE=21534947; PubMed=11677608; Enterobacteriaceae; Salmonella 15882 MW; Query Match Best Local Similarity 29.1% Matches 34; Conservative STANDARD; CURLIN MONOMERS 151 AA; SEQUENCE FROM N.A. SEQUENCE FROM N.A. Salmonella typhi NCBI\_TaxID=601; SALTI SEQUENCE 08Z7M3; RESULT 5 8 8

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                                                                                                                                                                                                                            94
                                                                                                                                                                                                                                           14 GAPGIATATNYDLARSEYNFAVNELSKSSFNQAAIIGQVGTDNSARVRQEGSKLLSVISQ 73
                                                                                                                                                                                                                                                                                                        74 EĞENNRAKVDQAGNYNFAY-IEQTGNANDASISQSAYGNSAAIIQKGSGNKANITQY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fimbriae.";
J. Bacteriol. 178:662-667(1996).
-i. EMUCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI ARE COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DECREES CELSTUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                95 NGFRINNATYDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES-S.typhimurium, STRAIN-LTZ / SGSC1412 / ATCC 700720; MEDLINE-21534948; PubMed=11677609; MEDLINE-21534948; PubMed=11677609; MCClelland M., Sanderson K.E., Spiech J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                            ----IELTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES=S.typhimurium; STRAIN=SR-11;
MEDLINE=98117058; PubMed=9457880;
Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;
"Curli fibers are highly conserved between Salmonella typhimurium and Escherichia coli with respect to operon structure and regulation.";
J. Bacteriol. 180:722-731(1998).
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FSB-2003 (Rel. 41, Last annotation update)
28-FSB-2003 (Rel. 41, Last annotation update)
Minor curlin subunit precursor (Fimbrin SEF17 minor subunit).
CSGB OR AGFB OR STM1143.
Salmonella typhimurium, and
Salmonella enteritidis.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriais (Enterobacteria).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SPECIES=S.enteritidis; STRAIN=27655-3B;
MEDLINE=96146512; Pubmed=8550497;
Collinson S.K., Cloutthier S.C., Doran J.L., Banser P.A., Kay W.W.
"Salmonella enteritidis agfBAC operon encoding thin, aggregative
                                                                                                                                                                                                 17;
                                                                                                                                                                     Length 151;
                                                                                                                                                                                                51; Indels
                                                                                                                                                                                                                         51 GSANAALALQSDARKSE----TTITQSGYGNGADVGQ-GADNST--
                                                                                                                          22 151 MINOR CURLIN SUBUNIT.
151 AA; 16254 MW; 161C54326E573495 CRC64;
                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURLIN MONOMERS.
SIMILARITY: BELONGS TO THE CSGA/CSGB FAMILY
                                                                                                                                                                  13.0%; Score 99.5; DB 1
28.2%; Pred. No. 0.088;
vative 16; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                  151 AA
                                                                EMBL; AL627269; CAD08267.1; -.
EMBL; AE016840; AA0669400.1; -.
Fimbria; Signal; Complete protecome.
SIGNAL
                                                                                                                                                                                              33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=602, 592;
                                                                                                                                                                                  Similarity
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X MEDLINE=91293102, PubMed=1712294;

XM FEDLINE=91293102, PubMed=1712294;

MEDLINE=91293102, PubMed=1712294;

MEDLINE=91293102, PubMed=1712294;

XT from to for form the foreaction of finger protein required for female germ line development.";

EMBO J. 10.2259-2266(1991)

LINE GELLS. PLAYS A ROLE IN GERM LINE SEX DETERMINATION.

-1. FUNGTION: REQUIRED FOR SURVIVAL AND DIFFERENTIATION OF FEMALE GERM LINE SEX DETERMINATION.

-1. DEVELOPMENTAL STAGE: FIRST APPEARS IN THE GERMARIUM AND ACCUMULATES IN UNTRS CELLS DURING OGGENESIS. STORED IN THE EGG, BUT IS RAPIDLY LOST IN THE EMBRYOS EXCEPT FOR ITS CONTINUED PRESENCE IN THE GERM LINE PRECURSOR POLE CELLS.

-1. SIMILARITY: Contains 4 C2H2-type zinc fingers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 EGGNNRAKVDQAGNYNFAY-IEQTGNANDASISQSAYGNSAAIIQKGSGNKANITQY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 GSANAALALQSDARKSE----TTITQSGYGNGADVGQ-GADNST-----IELTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAPGIATATNYDLARSEYNFAVNELSKSSFNQAAIIGOVGTDNSARVRQEGSKLLSVISO
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"Multiple products from the shavenbaby-ovo gene region of Drosophila
melanogaster: relationship to genetic complexity.";
Mol. Cell. Biol. 14:6809-6818(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95 NGFRINNATYDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bhydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.0%; Score 99.5; DB 1; Length 151; 28.2%; Pred. No. 0.088; ive 16; Mismatches 51; Indels 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stydene; Saraci, Content Proteome.
Fimblia; Signal; Complete proteome.
SIGNAL 1 21 POTENTIAL.
CHAIN 22 151 MINOR CURLIN SUBUNIT.
PPOTENTIAL.
POTENTIAL.
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01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ovo protein (Shaven baby protein) OVO OR SVB.
                                                                                                                                                                                                                                                                                    EMBL, AJ002301, CAA05316.1,
EMBL, AB008749; AAL20073.1; -
EMBL, U43280, AAC43598.1, -
PIR, JC6040, JC6040.
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Best Local Simil
Matches 33; C
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(TNKS-1) (TRF1

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Fankyrase 1 (EC 2.4.2.30) (TANK1) (Tankyrase I)
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                       27;
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15; Mismatches
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CALZ-TYPE 1.
CCH2-TYPE 2.
CCH2-TYPE 2.
CCH2-TYPE 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----NNNNGGQTSMMGHPFYGGNPSA 177
                                                                                                                  EMBL; U11383; AAB60216.1; -.
EMBL; X59772; CAB36921.1; ALT_SEQ.
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095271; 095272;
28-FEB-2003 (Rel.
28-FEB-2003 (Rel.
10-OCT-2003 (Rel.
                                                                                                                                                                                                                                                                                                                                                    Transcription
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SEQUENCE
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Last sequence update) Last annotation update)

Created)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isoid=095271-2; Sequence=VSP 004538, VSP 004539;
Note=No experimental confirmation available;
ISSUE SPECIFICITY: Ubiquitous; highest levels in testis.
PTM: Upon insulin-stimulation, phosphorylated on serine residues by MAPK kinases:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ŋ
                                                                                                                                                                                                                                           MEDIINE=99454782; PubMed=10523501;
Smith S., de Lange T.;
"Cell cycle dependent localization of the telomeric PARP, tankyrase,
                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION, AND MUTAGENESIS OF HIS-1184 AND GLU-1291.
MEDLINE=21602874; PubMed=11739745;
Cook B.D., Dynek J.N., Chang W., Shostak G., Smith S.;
"Role for the related poly(ADP-Ribose) polymerases tankyrase 1 and
                                                                                                                                                                                                                                                                                                                                     FUNCTION, AND PHOSPHORYLATION.
MEDLINE=20556282; PubMed=10988299;
Chi N.-W., Lodish H.F.;
Thix N.-W. a Golgi-associated mitogen-activated protein kinase substrate that interacts with IRAP in GLUT4 vesicles.";
J. Biol. Chem. 275:38437-38444(2000).
                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                         Smith S., Giriat I., Schmitt A., de Lange T.;
"Tankyrase, a poly(ADP-ribose) polymerase at human telomeres.";
Science 282:1484-1487(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by MAPK kinases.
PTM: ADP-ribosylated (-auto).
SIMILARITY: Belongs to the PARP family.
SIMILARITY: Contains 15 ANK repeats.
SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
             interacting ankyrin-related ADP-ribose polymerase). TNKS OR TNKSI OR TINI OR TINFI OR PARPL. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                       nuclear pore complexes and centrosomes."; Cell Sci. 112:3649-3656(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=095271-1; Sequence=Displayed;
                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. 22:332-342(2002).
                                                                                                                                                    MEDLINE=99040105; PubMed=9822378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF082556; AAC79841.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTERNATIVE PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at human telomeres.";
Mol. Cell. Biol. 22:33
                                                                                                                                                                                                                                SUBCELLULAR LOCATION
                                                                            Mammalia; Euther:
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=1;
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1656 AA

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                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2011 (Rel. 40, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen S) (Gas5) (Tompa)
(Tompa B) (Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR (By similarity).
-!- SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a slayer with hexagonal symmetry.
-!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Uchiyama T., "Sequencing of the gene encoding the protein rOmp B of Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       japonica.";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE 120 kDa SURFACE-EXFOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (By
                                                                                                                                                                                                                                                                                                                                        Rickettšia japonica.
Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 kDa SURFACE-EXPOSED PROTEIN.
32 kDa BETA PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB003681; BAA20138.1;
InterPro; IPR006315; Autotransport.
InterPro; IPR005546; Autotransporter.
Fam, PP03797; Autotransporter; I.
TIGRFAMs; TIGR01414; autotrans_barl; 2.
Antigen; S-layer; Cell wall.
                 STANDARD;
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1656 AA;
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/FTId='VSP 004538.
Missing (in isoform 2).
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H->A: LOSS OF ACTIVITY, WHEN ASSOCIATED
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E->A: LOSS OF ACTIVITY; WHEN ASSOCIATED
                                                                                                                                                                            MIM, 6030303, -. Gichromosome, telomeric region, IDA.
GO; GO:0000781; Cichromosome, telomeric region, IDA.
GO; GO:0003515; FinAD ADP-ribosyltransferase activity; IDA.
GO; GO:0005515; Fiprotein binding; IPI.
GO; GO:0007004; Pitelomerase-dependent telomere maintenance; NAS.
InterPro; IPR002110; ANK.
Pfam; PF0023; ank; 19.
Pfam; PF0053; ANK; 19.
Pfam; PF00536; SAM; 1.
SMART; SM00454; SAM; 1.
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PROSITE; PS50297, ANK REP REGION; 1.
PROSITE; PS50105; SAM DOWALN; 1.
Transferace; Glycosyltransferace; NAD; Golgi stack; Telomere; Nuclear protein; Repeat; ANK repeat; ADP-ribosylation;
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W; E14DE985C710B957 CRC64;
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EMBL; AF082558; AAC79843.1; --
EMBL; AF082559; AAC79844.1; --
HSSP; Q00420; LAWC.
Genew; HGNC:11941; TNKS.
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                                                                                                                                                    VAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARK 65
                                                                                                                                                                                  509 VLAAGAITLDGSATI-----TGDIGNGGG------GAALQSITLANDATK
                                                                                                            Gaps
                                                                                                            52;
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                                                                                                                                                                                                                                                                                                                                                              605 NAQTLTISGTIGIIGANNTTLGQFNIGSSKTTLNGGNVAINELVIGNNGS
                                                             11.7%; Score 90; DB 1; Length 1656; 23.5%; Pred. No. 8; ive 21; Mismatches 57; Indels E
                  168097 MW; 3132A69C9DD5999F CRC64;
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RESULT 9 OMPB\_RICJA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 SFGSKPVGSGSLFGQSNNTLGNTTN--NRNGLFGQM-----NSSNQGSSNSGLFGQNS 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 GGGGNHNGGGNSSGPDSTLSIY--QYGSANAALALQSDARKSETTITQSGYGN----GA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yeast 10:869-574 (1994).
-!- FUNCTION: Essential component of nuclear pore complex.
-!- FUNCTION: Essential component of nuclear pore complex.
Nucleoporins may be involved in both binding and translocation of the proteins during nucleocytoplasmic transport.
-!- SUBCEDLIULAR LOCATION: Nuclear pore complex.
-!- DOMAIN: Contains G-L-F-G repeats.
-!- DOMAIN: Belongs to the GLFG family of nucleoporins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                          MEDILINE=94378724; PubMed=8091863; Rasmussen S.W.; "Sequence of a 20.7 kb region of yeast chromosome XI includes the "Sequence of a 20.7 kb region of yeast chromosome XI includes the NUP100 gene, an open reading frame (ORF) possibly representing a nucleoside diphosphare kinase gene, tRNAs for His, Val and Trp in addition to seven ORFS with weak or no significant similarity to
15-WAR-2004 (Rel. 43, Last annotation update)
Nucleoporin NUPl00/NSPl00 (Nuclear pore protein NUPl00/NSPl00).
NUPl00 OR NSPl00 OR YKL068W OR YKL336.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 959;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Mismatches 52; Indels
                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=93054906; PubMed=1385442;
Wente S.R., Rout M.P., Blobel G.;
Manew family of yeast nuclear pore complex proteins.";
J. Cell Biol. 119:705-723(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D3985F9901BBAA51 CRC64;
                                                                                                   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.6%; Score 89; DB 1
25.9%; Pred. No. 5.3;
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GGD; GO: 0005643; C:nuclear pore; IDA.
InterPro; IPR007230; Nucleoporin2.
InterPro; IPR004325; Nucleoporin_FG.
Pfan; PF04096; Nucleoporins_I.
Pfan; PF0393; Nucleoporin_FG; 25.
Nuclear protein; Transport; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      959 AA; 99988 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z28068; CAA81905.1; -. PIR; B44402; B44402. GermOnline; 139824; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 294 MNSST---QGVFGQN 305
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Best Local Similarity 25.99
Matches 35, Conservative
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                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   known proteins.'
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                                                                                                                                                                                                                                                                                                                                                            MEDDING=ZIBEGGUI; FUDNEG=ILED9350,

RA WOOD V. GWIlliam R., Rajandream M.A. Lyne M., Lyne R., Stewart A.,

RA GOURDS J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA SGOUROS K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA COllins M., Connor R., Cronin A., Davis P., Hidalgo J., Hodgson G.,

RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Gentles S., Goles A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Muchle E.J., Hunt S., Jagels K.,

RA Mooney P., Moule S., Mingall K., Murphy L., Niblett D., Odell C.,

RA Mooney P., Moule S., Mangall K., Murphy L., Niblett D., Odell C.,

RA Mooney P., Saunders R., Squares R., Sharp S.,

RA Skelton J., Simmonds M., Squares R., Stavens K.,

RA Skelton J., Squares R., Squares R., Sharp S.,

RA Skelton J., Squares R., Squares R.,

RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

RA Goble C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., More K., Hurst S.M.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Wore K., Hurst S.M.,

RA Daga R.R., Cruzado L., Jümenez J., Sanchez M., del Rey F., Benito J.,

RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;

RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;

RA Merly M. Parker S., Schlzosaccharomyces pombe.',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEDLINE=22263608; PubMed=12376568;
MEDLINE=22263608; PubMed=12376568;
Tange Y., Hirata A., Niwa O.;
Tange Y., Hirata A., Niwa O.;
Tange Y., Hirata A., Niwa O.;
Tange Y., Hirata A., Niwa O.;
Tange Y., Hirata A., Niwa O.;
Tange Y., Hirata A., Niwa O.;
Tange Y., Hirata A., Niwa O.;
Tange Y., Hirata A., Niwa O.;
Tange Y., Hirata A., Nonomer.
Theracts with nedl.
The SUBUNIT: Monomer. Interacts with nedl.
The SUBCELLULAR LOCATION: Nuclear pore complex (By similarity).
The DOWAIN: Contains G-L-FG repeats.
The SIMILARITY: Belongs to the GLFG family of nucleoporins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Voshioka S., Kato K., Nakai K., Okayama H., Nojima H., "Identification of open reading frames in Schizosaccharomyces pombe
                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                 090TEA; P78796;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nucleoporin nupl89 (Nuclear pore protein nupl89).
NUP189 OR SPACI486.05.
1778 AA
                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98162722; PubMed=9501991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Res. 4:363-369(1997).
  STANDARD;
                                                                                                                                                                                                                                      Schizosaccharomyces
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             NCBI_TaxID=4896;
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Query Match
Best Local Similarity 44.8%;
Lines 26; Conservative
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590
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Leishmania donovani.
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MEROPS; M08.001;
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P23223;
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CHAIN
PROPEP
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Mol.
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                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the SMEL outstation the Duropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGTMGTGL - - - FGFGANNNTANNTAPTSTFGGNNSSNFSFGANNNAATKPSGFGFGFGTT 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITOSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGNNAALVNQT 129
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MEDLINE=87283911; PubMed=3302276;
MEDLINE=87283911; PubMed=3302276;
MIDA sequence of the solution of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the phage recognition site for the cellular receptor.

-!- MISCELLANEOUS: THIS PHAGE USE OUTER MEMBRANE PROTEINS OMPF AND TTR AS RECEPTORS.
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Viruses, dsDNA viruses, no RNA stage, Caudovirales, Myoviridae,
T4-like viruses.
REMBL; D89145; BAA13807.1; -.
RISEP; T25074; T50074.
RISEP; P22629; ISWF.
Genedba SPombe; SPACI486.05; -.
GG; GG: 0016020; C:membrane; ISS.
GG; GG: 00056643; C:muclear pore; ISS.
GG; GG: 00066606; P:protein-nucleus import; ISS.
RITHERPO; IPR004325; Nucleoporing;
RitterPro; IPR004325; Nucleoporing; I.
Refam; PF04096; Nucleoporing; I.
Refam; PF04096; Nucleoporing; I.
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PIR; S00275; S00275.
InterPro; IPR007932; Tail_fibre_GP38.
Pfam, PF05268; GP38.1.
Fiber protein; Phage recognition.
SEQUENCE 262 AA; 25801 MW; 056736
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                                                                                                                                                                               GGGRPFGVGGKIGSDSILS----GSNASL---TDAGTGGTTF-QYGAGNGGNVGAG 223
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Mol. Biochem. Parasicol. 48:173-184(1991).

-!- FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.

-!- CATALYTIC ACTIVITY: Preference for hydrophobic residues at P1 and P1. and basic residues at P2 and P3'. A model nonapeptide is cleaved at - Ala-Tyr-|-Leu-Lys-Lys-.

-!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).

-!- SUBCELLULAR LOCATION: Attached to the membrane by a GP1-anchor.

-!- SIMILARITY: Belongs to peptidase family M8.
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NCBI_TaxID=5661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92107220; PubMed=1762629;
Webb J.R., Button L.L., McMaster R.W.;
"Heterogeneity of the genes encoding the major surface glycoprotein of Leishmania donovani.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1991 (Rel. 20, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leishmanolysin precursor (EC 3, 4.24, 36) (Cell surface protease)
(Major șurface glycoprotein) (GP63 protein) (Promastigote surface
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د
Length 262;
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InterPro; IPR001577; Peptidase_M8.
InterPro; IPR001577; Peptidase_M8.
InterPro; IPR001577; Peptidase_M8.
IPR0718; PR00742; ISHMANOLYSIN
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Glycoprotein; Metal-binding; Symogen; Signal; Cell adhesion; GPI-anchor; Lipoprotein.
IPROPER 40 87 ACTIVATION PEPTIDE.
                                                                     Indels
                                                                     19;
DB 1;
                                                                                                                                                                                                                                                                                                                                                                                590 AA
Score 86.5; D
Pred. No. 2;
4; Mismatches
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01-NOV-1991 (Rel. 20, Last seq
10-OCT-2003 (Rel. 42, Last anno
11.3%;
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    DETERMINATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY 
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-!- FUNCTION: Has an integral role during the infection of macrophages in the mammalian host.
-!- CATALYTIC ACTIVITY: Preference for hydrophobic residues at Pl and Pl' and basic residues at P2 and P3'. A model nonapeptide is cleaved at -Ala-Tyr-|-Leu-Lys-Lys-... COFACTOR: Binds I zinc ion per subunit (By similarity).
-!- COFACTOR: Binds I zinc ion per subunit (By similarity).
                                                                                                                                                                                                       Gaps
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NCBL_TaxID=5665;
                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leisinanolysin C1 precursor (EC 3.4.24.36) (Cell surface protease)
(Major surface glycoprotein) (GP63 protein) (Promastigote surface
                                                                                                                                                                                                                                              103 YDQLVTRVVTHEMAHAGGNNAALVNQTASDSSVM-VRQVGFG----NNATA 148
                                                                                                                                                                                                                                                                         241 YDQLVIRVVTHEMAHALGFSVVFFRDARILESISNVRHKDFDVPVINSSTA 291
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
GPI-anchor amidated asparagine (By
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LEISHMANOLYSIN C1.
ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                              11.3%; Score 86.5; DB 1; Length 590; 47.1%; Pred. No. 4.9;
                                                                                                                                                                                                       Indels
                                                                                                    similarity).
OFB315D299659F58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amastigote forms.
-!- SIMILARITY: Belongs to peptidase family M8.
                                                                                                                                                                                                                                                                                                                                                                                         646 AA
                                                                                                                                                                                                         4; Mismatches
                                                                                                                          62950 MW;
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                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=MNYC/BZ/62/M379;
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102
646
266
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2846
565
565
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                                                                                                                          590 AA;
                                                                                                                                                                  Query Match
Best Local Similarity
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MEROPS; MO8.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       endopeptidase).
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P43150;
                                          DISULFID
                                                                                                                          SEQUENCE
                         DISULFID
                                                                                     LIPID
                                                                                                                                                                                                                                                                                                                                                                      LEIME
                                                                                                                                                                                                                                                                                                                                              RESULT 14
GP63_LEIME
                                                                                                                                                                                                         Matches
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Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales,
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                                                 SIMILARITY)
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ZINC (CATALYTIC)
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101-NOV-1990 (Rel. 16, Created)

01-NOV-1990 (Rel. 16, Last sequence update)

01-NOV-1990 (Rel. 16, Last sequence update)

10-NOV-1990 (Rel. 40, Last annotation update)

Ice nucleation protein.
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BY SIMILARITY
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Pred. No.
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MEDLINE=91080859; PubMed=2259339;
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94.4%;
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466
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Search completed: August 2, 2004, 14:49:33 Job time : 6.3 secs

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Sequence:

Database

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QBawa6 lampetra fl
Q94821 tetrathymena
Q7uw28 rhodopirell
Q89ck5 bradyrhizob
Q89d03 bradyrhizob
G87327 pseudomonas
Q89397 cyprinus ca
Q81327 pseudomonas
Q81327 pseudomonas
Q81327 pseudomonas
Q81328 secherichia
Q74455 pseudomonas
Q84218 escherichia
Q84218 escherichia
Q84218 enterobacteri
Q85155 bradyrhizob
Q8738 enterobacter
Q89155 bradyrhizob
Q95rs5 drosophila
Q7328 enterobacter
Q89156 bradyrhizob
Q95rs5 drosophila
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Q8916 bradyrhizob
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Q75283 enterobacter
Q8916 bradyrhizob
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EMBL. AJ000514; CAAQ4151.1; -.

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SEQÜENCE 152 AA; 15401 MW; 9DA7DADC2364B006 CRC64;
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Qxx40 citrobacter
Qxx37 enterobacte
Q5469 salmonella
Q8eh4 shewanella
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_fungi:*
5: sp_invertebrate:*
5: sp_invertebrate:*
5: sp_mammal:*
5: sp_mammal:*
5: sp_praga:*
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Gapop 10.0 , Gapext 0.5
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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_bacteriap:*
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Match Length
                                                 Copyright
                                                                                                                                                                        August
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Perfect score:
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570.5
534
536.5
435.5
435.5
126
112
111.2
111.2
105
104.5
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Score

Result

120 118

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RESULT 2 Q7X243

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1 MKLLKVAAFAAIVVSGSALAGVVPQW--GGNHHGGGSNYGPDSSLSIYQYGSNNSANALQ
                                                       61 SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGG
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MEDINE=2388244; PubMed=12471157;
MEDINE=2388244; PubMed=12471157;
MEICH REA., BURIAND V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
MayNew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U. S.A. 99:17020-17024(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
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Enterobacteriaceae; Enterobacter:
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Last annotation update)
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69.1%; Pred. No. 4.9e-33;
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Matches 105; Conservative
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01-OCT-2003 (TrEMBLr
Curlin-csgA protein.
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SEQUENCE 152 AA
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"Production of Cellulose and Curli Fimbriae by Members of the Family
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.";
Infect. Immun. 72:4151-4158 (2003).
EMBL; AJS19700; CADS6672.1; -.
SEQUENCE 150 AA; 15016 MW; 1D7141B8D6973DC6 CRC64;
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"Production of Cellulose and Curli Fimbriae by Members of the Famil
Enterobacteriacaea Isolated from the Human Gastrointestinal Tract..
Infect. Immun. 72-4151-4158 (2003).
EMBL; AJS15701; CAD56675.1; -.
SEQUENCE 149 AA; 15260 MM; 946DD52017F648FD CRC64;
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NCBI_TaxID=546;
                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
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74.3%; Score 570.5; DB 2
Best Local Similarity 77.5%; Pred. No. 3.7e-38;
Matches 117; Conservative 14; Mismatches 19
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  121 NNAALVNQTASDSSVMVRQVGFGNNATANQY
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Citrobacter freundii.
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SEQUENCE FROM N.A.
STRAIN=Fec4;
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01-OCT-2003
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CSGA.
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62 DARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATYDQLVTRVVTHEMAHAGGN 121
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                                        PEDINES. 2297686; PubMed=12368813; MEDINES. 2297686; PubMed=12368813; MEDINES. 2297686; PubMed=12368813; Medicalberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Meder T.D., Eisen J.A., Seahadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vanathevan J., Weighan J., Impraim M., Lee K., Berry K., Lee C., Peldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; Genome sequence of the dissimilatory metal ion-reducing bacterium
                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                ll protein, Complete proteome.
502 AA; 52441 MW; D08CA23D6C46B62D CRC64;
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Pred. No. 0.048;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350 NELVAFATGEDNSIEISQEGDANFAYVDATGN 381
                                                                                                                                                                                                                                                                                                  16.4%; Scc. 27.0%; Pred. No. 0.c.
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EMBL; AE015532; AAN53941.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.9%;
89.7%;
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                                                                                                                                                                                                          Shewanella oneidensis.";
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                                                                                                                                                                                                                                                                                                                        Local Similarity
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 NCBI_TaxID=70863;
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Hypothetical prot
SEQUENCE 502 AP
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NON TER
SEQUENCE
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Best Local
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0983J5
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                                                                                                                                                1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                 1 MKFIKVAALAAIVVSGSAMAGMINQ-GGWGHGHGHGGYGGPNSTLNIYQNGGGNSALALQ
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                                                                                                                    Gaps
"Production of Cellulose and Curli Fimbriae by Members of the Fami
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract.
Infect. Immun. 72-4151-4158(2003).
EMBL; AJ515702; CAD56(78.1; -.
SEQUENCE 150 AA; 15112 MW; 5D8BB2D872DF15F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
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                                                                                        Length 150;
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                                                                                     56.7%; Score 435.5; DB 2; Length 60.3%; Pred. No. 2.2e-27; ive 26; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-SE30;
Cox J.M., Eglezos S., Woolcock J.B.;
Virulence of Salmonella enteritidis in chickens correla colony morphology and expression of SEB17 fimbriae.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, U53207; AAA98671.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 AA; 7704 MW; 2FD5411241A7BCB1 CRC64;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                    120 LNGALVDQTASNSTVNVTQIGFGNHATAHQY 150
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-NRC-2001 (TrEMBLrel. 19,
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                                                                                                   Best Local Similarity 60.3%
Matches 91; Conservative
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Q8EIH4;
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Q54069
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32;

SEQUENCE FROM N.A.
TRANSPOSON=Insertion sequence 181;
MRDLINE=99314153; PubMed=1038631;
MRDLINE=99314153; PubMed=1038631;
La Ragione R.M., Collighan R.J., Woodward M.J.;
Is Ragione R.M., Collighan R.J., Woodward M.J.;
"Non-curliation of Escherichia coli 078;K80 isolates associated with
IS1 inserti on in csgB and reduced persistence in poultry infection.";
PEMS Microbiol. Lett. 175:247-253(1999).
NON\_TER 29 29 Gaps Escherichia coli. Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia. . 0 Score 122; DB 2; Length 29; Pred. No. 0.0035; 2; Indels 29 AA; 2789 MW; E290DFC07ABBB243 CRC64; 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2001 (TrEMBLrel. 16, Last annotation update)
01-MII subunit monomer (Fragment).

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Shigella flexneri.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
    DB 16;
14.5%; Score 111.5; DE 24.8%; Pred. No. 0.19; iive 24; Mismatches
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01-0CT-2003 (TrEMBLrel. 25,
01-0CT-2003 (TrEMBLrel. 25,
Minor curlin subunit.
CSGB OR S1108.
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    Query Match
Best Local Similarity 24.8%
Matches 40; Conservative
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01-JUN-2003 (TrEMBLrel.
Bl15299 protein.
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SEQUENCE 130 AA
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Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.,
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DNA Res. 9:189-197(2002).
EMBL; APD005954; BAC50565.1; -.
Complete protecom
SEQUENCE 171 AA; 17448 MW; 995DB08C01498381 CRC64;
                                                                                                                                                                                                           Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Alteromonadaceae, Shewanella.
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Bracteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Bradyrhizobiaceae, Bradyrhizobium.
NCBI_TaxID=375;
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Last annotation update)
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(TrEMBLrel. 23, Last seq
(TrEMBLrel. 23, Last ann
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EMBL; AE015532; AAN53942.1; -.
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Best Local Similarity 28.34
Matches 32; Conservative
                                PRELIMINARY;
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CSGA OR BLL53
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01-MAR-2003
01-MAR-2003
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Q89JI3;
                                Q8EIH3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
Bradyxhizobium japonicum USDA110.";
DNA Res. 9:189-197(2002)
EMBL; AP005954; BACS0564.1; -.
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                                               43;
Length 171;
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Bradyrhizobiaceae; Bradyrhizobium.
NCBI_TaxID=375;
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MEDLINE=22388234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Masko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.*, Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
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                                                                                                                                                                                        Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A., Mau B., Perra M.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R., "Complete genome sequence and comparative genomics of Shigella flexneri serctype 2a strain 2457T."; Infect. Immun. 712775-2786(2003).

EMBL, AE016981; AAP16422.1; -SEQUENCE 151 AA; 15868 MW; 5D5D266B964014A0 CRC64;
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Minor curlin subunit precursor.
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29.1%; Pred. No. 0.65;
:ive 15; Mismatches
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                                                                                          SEQUENCE FROM N.A.
STRAIN=2457T / ATCC 700930 / Seroty
MEDLINE=22590274; PubMed=12704152;
Enterobacteriaceae; Shigella
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nes 34; Conservative
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SEQUENCE 160 AA;
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01-MAR-2003
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Q8CW64
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EMBL; AE015131; AAN42658.1; -. Complete protecome. SEQUENCE 160 AA; 16919 NW; 50269F5268D2A32F CRC64;
                                                                                                                                                                                                                                              SECUENCE FROM N.A.
STRAIN=201 / Sertotype 2a,
STRAIN=20272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang G., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A. (Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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                                                                                                                                              Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Shigella.
NCBI_TaxID=623;
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Pseudomonadaceae; Pseudomonas
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EMBL; AE016786; AAN69002.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1-2003 (TrEMBLrel. 24, Last sequence update)
1-2003 (TrEMBLrel. 25, Last annotation update)
fiber surface-exposed nucleator CsgB, putative.
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Minor curlin subunit precursor, similar ro CsgA.
CSGB OR SF1035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.6%; Score 104.5; DB
29.1%; Pred. No. 0.65;
tive 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000437; Prok lipoprot S.
PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
COMPLETE PROCESSE 157 AA; 16175 MW; C385E9846;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas putida (strain KT2440)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 24, (TrEMBLrel. 24, (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 29.18
Matches 34; Conservative
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4; Query Match
Best Local Similarity 26.4%; Pred. No. 0.69;
Matches 37; Conservative 20; Mismatches 57; Indels 26; Gaps Пр ΘŻ

qq

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Search completed: August 2, 2004, 14:54:42 Job time: 29.7 secs